target gene, herein designated TARGET GENE. FLJ35487 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35487, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35487 BINDING SITE, designated SEQ ID:18431, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24788] Another function of GAM148 is therefore inhibition of FLJ35487 (Accession NP_776181.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35487.

[24789] FLJ40584 (Accession XP_069189.2) is another GAM148 target gene, herein designated TARGET GENE. FLJ40584 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ40584, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ40584 BINDING SITE, designated SEQ ID:10385, to the nucleotide sequence of GAM148 RNA, herein designated

GAM RNA, also designated SEQ ID:280.

[24790] Another function of GAM148 is therefore inhibition of FLJ40584 (Accession XP_069189.2) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ40584.

[24791] Glutamic pyruvate transaminase (alanine aminotransferase) 2 (GPT2, Accession NP_597700.1) is another GAM148 target gene, herein designated TARGET GENE. GPT2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPT2 BINDING SITE, designated SEQ ID:580, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24792] Another function of GAM148 is therefore inhibition of Glutamic pyruvate transaminase (alanine aminotransferase) 2 (GPT2, Accession NP_597700.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPT2.

[24793] GRTP1 (Accession NP_078995.1) is another GAM148 target gene, herein designated TARGET GENE. GRTP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRTP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRTP1 BINDING SITE, designated SEQ ID:6509, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24794] Another function of GAM148 is therefore inhibition of GRTP1 (Accession NP_078995.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRTP1.

[24795] Huntingtin interacting protein 2 (HIP2, Accession NP_005330.1) is another GAM148 target gene, herein designated TARGET GENE. HIP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HIP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIP2 BINDING SITE, designated SEQ ID:8300, to the nucleotide sequence of GAM148 RNA,

herein designated GAM RNA, also designated SEQ ID:280.

[24796] Another function of GAM148 is therefore inhibition of Huntingtin interacting protein 2 (HIP2, Accession NP_005330.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIP2.

[24797] Homeo box a7 (HOXA7, Accession NP_008827.2) is another GAM148 target gene, herein designated TARGET GENE. HOXA7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HOXA7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HOXA7 BINDING SITE, designated SEQ ID:6135, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24798] Another function of GAM148 is therefore inhibition of Homeo box a7 (HOXA7, Accession NP_008827.2), a gene which provides cells with specific positional identities on the anterior- posterior axis. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXA7.

[24799] The function of HOXA7 has been established by previous

studies. The homeotic genes, whose products serve as determinants of embryonic cell fate, are expressed in a series of different but partially overlapping domains that extend along the anterior- posterior (A- P) axis of the embryo. The Hox genes share a 180- bp homeo box, which encodes a 60- amino acid homeodomain that binds specifically to DNA. There are 4 Hox gene clusters: HOXA (formerly HOX1) on chromosome 7, HOXB (formerly HOX2) on chromosome 17, HOXC (formerly HOX3) on chromosome 12, and HOXD (formerly HOX4) on chromosome 2. By sequence comparison, the genes of each cluster are assigned to 1 of 13 groups. The order of the HOX genes along the chromosome reflects where they are expressed along the body axis. This principle is followed in homeo box gene nomenclature. For a review of homeo box gene nomenclature, see Scott (1992). The homeo box is a 180-bp DNA sequence conserved in Drosophila homeotic genes which regulate early development (review by Gehring, 1985). These DNA sequences are present in open reading frames and have been identified in Drosophila and Xenopus embryos. They share structural features with genes encoding some DNA- binding proteins. Homologous homeo box sequences have been detected in species

ranging from insects and annelids to vertebrates. The high degree of sequence conservation (70 to 90%) suggests a common role in embryonic development. Schughart et al. (1989) pointed to evidence of duplication of large genomic regions during evolution of the mouse homeo box genes. The findings were considered consistent with the hypothesis of Ohno (1970) that during vertebrate evolution duplications of the entire genome occurred. Such are likely to be less deleterious than duplications of individual chromosomes. Ferguson- Smith et al. (1989) showed that the sequence of the HOX1 gene has 100% identity to the deduced amino acid sequence of the mouse HOX1.4 homeo box. They detected no RFLPs with the 14- kD clone, which was devoid of any moderately repetitive DNA sequences. This implied an inability of this region to tolerate change in sequence, consistent with a function highly conserved throughout evolution

[24800] Animal model experiments lend further support to the function of HOXA7. As reviewed by Gaunt and Singh (1990), in both the mouse and Drosophila, Antennapedia-like homeo box- containing genes (homeogenes) display a strict correspondence between the order of genes (3-prime to 5- prime) along the chromosome and the order

of their expression domains (anterior to posterior) in the developing embryo. Gaunt and Singh (1990) suggested that this and other points of similarity indicate that the 2 species use a common mechanism of chromosomal imprinting in order to retain cellular memory of homeogene expression patterns throughout embryonic development. The 'open for transcription' model suggests that imprinting is a matter of open and closed chromatin, the molecular nature of which is not clear. It is possible that a clue to the mechanism of memory used within the homeogene complex, at least in Drosophila, is provided by the Drosophila mutant 'Polycomb' (Pc). The product of the Pc gene, which presumably has a homolog in man, appears to act as a repressor of 'posterior' genes in anterior segments. Thus, it may be involved in restricting the state of 'openness' of the homeotic gene complex.

[24801] It is appreciated that the abovementioned animal model for HOXA7 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[24802] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[24803] Schughart, K.; Kappen, C.; Ruddle, F. H. : Duplication of large genomic regions during the evolution of vertebrate homeobox genes. Proc. Nat. Acad. Sci. 86: 7067- 7071, 1989. ; and

[24804] Scott, M. P. : Vertebrate homeobox gene nomenclature. (Letter) Cell 71: 551- 553, 1992.

[24805] Further studies establishing the function and utilities of HOXA7 are found in John Hopkins OMIM database record ID 142950, and in cited publications listed in Table 5, which are hereby incorporated by reference.Histamine receptor h3 (HRH3, Accession NP_009163.1) is another GAM148 target gene, herein designated TARGET GENE. HRH3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HRH3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HRH3 BINDING SITE, designated SEQ ID:6908, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24806] Another function of GAM148 is therefore inhibition of Histamine receptor h3 (HRH3, Accession NP_009163.1) . Accordingly, utilities of GAM148 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with HRH3.

[24807] Insulin-like growth factor 2 (somatomedin a) (IGF2, Accession NP_000603.1) is another GAM148 target gene, herein designated TARGET GENE. IGF2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IGF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IGF2 BINDING SITE, designated SEQ ID:12962, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24808] Another function of GAM148 is therefore inhibition of Insulin-like growth factor 2 (somatomedin a) (IGF2, Accession NP_000603.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IGF2.

[24809] Integrin, alpha l (antigen cd11a (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL, Accession NP_002200.1) is another GAM148 target gene, herein designated TARGET GENE. ITGAL BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by ITGAL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITGAL BINDING SITE, designated SEQ ID:15602, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24810] Another function of GAM148 is therefore inhibition of Integrin, alpha l (antigen cd11a (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL, Accession NP_002200.1), a gene which s a receptor for icam1, icam2, icam3 and icam4. it is involved in a variety of immune phenomena including leukocyte- endothelial cell interaction, cytotoxic t- cell mediated killing, and antibody dependent killing by granulocytes and monocytes. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAL.

[24811] The function of ITGAL has been established by previous studies. See 120980 and 151510. Lymphocyte function-associated antigen- 1 (LFA- 1) shares a beta subunit (see OMIM Ref. No. 116920) with other members of a family of leukocyte surface membrane antigens but has a unique

alpha subunit (Sanchez- Madrid et al., 1983). LFA- 1 is expressed on lymphocytes and phagocytic cells. The LFA- 1 molecule is involved in the adhesion of cytotoxic T cells to their target cells. Patients with LFA- 1 immunodeficiency disease (see OMIM Ref. No. 116920) have recurrent life- threatening infections, show deficiency of the beta chain of all 3 molecules, LFA- 1, Mac- 1 (macrophage antigen- 1), and p150,95, and display profound defects in adhesion- dependent granulocyte, monocyte, and B- and T- lymphocyte functions. The alpha subunits were designated by Marlin et al. (1986) as alpha- L for LFA- 1, alpha- M for Mac- 1, and alpha- X for p150,95. Lu and Cyster (2002) studied the mechanisms that control localization of marginal zone B cells. They demonstrated that marginal zone B cells express elevated levels of the integrins LFA- 1 and alpha- 4- beta- 1 (see OMIM Ref. No. 192975 and 135630) and that the marginal zone B cells bind to the ligands ICAM1 (OMIM Ref. No. 147840) and VCAM1 (OMIM Ref. No. 192225). These ligands are expressed within the marginal zone in a lymphotoxin- dependent manner. Combined inhibition of LFA- 1 and alpha- 4- beta- 1 causes a rapid and selective release of B cells from the marginal zone. Furthermore, lipopolysac-

charide- triggered marginal zone B cell relocalization involves downregulation of integrin- mediated adhesion. Lu and Cyster (2002) concluded that their studies identified key requirements for marginal zone B cell localization and established a role for integrins in peripheral lymphoid tissue compartmentalization

[24812]

[24813] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[24814] Lu, T. T.; Cyster, J. G. : Integrin- mediated long- term B cell retention in the splenic marginal zone. Science 297: 409- 412, 2002. ; and

[24815] Marlin, S. D.; Morton, C. C.; Anderson, D. C.; Springer, T. A. : LFA- 1 immunodeficiency disease: definition of the genetic defect and chromosomal mapping of alpha and beta subunits of t.

[24816] Further studies establishing the function and utilities of ITGAL are found in John Hopkins OMIM database record ID 153370, and in cited publications listed in Table 5, which are hereby incorporated by reference.KIAA0062 (Accession XP_046677.3) is another GAM148 target gene, herein designated TARGET GENE. KIAA0062 BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0062, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0062 BINDING SITE, designated SEQ ID:17664, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24817] Another function of GAM148 is therefore inhibition of KIAA0062 (Accession XP_046677.3) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0062.

[24818] KIAA0101 (Accession NP_055551.1) is another GAM148 target gene, herein designated TARGET GENE. KIAA0101 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0101 BINDING SITE, designated SEQ ID:11332, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24819] Another function of GAM148 is therefore inhibition of KIAA0101 (Accession NP_055551.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0101.

[24820] KIAA0522 (Accession XP_291345.1) is another GAM148 target gene, herein designated TARGET GENE. KIAA0522 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0522, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0522 BINDING SITE, designated SEQ ID:9466, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24821] Another function of GAM148 is therefore inhibition of KIAA0522 (Accession XP_291345.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0522.

[24822] KIAA1458 (Accession XP_044434.1) is another GAM148 target gene, herein designated TARGET GENE. KIAA1458 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1458, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1458 BINDING SITE, designated SEQ ID:9176, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24823] Another function of GAM148 is therefore inhibition of KIAA1458 (Accession XP_044434.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1458.

[24824] KIAA1656 (Accession XP_038022.1) is another GAM148 target gene, herein designated TARGET GENE. KIAA1656 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1656, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1656 BINDING SITE, designated SEQ ID:7823, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24825] Another function of GAM148 is therefore inhibition of

KIAA1656 (Accession XP_038022.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1656.

[24826] KIAA1909 (Accession XP_291137.1) is another GAM148 target gene, herein designated TARGET GENE. KIAA1909 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1909, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1909 BINDING SITE, designated SEQ ID:6342, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24827] Another function of GAM148 is therefore inhibition of KIAA1909 (Accession XP_291137.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1909.

[24828] Kinesin family member 5a (KIF5A, Accession NP_004975.1) is another GAM148 target gene, herein designated TARGET GENE. KIF5A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA

encoded by KIF5A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIF5A BINDING SITE, designated SEQ ID:5352, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24829] Another function of GAM148 is therefore inhibition of Kinesin family member 5a (KIF5A, Accession NP_004975.1), a gene which is a microtubule- associated force- producing protein that may play a role in organelle transport. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF5A.

[24830] The function of KIF5A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.LCX (Accession XP_167612.2) is another GAM148 target gene, herein designated TARGET GENE. LCX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

LCX BINDING SITE, designated SEQ ID:12109, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24831] Another function of GAM148 is therefore inhibition of LCX (Accession XP_167612.2) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCX.

[24832] LOC122183 (Accession XP_062994.2) is another GAM148 target gene, herein designated TARGET GENE. LOC122183 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC122183, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC122183 BINDING SITE, designated SEQ ID:5819, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24833] Another function of GAM148 is therefore inhibition of LOC122183 (Accession XP_062994.2) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122183.

[24834] LOC126299 (Accession XP_059019.2) is another GAM148

target gene, herein designated TARGET GENE. LOC126299 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC126299, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126299 BINDING SITE, designated SEQ ID:3713, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24835] Another function of GAM148 is therefore inhibition of LOC126299 (Accession XP_059019.2) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126299.

[24836] LOC145268 (Accession XP_085072.1) is another GAM148 target gene, herein designated TARGET GENE. LOC145268 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145268 BINDING SITE, designated SEQ ID:10503, to the nucleotide sequence of GAM148 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:280.

[24837] Another function of GAM148 is therefore inhibition of LOC145268 (Accession XP_085072.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145268.

[24838] LOC150095 (Accession XP_097805.1) is another GAM148 target gene, herein designated TARGET GENE. LOC150095 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150095, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150095 BINDING SITE, designated SEQ ID:553, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24839] Another function of GAM148 is therefore inhibition of LOC150095 (Accession XP_097805.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150095.

[24840] LOC150297 (Accession XP_086894.2) is another GAM148 target gene, herein designated TARGET GENE. LOC150297

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150297, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150297 BINDING SITE, designated SEQ ID:14830, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24841] Another function of GAM148 is therefore inhibition of LOC150297 (Accession XP_086894.2) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150297.

[24842] LOC196337 (Accession XP_113696.1) is another GAM148 target gene, herein designated TARGET GENE. LOC196337 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196337, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196337 BINDING SITE, designated SEQ ID:18591, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24843] Another function of GAM148 is therefore inhibition of LOC196337 (Accession XP_113696.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196337.

[24844] LOC199906 (Accession XP_114052.1) is another GAM148 target gene, herein designated TARGET GENE. LOC199906 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC199906, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199906 BINDING SITE, designated SEQ ID:1048, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24845] Another function of GAM148 is therefore inhibition of LOC199906 (Accession XP_114052.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199906.

[24846] LOC219649 (Accession XP_167562.1) is another GAM148 target gene, herein designated TARGET GENE. LOC219649 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC219649, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219649 BINDING SITE, designated SEQ ID:1391, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24847] Another function of GAM148 is therefore inhibition of LOC219649 (Accession XP_167562.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219649.

[24848] LOC283007 (Accession XP_210849.1) is another GAM148 target gene, herein designated TARGET GENE. LOC283007 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283007, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283007 BINDING SITE, designated SEQ ID:3635, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24849] Another function of GAM148 is therefore inhibition of

LOC283007 (Accession XP_210849.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283007.

[24850] LOC283511 (Accession XP_211077.1) is another GAM148 target gene, herein designated TARGET GENE. LOC283511 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283511, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283511 BINDING SITE, designated SEQ ID:9199, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24851] Another function of GAM148 is therefore inhibition of LOC283511 (Accession XP_211077.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283511.

[24852] LOC283767 (Accession XP_208835.1) is another GAM148 target gene, herein designated TARGET GENE. LOC283767 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283767, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283767 BINDING SITE, designated SEQ ID:640, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24853] Another function of GAM148 is therefore inhibition of LOC283767 (Accession XP_208835.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283767.

[24854] LOC283868 (Accession XP_211243.1) is another GAM148 target gene, herein designated TARGET GENE. LOC283868 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283868, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283868 BINDING SITE, designated SEQ ID:7128, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24855] Another function of GAM148 is therefore inhibition of LOC283868 (Accession XP_211243.1) . Accordingly, utili-

ties of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283868.

[24856] LOC284169 (Accession XP_211360.1) is another GAM148 target gene, herein designated TARGET GENE. LOC284169 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284169, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284169 BINDING SITE, designated SEQ ID:18426, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24857] Another function of GAM148 is therefore inhibition of LOC284169 (Accession XP_211360.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284169.

[24858] LOC284175 (Accession XP_211364.1) is another GAM148 target gene, herein designated TARGET GENE. LOC284175 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284175, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284175 BINDING SITE, designated SEQ ID:1975, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24859] Another function of GAM148 is therefore inhibition of LOC284175 (Accession XP_211364.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284175.

[24860] LOC284927 (Accession XP_211689.1) is another GAM148 target gene, herein designated TARGET GENE. LOC284927 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284927, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284927 BINDING SITE, designated SEQ ID:5418, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24861] Another function of GAM148 is therefore inhibition of LOC284927 (Accession XP_211689.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284927.

[24862] LOC285194 (Accession XP_211803.1) is another GAM148 target gene, herein designated TARGET GENE. LOC285194 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285194 BINDING SITE, designated SEQ ID:16431, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24863] Another function of GAM148 is therefore inhibition of LOC285194 (Accession XP_211803.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285194.

[24864] LOC285587 (Accession XP_211947.1) is another GAM148 target gene, herein designated TARGET GENE. LOC285587 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC285587 BINDING SITE, designated SEQ ID:5312, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24865] Another function of GAM148 is therefore inhibition of LOC285587 (Accession XP_211947.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285587.

[24866] LOC285594 (Accession XP_211946.2) is another GAM148 target gene, herein designated TARGET GENE. LOC285594 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285594, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285594 BINDING SITE, designated SEQ ID:2211, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24867] Another function of GAM148 is therefore inhibition of LOC285594 (Accession XP_211946.2) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285594.

[24868] LOC285843 (Accession XP_212034.1) is another GAM148 target gene, herein designated TARGET GENE. LOC285843 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285843, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285843 BINDING SITE, designated SEQ ID:14325, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24869] Another function of GAM148 is therefore inhibition of LOC285843 (Accession XP_212034.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285843.

[24870] LOC286058 (Accession XP_212158.1) is another GAM148 target gene, herein designated TARGET GENE. LOC286058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC286058 BINDING SITE, designated SEQ ID:15183, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24871] Another function of GAM148 is therefore inhibition of LOC286058 (Accession XP_212158.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286058.

[24872] LOC286063 (Accession XP_212159.1) is another GAM148 target gene, herein designated TARGET GENE. LOC286063 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286063, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286063 BINDING SITE, designated SEQ ID:1688, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24873] Another function of GAM148 is therefore inhibition of LOC286063 (Accession XP_212159.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286063.

[24874] LOC338817 (Accession XP_290588.1) is another GAM148 target gene, herein designated TARGET GENE. LOC338817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338817 BINDING SITE, designated SEQ ID:15148, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24875] Another function of GAM148 is therefore inhibition of LOC338817 (Accession XP_290588.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338817.

[24876] LOC338991 (Accession XP_290663.1) is another GAM148 target gene, herein designated TARGET GENE. LOC338991 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338991, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338991 BINDING SITE, designated SEQ ID:640, to

the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24877] Another function of GAM148 is therefore inhibition of LOC338991 (Accession XP_290663.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338991.

[24878] LOC338999 (Accession XP_290659.1) is another GAM148 target gene, herein designated TARGET GENE. LOC338999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338999 BINDING SITE, designated SEQ ID:640, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24879] Another function of GAM148 is therefore inhibition of LOC338999 (Accession XP_290659.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338999.

[24880] LOC339717 (Accession XP_295040.1) is another GAM148

target gene, herein designated TARGET GENE. LOC339717 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339717, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339717 BINDING SITE, designated SEQ ID:7535, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24881] Another function of GAM148 is therefore inhibition of LOC339717 (Accession XP_295040.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339717.

[24882] LOC340150 (Accession XP_295167.1) is another GAM148 target gene, herein designated TARGET GENE. LOC340150 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340150, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340150 BINDING SITE, designated SEQ ID:5873, to the nucleotide sequence of GAM148 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:280.

[24883] Another function of GAM148 is therefore inhibition of LOC340150 (Accession XP_295167.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340150.

[24884] LOC340385 (Accession XP_291261.1) is another GAM148 target gene, herein designated TARGET GENE. LOC340385 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340385, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340385 BINDING SITE, designated SEQ ID:12963, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24885] Another function of GAM148 is therefore inhibition of LOC340385 (Accession XP_291261.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340385.

[24886] LOC343095 (Accession XP_291404.1) is another GAM148 target gene, herein designated TARGET GENE. LOC343095

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC343095, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC343095 BINDING SITE, designated SEQ ID:5934, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24887] Another function of GAM148 is therefore inhibition of LOC343095 (Accession XP_291404.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC343095.

[24888] LOC348113 (Accession XP_300623.1) is another GAM148 target gene, herein designated TARGET GENE. LOC348113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348113 BINDING SITE, designated SEQ ID:640, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24889] Another function of GAM148 is therefore inhibition of LOC348113 (Accession XP_300623.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348113.

[24890] LOC348137 (Accession XP_300635.1) is another GAM148 target gene, herein designated TARGET GENE. LOC348137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348137 BINDING SITE, designated SEQ ID:640, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24891] Another function of GAM148 is therefore inhibition of LOC348137 (Accession XP_300635.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348137.

[24892] LOC348142 (Accession XP_300636.1) is another GAM148 target gene, herein designated TARGET GENE. LOC348142 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC348142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348142 BINDING SITE, designated SEQ ID:640, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24893] Another function of GAM148 is therefore inhibition of LOC348142 (Accession XP_300636.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348142.

[24894] LOC348180 (Accession XP_300650.1) is another GAM148 target gene, herein designated TARGET GENE. LOC348180 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348180, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348180 BINDING SITE, designated SEQ ID:12165, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24895] Another function of GAM148 is therefore inhibition of

LOC348180 (Accession XP_300650.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348180.

[24896] LOC348361 (Accession XP_302730.1) is another GAM148 target gene, herein designated TARGET GENE. LOC348361 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348361, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348361 BINDING SITE, designated SEQ ID:624, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24897] Another function of GAM148 is therefore inhibition of LOC348361 (Accession XP_302730.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348361.

[24898] LOC348369 (Accession XP_302732.1) is another GAM148 target gene, herein designated TARGET GENE. LOC348369 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348369, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348369 BINDING SITE, designated SEQ ID:15542, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24899] Another function of GAM148 is therefore inhibition of LOC348369 (Accession XP_302732.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348369.

[24900] LOC348911 (Accession XP_302915.1) is another GAM148 target gene, herein designated TARGET GENE. LOC348911 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348911, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348911 BINDING SITE, designated SEQ ID:15228, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24901] Another function of GAM148 is therefore inhibition of LOC348911 (Accession XP_302915.1) . Accordingly, utili-

ties of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348911.

[24902] LOC349251 (Accession XP_300251.1) is another GAM148 target gene, herein designated TARGET GENE. LOC349251 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349251, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349251 BINDING SITE, designated SEQ ID:4297, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24903] Another function of GAM148 is therefore inhibition of LOC349251 (Accession XP_300251.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349251.

[24904] LOC55924 (Accession NP_061972.1) is another GAM148 target gene, herein designated TARGET GENE. LOC55924 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC55924, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC55924 BINDING SITE, designated SEQ ID:3949, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24905] Another function of GAM148 is therefore inhibition of LOC55924 (Accession NP_061972.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC55924.

[24906] Mitogen-activated protein kinase kinase kinase 13 (MAP3K13, Accession NP_004712.1) is another GAM148 target gene, herein designated TARGET GENE. MAP3K13 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MAP3K13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAP3K13 BINDING SITE, designated SEQ ID:16657, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24907] Another function of GAM148 is therefore inhibition of Mitogen-activated protein kinase kinase kinase 13

(MAP3K13, Accession NP_004712.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K13.

[24908] Membrane-bound transcription factor protease, site 1 (MBTPS1, Accession NP_003782.1) is another GAM148 target gene, herein designated TARGET GENE. MBTPS1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MBTPS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MBTPS1 BINDING SITE, designated SEQ ID:10515, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24909] Another function of GAM148 is therefore inhibition of Membrane-bound transcription factor protease, site 1 (MBTPS1, Accession NP_003782.1), a gene which catalyzes the first step in the proteolytic activation of the sterol regulatory element- binding proteins (srebps). Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBTPS1.

[24910] The function of MBTPS1 has been established by previous studies. The lipid composition of animal cells is controlled by sterol regulatory element binding proteins (SREBPs; OMIM Ref. No. 184756), transcription factors released from membranes by sterol- regulated proteolysis (Brown and Goldstein, 1997). Release is initiated by site- 1 protease (S1P), which cleaves SREBPs in the endoplasmic reticulum (ER) luminal loop between 2 membrane- spanning regions (Sakai et al., 1996). The cleavage recognition sequence of S1P is the pentapeptide RSVLS (Duncan et al., 1997). To clone S1P, Sakai et al. (1998) prepared pCMV- PLAP- BP2, which encodes a fusion protein that contains placental alkaline phosphatase (PLAP; 171800) in the ER lumen flanked by cleavage sites for signal peptidase and S1P. In sterol- deprived cells, cleavage by both proteases leads to PLAP secretion. PLAP is not secreted by SRD- 12B cells, cholesterol auxotrophs that lack S1P. Sakai et al. (1998) transfected SRD- 12B cells with pCMV- PLAP- BP2 plus pools of CHO cDNAs and identified a cDNA that restored site- 1 cleavage and PLAP secretion. The cDNA encodes S1P, an intraluminal 1,052- amino acid membrane- bound subtilisin- like protease. The authors proposed that S1P is the sterol- regulated protease that controls

lipid metabolism in animal cells. Nakajima et al. (2000) localized the human S1P gene to 16q24 by FISH and radiation hybrid mapping. They showed that the gene is more than 60 kb long and contains 23 exons. Its transcription initiation site within exon 1 is separate from the initiation codon in exon 2. Analysis of the exon/intron structure showed that the S1P gene consists of a mosaic of functional units: exon 1 encodes the 5- prime untranslated region; exon 2 encodes the NH2- terminal signal sequence; and exons 2 and 3 encode the propeptide sequence that is released when S1P is self- activated by intramolecular cleavage. Exons 5- 10 encode the subtilisin-homology domain that is critical for catalytic activity, and exon 23 encodes the transmembrane region. Analysis of the putative promoter region revealed a highly GC- rich region containing a binding site for SREBP1, as well as Sp1 (OMIM Ref. No. 189906) and AP2 (OMIM Ref. No. 107580) sites. Therefore, expression of the S1P gene may be under the control of SREBP1, a key regulator of the expression of genes essential for intracellular lipid metabolism.

[24911]

[24912] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[24913] Sakai, J.; Rawson, R. B.; Espenshade, P. J.; Cheng, D.; Seegmiller, A. C.; Goldstein, J. L.; Brown, M. S. : Molecular identification of the sterol- regulated luminal protease that cleaves SREBPs and controls lipid composition of animal cells. Molec. Cell 2: 505- 514, 1998. ; and

[24914] Nakajima, T.; Iwaki, K.; Kodama, T.; Inazawa, J.; Emi, M. : Genomic structure and chromosomal mapping of the human site- 1 protease (S1P) gene. J. Hum. Genet. 45: 212-217, 2000.

[24915] Further studies establishing the function and utilities of MBTPS1 are found in John Hopkins OMIM database record ID 603355, and in cited publications listed in Table 5, which are hereby incorporated by reference.MEP50 (Accession NP_077007.1) is another GAM148 target gene, herein designated TARGET GENE. MEP50 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MEP50, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MEP50 BINDING SITE, designated SEQ ID:13864, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA,

also designated SEQ ID:280.

[24916] Another function of GAM148 is therefore inhibition of MEP50 (Accession NP_077007.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEP50.

[24917] MGC13017 (Accession NP_542387.1) is another GAM148 target gene, herein designated TARGET GENE. MGC13017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13017 BINDING SITE, designated SEQ ID:18039, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24918] Another function of GAM148 is therefore inhibition of MGC13017 (Accession NP_542387.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13017.

[24919] MGC17403 (Accession NP_689847.1) is another GAM148 target gene, herein designated TARGET GENE. MGC17403 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC17403, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC17403 BINDING SITE, designated SEQ ID:2263, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24920] Another function of GAM148 is therefore inhibition of MGC17403 (Accession NP_689847.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC17403.

[24921] MGC35136 (Accession NP_689640.1) is another GAM148 target gene, herein designated TARGET GENE. MGC35136 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35136 BINDING SITE, designated SEQ ID:13560, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24922] Another function of GAM148 is therefore inhibition of

MGC35136 (Accession NP_689640.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35136.

[24923] Myotubularin related protein 3 (MTMR3, Accession NP_694691.1) is another GAM148 target gene, herein designated TARGET GENE. MTMR3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MTMR3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTMR3 BINDING SITE, designated SEQ ID:17072, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24924] Another function of GAM148 is therefore inhibition of Myotubularin related protein 3 (MTMR3, Accession NP_694691.1), a gene which could be a tyrosine- phosphatase. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTMR3.

[24925] The function of MTMR3 has been established by previous studies. Zhao et al. (2001) showed that an isoform of

MTMR3, missing exon 17, dephosphorylates para- nitro- phenylphosphate and phosphatidylinositol 3- phosphate.

[24926]

[24927] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[24928] Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. : Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro. DNA Res. 4: 141- 150, 1997. ; and

[24929] Zhao, R.; Qi, Y.; Chen, J.; Zhao, Z. J. : FYVE- DSP2, a FYVE domain- containing dual specificity protein phosphatase that dephosphorylates phosphotidylinositol (sic) 3- phosphate. Exp. Cel.

[24930] Further studies establishing the function and utilities of MTMR3 are found in John Hopkins OMIM database record ID 603558, and in cited publications listed in Table 5, which are hereby incorporated by reference.Myotubularin related protein 3 (MTMR3, Accession NP_066576.1) is another GAM148 target gene, herein designated TARGET GENE. MTMR3 BINDING SITE is a target binding site found

in the 3` untranslated region of multiple transcripts of mRNA encoded by MTMR3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTMR3 BINDING SITE, designated SEQ ID:17072, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24931] Another function of GAM148 is therefore inhibition of Myotubularin related protein 3 (MTMR3, Accession NP_066576.1), a gene which could be a tyrosine- phosphatase. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTMR3.

[24932] The function of MTMR3 has been established by previous studies. Zhao et al. (2001) showed that an isoform of MTMR3, missing exon 17, dephosphorylates para- nitrophenylphosphate and phosphatidylinositol 3- phosphate.

[24933]

[24934] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[24935] Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.;

Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. : Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro. DNA Res. 4: 141- 150, 1997. ; and

[24936] Zhao, R.; Qi, Y.; Chen, J.; Zhao, Z. J. : FYVE- DSP2, a FYVE domain- containing dual specificity protein phosphatase that dephosphorylates phosphotidylinositol (sic) 3- phosphate. Exp. Cel.

[24937] Further studies establishing the function and utilities of MTMR3 are found in John Hopkins OMIM database record ID 603558, and in cited publications listed in Table 5, which are hereby incorporated by reference.Myotubularin related protein 3 (MTMR3, Accession NP_694690.1) is another GAM148 target gene, herein designated TARGET GENE. MTMR3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MTMR3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTMR3 BINDING SITE, designated SEQ ID:17072, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA,

also designated SEQ ID:280.

[24938] Another function of GAM148 is therefore inhibition of Myotubularin related protein 3 (MTMR3, Accession NP_694690.1), a gene which could be a tyrosine- phosphatase. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTMR3.

[24939] The function of MTMR3 has been established by previous studies. Zhao et al. (2001) showed that an isoform of MTMR3, missing exon 17, dephosphorylates para- nitrophenylphosphate and phosphatidylinositol 3- phosphate.

[24940]

[24941] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[24942] Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. : Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro. DNA Res. 4: 141- 150, 1997. ; and

[24943] Zhao, R.; Qi, Y.; Chen, J.; Zhao, Z. J. : FYVE- DSP2, a FYVE domain- containing dual specificity protein phosphatase

that dephosphorylates phosphotidylinositol (sic) 3- phosphate. Exp. Cel.

[24944] Further studies establishing the function and utilities of MTMR3 are found in John Hopkins OMIM database record ID 603558, and in cited publications listed in Table 5, which are hereby incorporated by reference.Myeloid differentiation primary response gene (88) (MYD88, Accession NP_002459.1) is another GAM148 target gene, herein designated TARGET GENE. MYD88 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYD88, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYD88 BINDING SITE, designated SEQ ID:10785, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24945] Another function of GAM148 is therefore inhibition of Myeloid differentiation primary response gene (88) (MYD88, Accession NP_002459.1), a gene which is involved in the toll- like receptor and il- 1 receptor signaling pathway in the innate immune response. Accordingly, utilities of GAM148 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with MYD88.

[24946] The function of MYD88 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.NECAB2 (Accession NP_061938.1) is another GAM148 target gene, herein designated TARGET GENE. NECAB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NECAB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NECAB2 BINDING SITE, designated SEQ ID:5818, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24947] Another function of GAM148 is therefore inhibition of NECAB2 (Accession NP_061938.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NECAB2.

[24948] Neuronal cell adhesion molecule (NRCAM, Accession NP_005001.1) is another GAM148 target gene, herein designated TARGET GENE. NRCAM BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by NRCAM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRCAM BINDING SITE, designated SEQ ID:12857, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24949] Another function of GAM148 is therefore inhibition of Neuronal cell adhesion molecule (NRCAM, Accession NP_005001.1), a gene which functions as a cell surface protein and belongs to the immunoglobulin superfamily. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRCAM.

[24950] The function of NRCAM has been established by previous studies. The cell adhesion molecules (CAMs) are a subset of the immunoglobin (Ig) superfamily found in the nervous systems of both vertebrates and invertebrates. They are usually surface membrane proteins with multiple Ig domains at their N termini followed by several fibronectin type III repeats and either a transmembrane intracellular domain or a glycophosphatidylinositol- linked membrane

anchor at the C terminus (Lane et al., 1996). The chicken Bravo/Nr- CAM was described by Grumet et al. (1991) and Kayyem et al. (1992) and shown to play a role in nervous system development. The protein interacts with other cell surface molecules of the Ig superfamily and appears to be necessary for specific pathfinding by axonal growth cones during development (Lane et al., 1996). Lane et al. (1996) cloned the human homolog (NRCAM) of the chicken gene from a fetal brain library. Like its chicken counterpart, the predicted 1,275- amino acid protein has 6 V- like Ig domains and 5 fibronectin type III repeats. The transmembrane and intracellular domains of human and chicken NRCAM are entirely conserved and the proteins are 82% identical overall. Alternative splice variants were observed involving sequence around the fifth fibronectin repeat. Northern blots showed an approximately 7- kb transcript in all tissues of adult human brain examined.

[24951]

[24952] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[24953] Kayyem, J. F.; Roman, J. M.; de la Rosa, E. J.; Schwarz, U.; Dreyer, W. J. : Bravo/Nr- CAM is closely related to the cell

adhesion molecules L1 and Ng- CAM and has a similar heterodimer structure. J. Cell. Biol. 118: 1259- 1270, 1992. ; and

[24954] Lane, R. P.; Chen, X.- N.; Yamakawa, K.; Vielmetter, J.; Korenberg, J. R.; Dreyer, W. J. : Characterization of a highly conserved human homolog to the chicken neural cell surface protein.

[24955] Further studies establishing the function and utilities of NRCAM are found in John Hopkins OMIM database record ID 601581, and in cited publications listed in Table 5, which are hereby incorporated by reference.Nucleoporin 50kda (NUP50, Accession NP_009103.2) is another GAM148 target gene, herein designated TARGET GENE. NUP50 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NUP50, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUP50 BINDING SITE, designated SEQ ID:7777, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24956] Another function of GAM148 is therefore inhibition of Nucleoporin 50kda (NUP50, Accession NP_009103.2), a gene

which is transported through the nuclear pore complex (NPC) by the importin- alpha:beta receptor. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUP50.

[24957] The function of NUP50 has been established by previous studies. Using exon trapping and genomic sequence analysis to identify genes within 22q13.3, Trichet et al. (1999) identified NUP50, a human homolog of rat Npap60, is distantly related to the yeast Nup2 protein and belongs to the FG (phe- gly) nucleoporin family. The authors isolated a cDNA corresponding to the entire NUP50 coding sequence. The deduced 468- amino acid NUP50 protein contains 5 FG repeats. NUP50 shares 70% sequence identity with rat Npap60. However, the C- terminal end of NUP50 is 87 amino acids longer than that of Npap60. Northern blot analysis of various human tissues detected several NUP50 transcripts with different tissue specificities: a 2- kb transcript expressed at low levels in all tissues tested, but with considerably higher expression in testis, peripheral blood leukocytes, and fetal liver; a 2.8- kb transcript expressed in all tissues tested, but with highest expression in testis; a 4- kb transcript expressed

only in peripheral blood leukocytes; a 5- kb transcript expressed at similar levels in all tissues tested; and an 8- kb transcript weakly expressed in spleen, testis, ovary, and blood leukocytes. In addition, RT- PCR detected the 8- kb transcript in fetal brain. Trichet et al. (1999) found that NUP50 transcripts use at least 3 alternative polyadenylation sites and possibly have alternative 5- prime ends; they did not detect alternative splicing. Many nuclear-targeted proteins are transported through the NPC by the importin- alpha:importin- beta heterodimer (see OMIM Ref. No. 602738). Lindsay et al. (2002) showed that NUP50, a protein previously believed to be a structural component of the NPC, is a RAN (OMIM Ref. No. 601179)-binding protein and a cofactor for importin- alpha:importin- beta- mediated import. NUP50 is a tristable switch that alternates between binding modes. The C terminus binds importin- beta through RAN- GTP. The N terminus binds the C terminus of importin- alpha, while a central domain binds importin- beta. NUP50:importin- alpha:importin- beta binds cargo and can stimulate nuclear import. Endogenous NUP50 can shuttle and is accessible from the cytoplasmic side of the nuclear envelope. These findings identified NUP50 as a cofactor for importin- al-

pha:importin- beta nuclear import and as a subunit of the importin complex.

[24958]

[24959] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[24960] Lindsay, M. E.; Plafker, K.; Smith, A. E.; Clurman, B. E.; Macara, I. G. : Npap60/Nup50 is a tri- stable switch that stimulates importin- alpha:beta- mediated nuclear protein import. Cell 110: 349- 360, 2002. ; and

[24961] Trichet, V.; Shkolny, D.; Dunham, I.; Beare, D.; McDermid, H. E. : Mapping and complex expression pattern of the human NPAP60L nucleoporin gene. Cytogenet. Cell Genet. 85: 221- 226, 199.

[24962] Further studies establishing the function and utilities of NUP50 are found in John Hopkins OMIM database record ID 604646, and in cited publications listed in Table 5, which are hereby incorporated by reference.Nucleoporin 50kda (NUP50, Accession NP_710151.1) is another GAM148 target gene, herein designated TARGET GENE. NUP50 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NUP50, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUP50 BINDING SITE, designated SEQ ID:7777, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24963] Another function of GAM148 is therefore inhibition of Nucleoporin 50kda (NUP50, Accession NP_710151.1), a gene which is transported through the nuclear pore complex (NPC) by the importin- alpha:beta receptor. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUP50.

[24964] The function of NUP50 has been established by previous studies. Using exon trapping and genomic sequence analysis to identify genes within 22q13.3, Trichet et al. (1999) identified NUP50, a human homolog of rat Npap60, is distantly related to the yeast Nup2 protein and belongs to the FG (phe- gly) nucleoporin family. The authors isolated a cDNA corresponding to the entire NUP50 coding sequence. The deduced 468- amino acid NUP50 protein contains 5 FG repeats. NUP50 shares 70% sequence identity with rat Npap60. However, the C- terminal end of NUP50 is 87 amino acids longer than that of Npap60.

Northern blot analysis of various human tissues detected several NUP50 transcripts with different tissue specificities: a 2- kb transcript expressed at low levels in all tissues tested, but with considerably higher expression in testis, peripheral blood leukocytes, and fetal liver; a 2.8-kb transcript expressed in all tissues tested, but with highest expression in testis; a 4- kb transcript expressed only in peripheral blood leukocytes; a 5- kb transcript expressed at similar levels in all tissues tested; and an 8- kb transcript weakly expressed in spleen, testis, ovary, and blood leukocytes. In addition, RT- PCR detected the 8- kb transcript in fetal brain. Trichet et al. (1999) found that NUP50 transcripts use at least 3 alternative polyadenylation sites and possibly have alternative 5- prime ends; they did not detect alternative splicing. Many nuclear-targeted proteins are transported through the NPC by the importin- alpha:importin- beta heterodimer (see OMIM Ref. No. 602738). Lindsay et al. (2002) showed that NUP50, a protein previously believed to be a structural component of the NPC, is a RAN (OMIM Ref. No. 601179)-binding protein and a cofactor for importin- alpha:importin- beta- mediated import. NUP50 is a tristable switch that alternates between binding modes. The C ter-

minus binds importin- beta through RAN- GTP. The N terminus binds the C terminus of importin- alpha, while a central domain binds importin- beta. NUP50:importin- alpha:importin- beta binds cargo and can stimulate nuclear import. Endogenous NUP50 can shuttle and is accessible from the cytoplasmic side of the nuclear envelope. These findings identified NUP50 as a cofactor for importin- alpha:importin- beta nuclear import and as a subunit of the importin complex.

[24965]

[24966] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[24967] Lindsay, M. E.; Plafker, K.; Smith, A. E.; Clurman, B. E.; Macara, I. G. : Npap60/Nup50 is a tri- stable switch that stimulates importin- alpha:beta- mediated nuclear protein import. Cell 110: 349- 360, 2002. ; and

[24968] Trichet, V.; Shkolny, D.; Dunham, I.; Beare, D.; McDermid, H. E. : Mapping and complex expression pattern of the human NPAP60L nucleoporin gene. Cytogenet. Cell Genet. 85: 221- 226, 199.

[24969] Further studies establishing the function and utilities of NUP50 are found in John Hopkins OMIM database record

ID 604646, and in cited publications listed in Table 5, which are hereby incorporated by reference.Orthopedia homolog (drosophila) (OTP, Accession NP_115485.1) is another GAM148 target gene, herein designated TARGET GENE. OTP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OTP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OTP BINDING SITE, designated SEQ ID:2151, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24970] Another function of GAM148 is therefore inhibition of Orthopedia homolog (drosophila) (OTP, Accession NP_115485.1), a gene which involves in the development of the forebrain and spinal cord. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OTP.

[24971] The function of OTP has been established by previous studies. Homeodomain genes are helix- turn- helix transcription factors that play key roles in the specification of cell fates. In the central nervous system, homeodomain genes not only position cells along an axis, but also spec-

ify cell migration patterns and may influence axonal connectivity. In an effort to identify novel homeodomain genes involved in the development of the human central nervous system, Lin et al. (1999) cloned, characterized, and mapped the human homolog of the murine homeodomain gene Orthopedia (Otp), whose product is found in multiple cell groups within the mouse hypothalamus, amygdala, and brain stem. The human OTP cDNA encodes a protein of 325 amino acids. The deduced amino acid sequence is 99% homologous to mouse Otp and demonstrated a high degree of conservation when compared to sea urchin and Drosophila Otp proteins. A single putative OTP gene product was found in 17- week human fetal brain tissue by Western blot analysis using a novel polyclonal antibody raised against a conserved 13- amino acid sequence in the C terminus of the OTP protein. Expression in the developing human hypothalamus was confirmed by immunohistochemistry. Lin et al. (1999) mapped the human OTP gene to chromosome 5q13.3 using analysis of a radiation hybrid panel and by fluorescence in situ hybridization.

[24972] Animal model experiments lend further support to the function of OTP. Acampora et al. (1999) generated mice

deficient in Otp by homologous recombination. Homozygous Otp - /- mice died soon after birth and displayed progressive impairment of crucial neuroendocrine developmental events such as reduced cell proliferation, abnormal cell migration, and failure in terminal differentiation of the parvocellular and magnocellular neurons of the anterior periventricular, paraventricular, supraoptic, and arcuate nuclei. Acampora et al. (1999) suggested that Otp and Sim1 (OMIM Ref. No. 603128) are required to maintain Brn2 (OMIM Ref. No. 600494) expression which, in turn, is required for neuronal cell lineages secreting oxytocin (OMIM Ref. No. 167050), arginine vasopressin (OMIM Ref. No. 192340), and corticotropin- releasing (OMIM Ref. No. 122560) hormones.

[24973] It is appreciated that the abovementioned animal model for OTP is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[24974] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[24975] Acampora, D.; Postiglione, M. P.; Avantaggiato, V.; Di Bonito, M.; Vaccarino, F. M.; Michaud, J.; Simeone, A. :

Progressive impairment of developing neuroendocrine cell lineages in the hypothalamus of mice lacking the Orthopedia gene. Genes Dev. 13: 2787- 2800, 1999. ; and

[24976] Lin, X.; State, M. W.; Vaccarino, F. M.; Greally, J.; Hass, M.; Leckman, J. F. : Identification, chromosomal assignment, and expression analysis of the human homeodomain-containing gene.

[24977] Further studies establishing the function and utilities of OTP are found in John Hopkins OMIM database record ID 604529, and in cited publications listed in Table 5, which are hereby incorporated by reference.Procollagen c-endopeptidase enhancer (PCOLCE, Accession NP_002584.1) is another GAM148 target gene, herein designated TARGET GENE. PCOLCE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCOLCE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCOLCE BINDING SITE, designated SEQ ID:4646, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24978] Another function of GAM148 is therefore inhibition of

Procollagen c-endopeptidase enhancer (PCOLCE, Accession NP_002584.1), a gene which binds to the cooh- terminal propeptide of type i procollagen and enhances procollagen c- proteinase activity. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCOLCE.

[24979] The function of PCOLCE has been established by previous studies. Fibrillar collagen types I- III are synthesized as precursor molecules known as procollagens. These precursors contain amino- and carboxyl- terminal peptide extensions known as N- and C- propeptides, respectively, which are cleaved, upon secretion of procollagen from the cell, to yield the mature triple helical, highly structured fibrils. In the mouse, procollagen C- proteinase depends for full expression upon the presence of either a 55- kD glycoprotein or smaller 36- and 34- kD proteolytically processed forms of the same protein. None of the 3 enhancer proteins exhibits intrinsic procollagen processing activity, but all are capable of enhancing the activity of the C- proteinase by approximately one order of magnitude. Takahara et al. (1994) purified type I procollagen COOH-terminal proteinase enhancer, a glycoprotein that binds to the COOH- terminal propeptide of type I procollagen and

enhances C- proteinase activity, from mouse fibroblast culture medium. Sequences of mouse enhancer cDNA predicted a protein of approximately 50 kD and 468 amino acids. Human cDNAs encoded an enhancer of 449 amino acids. Mouse enhancer RNA was shown to be at highest levels in collagen- rich tissues, especially tendon. By Southern analysis of genomic DNA from panels of human/mouse cell hybrids and by fluorescence in situ hybridization, Takahara et al. (1994) localized the PCOLCE gene to 7q21.3- q22, the same region containing the type I collagen alpha- 2 chain gene (COL1A2; 120160). Takahara et al. (1996) investigated further the apparent proximity of the 2 genes by the study of somatic cell hybrids, cosmid contigs, and interspecific backcross mice. They found that PCOLCE and COL1A2 are separated by at least 6 Mb and that Pcolce and Col1a2 are located on separate chromosomes in the mouse, chromosomes 5 and 6, respectively.

[24980]

[24981] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[24982] Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R. L.; Jani- Sait, S.; Shows, T. B.; Greenspan, D. S. : Type I

procollagen COOH- terminal proteinase enhancer protein: identification, primary structure, and chromosomal localization of the cognate human gene (PCOLCE). J. Biol. Chem. 269: 26280- 26285, 1994. ; and

[24983] Takahara, K.; Osborne, L.; Elliott, R. W.; Tsui, L.- C.; Scherer, S. W.; Greenspan, D. S. : Fine mapping of the human and mouse genes for the type I procollagen COOH-terminal proteinase.

[24984] Further studies establishing the function and utilities of PCOLCE are found in John Hopkins OMIM database record ID 600270, and in cited publications listed in Table 5, which are hereby incorporated by reference.Phospholipase c, delta 1 (PLCD1, Accession NP_006216.1) is another GAM148 target gene, herein designated TARGET GENE. PLCD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLCD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PLCD1 BINDING SITE, designated SEQ ID:8152, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24985] Another function of GAM148 is therefore inhibition of

Phospholipase c, delta 1 (PLCD1, Accession NP_006216.1), a gene which acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5- trisphosphate and therefore may be associated with Alzheimer disease. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of Alzheimer disease, and of other diseases and clinical conditions associated with PLCD1.

[24986] The function of PLCD1 has been established by previous studies. Phosphoinositide- specific phospholipase C acts as a signal transducer that generates 2 messengers, diacylglycerol and inositol 1,4,5- trisphosphate, by hydrolyzing inositol phospholipids. Molecules belonging to the PLC family are divided into subfamilies, PLC- beta (see OMIM Ref. No. 600810), PLC- gamma (see OMIM Ref. No. 172420), and PLC- delta, whose amino acid sequences are highly conserved in 2 distinct regions designated X and Y. PLC- delta- 1 is distinguished from PLC- gamma by lack of the SH2 and SH3 domains that are essential for activation of PLC- gamma by tyrosine protein kinases, and from PLC- beta by lack of the C- terminal region of PLC- beta that is responsible for binding and activation by G proteins. Cheng et al. (1995) cloned cDNA for human PLC-

delta- 1 and localized the gene to chromosome 3 by means of a human/rodent somatic cell panel (Lyu et al., 1996). In the course of a large- scale sequencing analysis of genomic DNA in the vicinity of the homozygous deletion on chromosome 3p found in a lung cancer cell line, Ishikawa et al. (1997) found that the gene encoding phospholipase C, delta- 1 (PLCD1) is located just distal to the region removed by the deletion. They found that the gene consists of 15 exons and spans about 22 kb. By fluorescence in situ hybridization, they localized the PLCD1 gene to 3p22- p21.3. Shimohama et al. (1998) examined the entire sequences corresponding to protein- coding exons 2- 15 of the hamster PLC- delta- 1 gene in genomic DNA derived from the leukocytes of 13 unrelated patients with early- onset sporadic Alzheimer disease (OMIM Ref. No. 104300). In 1 of these patients whose clinical features and course did not differ from those of the other 12 cases, they found a change of codon CGC (arg) to CAC (his), located in the pleckstrin homology domain of the PLCD1 gene. They stated that this was the first mutation found in the human PLC genes. Site- directed mutagenesis of the glutathione- S- transferase (GST/PLCD1) fusion protein changing arg105 to his resulted in a 4- fold decrease in

the affinity of specific binding and a reduction in hydrolyzing activity to about 40% of that of the wildtype enzyme. This remarkable loss of function could be interpreted in terms of a conformational change in the pleckstrin homology domain. Shimohama et al. (1998) found that the arg105- to- his mutation was present in heterozygous state in the patient with AD. The mutation was not found in DNA extracted from leukocytes of 23 unrelated patients with familial AD, 23 unrelated patients with early- onset sporadic AD, 46 unrelated patients with late-onset sporadic AD, and 456 nondemented control subjects. Thus the change did not appear to be a common polymorphism. However, determination of the possible pathologic role required transgenic studies of the mutant gene to determine the role of the enzyme and the mutation and a search for other mutations in the pleckstrin homology domain of PLC genes in human subjects with genetic disorders. They pointed out that mutations in the pleckstrin homology domain of the BTK gene occur in patients with Bruton agammaglobulinemia (OMIM Ref. No. 300300).

[24987]

[24988] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[24989] Cheng, H. F.; Jiang, M. J.; Chen, C. L.; Liu, S. M.; Wong, L. P.; Lomasney, J. W.; King, K. : Cloning and identification of amino acid residues of human phospholipase C delta 1 essential for catalysis. J. Biol. Chem. 270: 5495- 5505, 1995. ; and

[24990] Ishikawa, S.; Takahashi, T.; Ogawa, M.; Nakamura, Y. : Genomic structure of the human PLCD1 (phospholipase C delta 1) locus on 3p22- p21.3. Cytogenet. Cell Genet. 78: 58- 60, 1997.

[24991] Further studies establishing the function and utilities of PLCD1 are found in John Hopkins OMIM database record ID 602142, and in cited publications listed in Table 5, which are hereby incorporated by reference.PP2447 (Accession NP_079480.1) is another GAM148 target gene, herein designated TARGET GENE. PP2447 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PP2447, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP2447 BINDING SITE, designated SEQ ID:10796, to the nucleotide se-

quence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24992] Another function of GAM148 is therefore inhibition of PP2447 (Accession NP_079480.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP2447.

[24993] Protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11, Accession NP_740751.1) is another GAM148 target gene, herein designated TARGET GENE. PPP1R11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R11 BINDING SITE, designated SEQ ID:15269, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24994] Another function of GAM148 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11, Accession NP_740751.1), a gene which inhibits rabbit muscle protein phosphatase- 1 in vitro . Accordingly, utilities of GAM148 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with PPP1R11.

[24995] The function of PPP1R11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11, Accession NP_068778.1) is another GAM148 target gene, herein designated TARGET GENE. PPP1R11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R11 BINDING SITE, designated SEQ ID:15269, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24996] Another function of GAM148 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11, Accession NP_068778.1), a gene which inhibits rabbit muscle protein phosphatase- 1 in vitro . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with PPP1R11.

[24997] The function of PPP1R11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Protein phosphatase 2a, regulatory subunit b' (pr 53) (PPP2R4, Accession NP_821069.1) is another GAM148 target gene, herein designated TARGET GENE. PPP2R4 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PPP2R4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP2R4 BINDING SITE, designated SEQ ID:14893, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[24998] Another function of GAM148 is therefore inhibition of Protein phosphatase 2a, regulatory subunit b' (pr 53) (PPP2R4, Accession NP_821069.1), a gene which is a regulatory subunit of protein phosphatase 2A. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R4.

[24999] The function of PPP2R4 has been established by previous studies. McCright et al. (1996) stated that PP2A contains a 36- kD catalytic C subunit (OMIM Ref. No. 176915) and a 65- kD structural/regulatory A subunit. Association of this dimeric core of PP2A with a third regulatory subunit (PR54, PR55, PR72, PR74, PR130, etc.) results in the formation of a specific trimeric holoenzyme. The PPP2R4 gene (which the authors symbolized PTPA) encodes a specific phosphotyrosyl phosphatase activator of the dimeric form of protein phosphatase 2A. Van Hoof et al. (1995) demonstrated that human PTPA is encoded by a single-copy gene composed of 10 exons and 9 introns with a total length of about 60 kb. The 5- prime flanking sequence of the transcription start site was analyzed for its potential as a promoter. This region lacks a TATA sequence in the appropriate position relative to the transcription start. However, this region is very GC- rich and contains four Sp1 sites (SP1; 189906) upstream of the transcription start site, a feature common to many TATA- less promoters. Based on homology with DNA- binding consensus sequences of transcription factors, Van Hoof et al. (1995) identified several additional putative transcription factor binding sites in the promoter region. Transfection experi-

ments with a construct containing the PTPA promoter region inserted 5- prime of a luciferase reporter gene demonstrated that the 5- prime flanking sequence of the PTPA gene indeed has promoter activity that seems to be cell- line dependent. By fluorescence in situ hybridization, Van Hoof et al. (1995) mapped the PTPA gene to 9q34. Fluorescence in situ analysis of metaphase chromosomes of patients bearing the Philadelphia chromosome indicated that PTPA is positioned centromeric of ABL1 (OMIM Ref. No. 189980) and probably is not involved in chronic myeloid leukemia.

[25000]

[25001] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25002] McCright, B.; Rivers, A. M.; Audlin, S.; Virshup, D. M. : The B56 family of protein phosphatase 2A (PP2A) regulatory subunits encodes differentiation- induced phosphoproteins that target PP2A to both nucleus and cytoplasm. J. Biol. Chem. 271: 22081- 22089, 1996. ; and

[25003] Van Hoof, C.; Aly, M. S.; Garcia, A.; Cayla, X.; Cassiman, J. J.; Merlevede, W.; Goris, J. : Structure and chromosomal localization of the human gene of the phosphotyrosyl

phosphatase a.

[25004] Further studies establishing the function and utilities of PPP2R4 are found in John Hopkins OMIM database record ID 600756, and in cited publications listed in Table 5, which are hereby incorporated by reference.Proline rich 2 (PROL2, Accession NP_006804.1) is another GAM148 target gene, herein designated TARGET GENE. PROL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PROL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PROL2 BINDING SITE, designated SEQ ID:17200, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25005] Another function of GAM148 is therefore inhibition of Proline rich 2 (PROL2, Accession NP_006804.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROL2.

[25006] Prostaglandin f2 receptor negative regulator (PTGFRN, Accession XP_040709.3) is another GAM148 target gene, herein designated TARGET GENE. PTGFRN BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by PTGFRN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGFRN BINDING SITE, designated SEQ ID:14508, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25007] Another function of GAM148 is therefore inhibition of Prostaglandin f2 receptor negative regulator (PTGFRN, Accession XP_040709.3), a gene which inhibits the binding of prostaglandin f2- alpha (pgf2- alpha) to its specific fp receptor. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGFRN.

[25008] The function of PTGFRN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1) is another GAM148 target gene, herein designated TARGET GENE. PTGIS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGIS, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGIS BINDING SITE, designated SEQ ID:15201, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25009] Another function of GAM148 is therefore inhibition of Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1), a gene which catalyzes the isomerization of prostaglandin h2 to prostacyclin (= prostaglandin i2). Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGIS.

[25010] The function of PTGIS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1, Accession NP_542970.1) is another GAM148 target gene, herein designated TARGET GENE. PTPNS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTPNS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPNS1 BINDING SITE, designated SEQ ID:9261, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25011] Another function of GAM148 is therefore inhibition of Protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1, Accession NP_542970.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPNS1.

[25012] Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602295.1) is another GAM148 target gene, herein designated TARGET GENE. RAD52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAD52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE, designated SEQ ID:9644, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25013] Another function of GAM148 is therefore inhibition of Rad52 homolog (s. cerevisiae) (RAD52, Accession

NP_602295.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52.

[25014] SBLF (Accession NP_006864.2) is another GAM148 target gene, herein designated TARGET GENE. SBLF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SBLF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SBLF BINDING SITE, designated SEQ ID:5432, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25015] Another function of GAM148 is therefore inhibition of SBLF (Accession NP_006864.2) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SBLF.

[25016] Src family associated phosphoprotein 1 (SCAP1, Accession NP_003717.2) is another GAM148 target gene, herein designated TARGET GENE. SCAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAP1 BINDING SITE, designated SEQ ID:13627, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25017] Another function of GAM148 is therefore inhibition of Src family associated phosphoprotein 1 (SCAP1, Accession NP_003717.2) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAP1.

[25018] Sidekick homolog 1 (chicken) (SDK1, Accession NP_689957.1) is another GAM148 target gene, herein designated TARGET GENE. SDK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SDK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SDK1 BINDING SITE, designated SEQ ID:16745, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25019] Another function of GAM148 is therefore inhibition of Sidekick homolog 1 (chicken) (SDK1, Accession

NP_689957.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDK1.

[25020] Solute carrier family 21 (prostaglandin transporter), member 2 (SLC21A2, Accession NP_005621.1) is another GAM148 target gene, herein designated TARGET GENE. SLC21A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC21A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC21A2 BINDING SITE, designated SEQ ID:10394, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25021] Another function of GAM148 is therefore inhibition of Solute carrier family 21 (prostaglandin transporter), member 2 (SLC21A2, Accession NP_005621.1), a gene which is a Prostaglandin transporter. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC21A2.

[25022] The function of SLC21A2 has been established by previous studies. At physiologic pH, prostaglandins (PGs) traverse biologic membranes poorly. Accordingly, PG trans-

port is carrier- mediated in many tissues, including the lung, choroid plexus, liver, anterior chamber of the eye, vagina and uterus, and placenta. Kanai et al. (1995) cloned the rat prostaglandin transporter (symbolized PGT by them) and postulated 3 possible roles for the transporter. First, PGT might mediate the efflux of newly synthesized PGs from cells. Second, PGT might mediate epithelial PG transport. A third possible role of PGT is that of mediating PG clearance and degradation. Lu et al. (1996) favored the clearance role for PGT. Using a rat PGT probe on Northern blots of human kidney mRNA, they found evidence for the presence of a human PGT homolog. They screened a human kidney cDNA library and isolated human PGT. The gene encodes a 643- amino acid polypeptide with 82% identity to the rat protein. They expressed a full- length human cDNA clone in cultured cells and reported that both rat and human PGT transport PGD2, as well as PGE1, PGE2, and PGF2a. Although human PGT has cDNA and deduced amino acid sequences similar to those of the rat, the tissue distribution of mRNA transcripts is substantially broader in human. Additionally, the diversity of human PGT transcripts is greater and the affinity for thromboxane- 2 is greater. Lu et al. (1996) found strong

PGT mRNA expression in the human fetus. By PCR- based monochromosomal somatic cell hybrid mapping and fluorescence in situ hybridization, Lu and Schuster (1998) mapped the PGT gene to 3q21.

[25023]

[25024] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25025] Kanai, N.; Lu, R.; Satriano, J. A.; Bao, Y.; Wolkoff, A. W.; Schuster, V. L. : Identification and characterization of a prostaglandin transporter. Science 268: 866- 869, 1995. ; and

[25026] Lu, R.; Kanai, N.; Bao, Y.; Schuster, V. L. : Cloning, in vitro expression, and tissue distribution of a human prostaglandin transporter cDNA (hPGT). J. Clin. Invest. 98: 1142- 1149, 1996.

[25027] Further studies establishing the function and utilities of SLC21A2 are found in John Hopkins OMIM database record ID 601460, and in cited publications listed in Table 5, which are hereby incorporated by reference.Solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 (SLC25A1, Accession NP_005975.1) is another GAM148 target gene, herein designated TARGET GENE.

SLC25A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC25A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC25A1 BINDING SITE, designated SEQ ID:16041, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25028] Another function of GAM148 is therefore inhibition of Solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 (SLC25A1, Accession NP_005975.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC25A1.

[25029] SMO (Accession NP_005622.1) is another GAM148 target gene, herein designated TARGET GENE. SMO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SMO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMO BINDING SITE, designated SEQ ID:19323, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA,

also designated SEQ ID:280.

[25030] Another function of GAM148 is therefore inhibition of SMO (Accession NP_005622.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMO.

[25031] Small nuclear ribonucleoprotein d3 polypeptide 18kda (SNRPD3, Accession NP_004166.1) is another GAM148 target gene, herein designated TARGET GENE. SNRPD3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SNRPD3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNRPD3 BINDING SITE, designated SEQ ID:2958, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25032] Another function of GAM148 is therefore inhibition of Small nuclear ribonucleoprotein d3 polypeptide 18kda (SNRPD3, Accession NP_004166.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNRPD3.

[25033] SNX27 (Accession NP_112180.4) is another GAM148 tar-

get gene, herein designated TARGET GENE. SNX27 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNX27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX27 BINDING SITE, designated SEQ ID:19179, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25034] Another function of GAM148 is therefore inhibition of SNX27 (Accession NP_112180.4) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX27.

[25035] Spondin 1, (f-spondin) extracellular matrix protein (SPON1, Accession NP_006099.1) is another GAM148 target gene, herein designated TARGET GENE. SPON1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPON1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPON1 BINDING SITE, designated SEQ ID:2566, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA,

also designated SEQ ID:280.

[25036] Another function of GAM148 is therefore inhibition of Spondin 1, (f-spondin) extracellular matrix protein (SPON1, Accession NP_006099.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPON1.

[25037] Sprouty homolog 4 (drosophila) (SPRY4, Accession NP_112226.2) is another GAM148 target gene, herein designated TARGET GENE. SPRY4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPRY4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPRY4 BINDING SITE, designated SEQ ID:18907, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25038] Another function of GAM148 is therefore inhibition of Sprouty homolog 4 (drosophila) (SPRY4, Accession NP_112226.2) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPRY4.

[25039] Spectrin, beta, non-erythrocytic 2 (SPTBN2, Accession

NP_008877.1) is another GAM148 target gene, herein designated TARGET GENE. SPTBN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPTBN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPTBN2 BINDING SITE, designated SEQ ID:11121, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25040] Another function of GAM148 is therefore inhibition of Spectrin, beta, non-erythrocytic 2 (SPTBN2, Accession NP_008877.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPTBN2.

[25041] Steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2) (SRD5A2, Accession NP_000339.1) is another GAM148 target gene, herein designated TARGET GENE. SRD5A2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SRD5A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of SRD5A2 BINDING SITE, designated SEQ ID:13219, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25042] Another function of GAM148 is therefore inhibition of Steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2) (SRD5A2, Accession NP_000339.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRD5A2.

[25043] Steroidogenic acute regulatory protein (STAR, Accession NP_000340.1) is another GAM148 target gene, herein designated TARGET GENE. STAR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STAR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAR BINDING SITE, designated SEQ ID:10859, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25044] Another function of GAM148 is therefore inhibition of Steroidogenic acute regulatory protein (STAR, Accession

NP_000340.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAR.

[25045] Synaptotagmin xiii (SYT13, Accession NP_065877.1) is another GAM148 target gene, herein designated TARGET GENE. SYT13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYT13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYT13 BINDING SITE, designated SEQ ID:9376, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25046] Another function of GAM148 is therefore inhibition of Synaptotagmin xiii (SYT13, Accession NP_065877.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT13.

[25047] Tolloid-like 1 (TLL1, Accession NP_036596.3) is another GAM148 target gene, herein designated TARGET GENE. TLL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TLL1, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLL1 BINDING SITE, designated SEQ ID:13124, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25048] Another function of GAM148 is therefore inhibition of Tolloid-like 1 (TLL1, Accession NP_036596.3), a gene which is involved in bone morphogenesis. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLL1.

[25049] The function of TLL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.1.Transmembrane 7 superfamily member 2 (TM7SF2, Accession NP_003264.1) is another GAM148 target gene, herein designated TARGET GENE. TM7SF2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TM7SF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TM7SF2 BINDING SITE, designated SEQ ID:11046, to the

nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25050] Another function of GAM148 is therefore inhibition of Transmembrane 7 superfamily member 2 (TM7SF2, Accession NP_003264.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TM7SF2.

[25051] Tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) (TNFRSF14, Accession NP_003811.2) is another GAM148 target gene, herein designated TARGET GENE. TNFRSF14 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TNFRSF14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF14 BINDING SITE, designated SEQ ID:5580, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25052] Another function of GAM148 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) (TNFRSF14, Accession NP_003811.2), a gene which mediates entry of herpes

simplex virus (HSV). Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF14.

[25053] The function of TNFRSF14 has been established by previous studies. Members of the tumor necrosis factor receptor (TNFR) family play a key role in regulating the immune response to infection (see OMIM Ref. No. TNFR1, 191190). By screening for genes that mediate the entry of herpes simplex virus (HSV) into Chinese hamster ovary (CHO) cells, Montgomery et al. (1996) identified cDNAs encoding a member of the TNFR family. They designated the gene HVEM (herpesvirus entry mediator). The predicted 283-amino acid protein had characteristics of a type I membrane glycoprotein, with an N- terminal signal peptide, 2 potential sites for addition of N- linked glycans, and a putative membrane- spanning domain. Sequence analysis revealed that HVEM contained a cysteine- rich repeat region characteristic of TNFR family members, and shared 17 to 25% amino acid identity with other TNFRs. Montgomery et al. (1996) suggested that HVEM plays an important role in HSV pathogenesis because it enhanced the entry of several wildtype HSV strains of both serotypes into CHO cells, and mediated HSV entry into activated hu-

man T cells. Independently, Kwon et al. (1997) cloned cDNAs encoding HVEM, which they designated TR2. Northern blot analysis revealed that HVEM is expressed as a 1.7- kb mRNA in several tissues, with the highest expression in lung, spleen, and thymus. Several additional larger mRNAs were observed in some tissues and several of the cDNAs contained insertions in the coding region, leading Kwon et al. (1997) to suggest that HVEM is regulated at the level of mRNA maturation. These authors reported that the in vitro translation product was 32 kD by SDS- PAGE. HSV infection requires binding of the viral envelope glycoprotein D (gD) to cell surface receptors. Carfi et al. (2001) reported the x- ray structures of a soluble, truncated ectodomain of gD both alone and in complex with the ectodomain of its cellular receptor, TNFRSF14, which they called HVEA. Two bound anions suggested possible binding sites for another gD receptor, a 3- O- sulfonated heparan sulfate. The structures revealed a V- like immunoglobulin fold at the core of gD that is closely related to cellular adhesion molecules and flanked by large N- and C- terminal extensions. The receptor- binding segment of gD, an N- terminal hairpin, appeared conformationally flexible, suggesting that a conformational change accompanying binding

might be part of the viral entry mechanism.

[25054]

[25055] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25056] Kwon, B. S.; Tan, K. B.; Ni, J.; Oh, K.- O.; Lee, Z. H.; Kim, K. K.; Kim, Y.- J.; Wang, S.; Gentz, R.; Yu, G.- L.; Harrop, J.; Lyn, S. D.; Silverman, C.; Porter, T. G.; Truneh, A.; Young, P. R. : A newly identified member of the tumor necrosis factor receptor superfamily with a wide tissue distribution and involvement in lymphocyte activation. J. Biol. Chem. 272: 14272- 14276, 1997. ; and

[25057] Carfi, A.; Willis, S. H.; Whitbeck, J. C.; Krummenacher, C.; Cohen, G. H.; Eisenberg, R. J.; Wiley, D. C. : Herpes sim- plex virus glycoprotein D bound to the human receptor HveA. Molec.

[25058] Further studies establishing the function and utilities of TNFRSF14 are found in John Hopkins OMIM database record ID 602746, and in cited publications listed in Table 5, which are hereby incorporated by reference.Tankyrase 1 binding protein 1, 182kda (TNKS1BP1, Accession NP_203754.1) is another GAM148 target gene, herein designated TARGET GENE. TNKS1BP1 BINDING SITE is a

target binding site found in the 5` untranslated region of mRNA encoded by TNKS1BP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNKS1BP1 BINDING SITE, designated SEQ ID:5658, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25059] Another function of GAM148 is therefore inhibition of Tankyrase 1 binding protein 1, 182kda (TNKS1BP1, Accession NP_203754.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNKS1BP1.

[25060] TPCN1 (Accession NP_060371.2) is another GAM148 target gene, herein designated TARGET GENE. TPCN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TPCN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPCN1 BINDING SITE, designated SEQ ID:3418, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25061] Another function of GAM148 is therefore inhibition of TPCN1 (Accession NP_060371.2) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TPCN1.

[25062] Tnfrsf1a-associated via death domain (TRADD, Accession NP_700474.1) is another GAM148 target gene, herein designated TARGET GENE. TRADD BINDING SITE1 and TRADD BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRADD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRADD BINDING SITE1 and TRADD BINDING SITE2, designated SEQ ID:3225 and SEQ ID:605 respectively, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25063] Another function of GAM148 is therefore inhibition of Tnfrsf1a-associated via death domain (TRADD, Accession NP_700474.1), a gene which specifically interacts with the cytoplasmic domain of activated tnfr1. interacts with trafs (traf1 and traf2), fadd and rip. acts as an adaptor molecule for tnfr1 mediating its interaction with fadd.

overexpression of tradd leads to two major tnf- induced responses, apoptosis and activation of nf- kappa b. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRADD.

[25064] The function of TRADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.TRAP240 (Accession NP_005112.1) is another GAM148 target gene, herein designated TARGET GENE. TRAP240 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TRAP240, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAP240 BINDING SITE, designated SEQ ID:596, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25065] Another function of GAM148 is therefore inhibition of TRAP240 (Accession NP_005112.1), a gene which Subunit of TRAP thyroid hormone receptor- associated protein complex; coactivator for nuclear receptors. Accordingly, utilities of GAM148 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with TRAP240.

[25066] The function of TRAP240 has been established by previous studies. For background information on thyroid hormone receptor- associated proteins (TRAPs), see 300182. Using a HeLa cell line, Ito et al. (1999) cloned TRAP240, the gene encoding the 240- kD subunit of the TRAP complex. The TRAP240 cDNA encodes a 2,174- amino acid protein that shows a regional identity of 29% and a similarity of 46% with a hypothetical C. elegans protein (CEK08F8 and CEF07H5). It shows no obvious relationship with known consensus sequences, other than 2 ligand-dependent nuclear hormone receptor signature recognition motifs (LXXLL sequences) at positions 1188- 1192 and 1279- 1283, and a short leucine zipper at position 1331- 1352. Northern blot analysis of multiple human tissues showed that the TRAP240 gene is ubiquitously expressed as an approximately 11.5- kb transcript. Nagase et al. (1998) also cloned the cDNA encoding TRAP240, which they referred to as KIAA0593, from a human brain cDNA library. By analysis of a human- rodent hybrid panel, Nagase et al. (1998) mapped the TRAP240 gene to chromosome 17

[25067]

[25068] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25069] Ito, M.; Yuan, C.- X.; Malik, S.; Gu, W.; Fondell, J. D.; Yamamura, S.; Fu, Z.- Y.; Zhang, X.; Qin, J.; Roeder, R. G. : Identity between TRAP and SMCC complexes indicates novel pathways for the function of nuclear receptors and diverse mammalian activators. Molec. Cell 3: 361- 370, 1999. ; and

[25070] Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. : Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100.

[25071] Further studies establishing the function and utilities of TRAP240 are found in John Hopkins OMIM database record ID 603808, and in cited publications listed in Table 5, which are hereby incorporated by reference.Three prime repair exonuclease 1 (TREX1, Accession NP_338598.1) is another GAM148 target gene, herein designated TARGET GENE. TREX1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TREX1, correspond-

ing to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TREX1 BINDING SITE, designated SEQ ID:6080, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25072] Another function of GAM148 is therefore inhibition of Three prime repair exonuclease 1 (TREX1, Accession NP_338598.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TREX1.

[25073] Translin (TSN, Accession NP_004613.1) is another GAM148 target gene, herein designated TARGET GENE. TSN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TSN BINDING SITE, designated SEQ ID:15704, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25074] Another function of GAM148 is therefore inhibition of Translin (TSN, Accession NP_004613.1), a gene which is a

DNA binding protein and involved in DNA repair, replication, or recombination. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSN.

[25075] The function of TSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Ubiquitin associated protein 2 (UBAP2, Accession NP_680476.1) is another GAM148 target gene, herein designated TARGET GENE. UBAP2 BINDING SITE1 and UBAP2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by UBAP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBAP2 BINDING SITE1 and UBAP2 BINDING SITE2, designated SEQ ID:3406 and SEQ ID:6591 respectively, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25076] Another function of GAM148 is therefore inhibition of Ubiquitin associated protein 2 (UBAP2, Accession NP_680476.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with UBAP2.

[25077] Udp glycosyltransferase 2 family, polypeptide b4 (UGT2B4, Accession NP_066962.1) is another GAM148 target gene, herein designated TARGET GENE. UGT2B4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT2B4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT2B4 BINDING SITE, designated SEQ ID:8980, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25078] Another function of GAM148 is therefore inhibition of Udp glycosyltransferase 2 family, polypeptide b4 (UGT2B4, Accession NP_066962.1), a gene which is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds. Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT2B4.

[25079] The function of UGT2B4 has been established by previous studies. The UDP- glucuronosyltransferases, a group of isoenzymes located primarily in hepatic endoplasmic

reticulum and nuclear envelope, are encoded by a large multigene family that has evolved to produce catalysts with differing but overlapping substrate specificities. Two subfamilies are recognized by sequence identities (Burchell et al., 1991). UGT1 consists of at least 4 isoenzymes that catalyze the glucuronidation of phenols and bilirubin. All 4 map to chromosome 2 and probably derive from the same gene (UGT1; 191740). The UGT2 family contains at least 5 members catalyzing steroid or bile acid glucuronidation. Members of the subfamily share 65 to 90% amino acid sequence identity. However, unlike the phenol UGT cDNAs, where the high degree of identity is concentrated in the 3- prime region of the cDNA, the steroid UGTs have a high degree of sequence homology throughout the cDNA. Riedy et al. (2000) examined a genomic map spanning approximately 500 to 1000 kb in the 4q13 region. They placed UGT2B4 between UGT2B7 and UGT2B15. Also, access to a large reference DNA bank allowed them to calculate the allele frequencies for a single nucleotide polymorphism (SNP), Q458D, in UGT2B4 among 803 unrelated individuals representing 5 ethnic populations. The findings suggested a recent evolutionary history of gene duplication, mutation, and rearrangement.

[25080]

[25081] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25082] Burchell, B.; Nebert, D. W.; Nelson, D. R.; Bock, K. W.; Iyanagi, T.; Jansen, P. L. M.; Lancet, T.; Mulder, G. J.; Chowdhury, J. R.; Siest, G.; Tephly, T. R.; Mackenzie, P. I. : The UDP- glucuronosyltransferase gene superfamily: suggested nomenclature based on evolutionary divergence. DNA Cell Biol. 10: 487- 494, 1991. ; and

[25083] Riedy, M.; Wang, J. Y.; Miller, A. P.; Buckler, A.; Hall, J.; Guida, M. : Genomic organization of the UGT2b gene cluster on human chromosome 4q13. Pharmacogenetics 10: 251- 260, 2000.

[25084] Further studies establishing the function and utilities of UGT2B4 are found in John Hopkins OMIM database record ID 600067, and in cited publications listed in Table 5, which are hereby incorporated by reference.X-prolyl aminopeptidase (aminopeptidase p) 2, membrane-bound (XPNPEP2, Accession NP_003390.2) is another GAM148 target gene, herein designated TARGET GENE. XPNPEP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by XPNPEP2, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of XPNPEP2 BINDING SITE, designated SEQ ID:966, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25085] Another function of GAM148 is therefore inhibition of X-prolyl aminopeptidase (aminopeptidase p) 2, membrane-bound (XPNPEP2, Accession NP_003390.2), a gene which is a membrane- associated X- prolyl metallopeptidase . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XPNPEP2.

[25086] The function of XPNPEP2 has been established by previous studies. Aminopeptidase P is a widely distributed hydrolase that is specific for N- terminal imido bonds, which are common to several collagen degradation products, neuropeptides, vasoactive peptides, and cytokines. Structurally, the enzyme is a member of the 'pita bread fold' family and occurs in mammalian tissues in both soluble and GPI- anchored membrane- bound forms. By RT- PCR using degenerate oligonucleotides based on the pig aminopeptidase P amino acid sequence, and by 5- prime

and 3- prime RACE, Venema et al. (1997) isolated human kidney and lung cDNAs encoding XPNPEP2. The deduced XPNPEP2 protein has 673 amino acids and an estimated molecular mass of 75,490 Da. The authors stated that the human and pig XPNPEP2 amino acid sequences show significant evolutionary divergence, with 83% identity; 5 of 6 potential N- glycosylation sites, and 5 of 6 cysteine residues that are potentially involved in disulfide bond formation, are conserved. Northern blot analysis detected a 3.5- kb XPNPEP2 transcript in human kidney, lung, heart, placenta, liver, small intestine, and colon, but not in brain, skeletal muscle, pancreas, spleen, thymus, prostate, testis, ovary, or leukocytes. Based on these results and on RT- PCR studies, Venema et al. (1997) suggested that the membrane- bound form and the soluble form, which is found in brain and leukocytes, are the products of 2 different genes or of alternative splicing of a single primary transcript. Women with balanced translocations between the long arm of the X chromosome and an autosome frequently suffer premature ovarian failure (POF; 311360). Two critical regions for POF which extend from Xq13 to Xq22 and from Xq22 to Xq26 have been identified by cytogenetic studies. To gain insight into the mechanism(s)

responsible for ovarian failure in women with X/autosome translocations, Prueitt et al. (2000) molecularly characterized the translocation breakpoints of 9 X chromosomes. They mapped the breakpoints using somatic cell hybrids retaining the derivative autosome and densely spaced markers from the X- chromosome physical map. One of the POF- associated breakpoints in a critical region (Xq25) mapped to a sequenced PAC clone. The translocation disrupts XPNPEP2. XPNPEP2 mRNA was detected in fibroblasts that carried the translocation, suggesting that this gene at least partially escapes X inactivation. Although the physiologic substrates for the enzyme were not known, Prueitt et al. (2000) suggested that XPNPEP2 is a candidate gene for POF.

[25087]

[25088] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25089] Venema, R. C.; Ju, H.; Zou, R.; Venema, V. J.; Ryan, J. W. : Cloning and tissue distribution of human membrane-bound aminopeptidase P. Biochim. Biophys. Acta 1354: 45- 48, 1997. ; and

[25090] Prueitt, R. L.; Ross, J. L.; Zinn, A. R. : Physical mapping of

nine Xq translocation breakpoints and identification of XPNPEP2 as a premature ovarian failure candidate gene. Cytogenet.

[25091] Further studies establishing the function and utilities of XPNPEP2 are found in John Hopkins OMIM database record ID 300145, and in cited publications listed in Table 5, which are hereby incorporated by reference.Zinc finger protein 91 homolog (mouse) (ZFP91, Accession NP_739574.1) is another GAM148 target gene, herein designated TARGET GENE. ZFP91 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP91, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP91 BINDING SITE, designated SEQ ID:15418, to the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, also designated SEQ ID:280.

[25092] Another function of GAM148 is therefore inhibition of Zinc finger protein 91 homolog (mouse) (ZFP91, Accession NP_739574.1) . Accordingly, utilities of GAM148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP91.

[25093]

[25094] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 149 (GAM149), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25095] GAM149 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM149 was detected is described hereinabove with reference to Figs. 8-15.

[25096] GAM149 gene, herein designated GAM GENE, and GAM149 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25097] GAM149 gene encodes a GAM149 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM149 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM149 precursor RNA is designated SEQ ID:146, and is provided hereinbelow with reference to the sequence listing part.

[25098] GAM149 precursor RNA folds onto itself, forming GAM149

folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25099] GAM149 precursor RNA folds onto itself, forming GAM149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25100] Nucleotide sequence of GAM149 precursor RNA, designated SEQ-ID: 146, and a schematic representation of a predicted secondary folding of GAM149 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25101] An enzyme complex designated DICER COMPLEX, `dices`

the GAM149 folded precursor RNA into GAM149 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM149 RNA is designated SEQ ID:237, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25102] GAM149 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM149 target RNA, herein designated GAM TARGET RNA. GAM149 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25103] GAM149 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM149 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM149

RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM149 RNA may have a different number of target binding sites in untranslated regions of a GAM149 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25104] The complementary binding of GAM149 RNA, herein designated GAM RNA, to target binding sites on GAM149 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM149 target RNA into GAM149 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25105] It is appreciated that GAM149 target gene, herein designated TARGET GENE, in fact represents a plurality of

GAM149 target genes. The mRNA of each one of this plurality of GAM149 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM149 RNA, herein designated GAM RNA, and which when bound by GAM149 RNA causes inhibition of translation of respective one or more GAM149 target proteins.

[25106] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM149 gene, herein designated GAM GENE, on one or more GAM149 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25107] It is appreciated that specific functions and accordingly utilities of GAM149 correlate with, and may be deduced from, the identity of the target genes which GAM149 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25108]

[25109]

[25110] Centaurin, gamma 1 (CENTG1, Accession NM_014770.1) is a GAM149 target gene, herein designated TARGET GENE. CENTG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CENTG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENTG1 BINDING SITE, designated SEQ ID:18082, to the nucleotide sequence of GAM149 RNA, herein designated GAM RNA, also designated SEQ ID:237.

[25111] A function of GAM149 is therefore inhibition of Centaurin, gamma 1 (CENTG1, Accession NM_014770.1) . Accordingly, utilities of GAM149 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with CENTG1.

[25112] LCHN (Accession XM_098615.2) is another GAM149 target gene, herein designated TARGET GENE. LCHN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCHN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCHN BINDING SITE, designated SEQ ID:6008, to the nucleotide sequence of GAM149 RNA, herein designated GAM RNA, also designated SEQ ID:237.

[25113] Another function of GAM149 is therefore inhibition of LCHN (Accession XM_098615.2) . Accordingly, utilities of GAM149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCHN.

[25114] Leptin receptor overlapping transcript-like 1 (LEPROTL1, Accession NM_015344.1) is another GAM149 target gene, herein designated TARGET GENE. LEPROTL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LEPROTL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LEPROTL1

BINDING SITE, designated SEQ ID:8728, to the nucleotide sequence of GAM149 RNA, herein designated GAM RNA, also designated SEQ ID:237.

[25115] Another function of GAM149 is therefore inhibition of Leptin receptor overlapping transcript-like 1 (LEPROTL1, Accession NM_015344.1) . Accordingly, utilities of GAM149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LEP-ROTL1.

[25116] LOC203286 (Accession) is another GAM149 target gene, herein designated TARGET GENE. LOC203286 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC203286, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC203286 BINDING SITE, designated SEQ ID:5131, to the nucleotide sequence of GAM149 RNA, herein designated GAM RNA, also designated SEQ ID:237.

[25117] Another function of GAM149 is therefore inhibition of LOC203286 (Accession) . Accordingly, utilities of GAM149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC203286.

[25118]

[25119] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 150 (GAM150), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25120] GAM150 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM150 was detected is described hereinabove with reference to Figs. 8-15.

[25121] GAM150 gene, herein designated GAM GENE, and GAM150 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25122] GAM150 gene encodes a GAM150 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM150 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM150 precursor RNA is designated SEQ ID:6, and is provided hereinbelow with reference to the sequence listing part.

[25123] GAM150 precursor RNA folds onto itself, forming GAM150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25124] GAM150 precursor RNA folds onto itself, forming GAM150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25125] Nucleotide sequence of GAM150 precursor RNA, designated SEQ-ID: 6, and a schematic representation of a predicted secondary folding of GAM150 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25126] An enzyme complex designated DICER COMPLEX, `dices` the GAM150 folded precursor RNA into GAM150 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM150 RNA is designated SEQ ID:261, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25127] GAM150 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM150 target RNA, herein designated GAM TARGET RNA. GAM150 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25128] GAM150 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM150 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM150 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM150 RNA may have a different number of target binding sites in untranslated regions of a GAM150 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25129] The complementary binding of GAM150 RNA, herein designated GAM RNA, to target binding sites on GAM150 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM150 target RNA into GAM150 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25130] It is appreciated that GAM150 target gene, herein desig-

nated TARGET GENE, in fact represents a plurality of GAM150 target genes. The mRNA of each one of this plurality of GAM150 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM150 RNA, herein designated GAM RNA, and which when bound by GAM150 RNA causes inhibition of translation of respective one or more GAM150 target proteins.

[25131] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM150 gene, herein designated GAM GENE, on one or more GAM150 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[25132] It is appreciated that specific functions and accordingly utilities of GAM150 correlate with, and may be deduced from, the identity of the target genes which GAM150 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25133]

[25134]

[25135] Death-associated protein kinase 1 (DAPK1, Accession NM_004938.1) is a GAM150 target gene, herein designated TARGET GENE. DAPK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DAPK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DAPK1 BINDING SITE, designated SEQ ID:11771, to the nucleotide sequence of GAM150 RNA, herein designated GAM RNA, also designated SEQ ID:261.

[25136] A function of GAM150 is therefore inhibition of Death-associated protein kinase 1 (DAPK1, Accession NM_004938.1) . Accordingly, utilities of GAM150 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with DAPK1.

[25137] LOC128008 (Accession) is another GAM150 target gene, herein designated TARGET GENE. LOC128008 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC128008, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC128008 BINDING SITE, designated SEQ ID:16098, to the nucleotide sequence of GAM150 RNA, herein designated GAM RNA, also designated SEQ ID:261.

[25138] Another function of GAM150 is therefore inhibition of LOC128008 (Accession) . Accordingly, utilities of GAM150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128008.

[25139] LOC221399 (Accession XM_168134.1) is another GAM150 target gene, herein designated TARGET GENE. LOC221399 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221399, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC221399 BINDING SITE, designated SEQ ID:14194, to the nucleotide sequence of GAM150 RNA, herein designated GAM RNA, also designated SEQ ID:261.

[25140] Another function of GAM150 is therefore inhibition of LOC221399 (Accession XM_168134.1) . Accordingly, utilities of GAM150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221399.

[25141] LOC253216 (Accession XM_170765.2) is another GAM150 target gene, herein designated TARGET GENE. LOC253216 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC253216, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253216 BINDING SITE, designated SEQ ID:10298, to the nucleotide sequence of GAM150 RNA, herein designated GAM RNA, also designated SEQ ID:261.

[25142] Another function of GAM150 is therefore inhibition of LOC253216 (Accession XM_170765.2) . Accordingly, utilities of GAM150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC253216.

[25143] Solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10, Accession NM_030777.2) is another GAM150 target gene, herein designated TARGET GENE. SLC2A10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC2A10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC2A10 BINDING SITE, designated SEQ ID:1592, to the nucleotide sequence of GAM150 RNA, herein designated GAM RNA, also designated SEQ ID:261.

[25144] Another function of GAM150 is therefore inhibition of Solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10, Accession NM_030777.2) . Accordingly, utilities of GAM150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC2A10.

[25145]

[25146] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 151 (GAM151), which modulates expression of respective tar-

get genes thereof, the function and utility of which target genes is known in the art.

[25147] GAM151 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM151 was detected is described hereinabove with reference to Figs. 8-15.

[25148] GAM151 gene, herein designated GAM GENE, and GAM151 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25149] GAM151 gene encodes a GAM151 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM151 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM151 precursor RNA is designated SEQ ID:71, and is provided hereinbelow with reference to the sequence listing part.

[25150] GAM151 precursor RNA folds onto itself, forming GAM151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25151] GAM151 precursor RNA folds onto itself, forming GAM151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25152] Nucleotide sequence of GAM151 precursor RNA, designated SEQ-ID: 71, and a schematic representation of a predicted secondary folding of GAM151 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25153] An enzyme complex designated DICER COMPLEX, `dices` the GAM151 folded precursor RNA into GAM151 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM151 RNA is designated SEQ ID:205, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25154] GAM151 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM151 target RNA, herein designated GAM TARGET RNA. GAM151 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25155] GAM151 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM151 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM151 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated

that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM151 RNA may have a different number of target binding sites in untranslated regions of a GAM151 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25156] The complementary binding of GAM151 RNA, herein designated GAM RNA, to target binding sites on GAM151 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM151 target RNA into GAM151 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25157] It is appreciated that GAM151 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM151 target genes. The mRNA of each one of this plurality of GAM151 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM151 RNA, herein designated GAM RNA, and which when bound by

GAM151 RNA causes inhibition of translation of respective one or more GAM151 target proteins.

[25158] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM151 gene, herein designated GAM GENE, on one or more GAM151 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25159] It is appreciated that specific functions and accordingly utilities of GAM151 correlate with, and may be deduced from, the identity of the target genes which GAM151 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25160]

[25161]

[25162] LOC151816 (Accession) is a GAM151 target gene, herein designated TARGET GENE. LOC151816 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151816, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151816 BINDING SITE, designated SEQ ID:12621, to the nucleotide sequence of GAM151 RNA, herein designated GAM RNA, also designated SEQ ID:205.

[25163] A function of GAM151 is therefore inhibition of LOC151816 (Accession) . Accordingly, utilities of GAM151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151816.

[25164]

[25165] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 152 (GAM152), which modulates expression of respective tar-

get genes thereof, the function and utility of which target genes is known in the art.

[25166] GAM152 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM152 was detected is described hereinabove with reference to Figs. 8-15.

[25167] GAM152 gene, herein designated GAM GENE, and GAM152 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25168] GAM152 gene encodes a GAM152 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM152 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM152 precursor RNA is designated SEQ ID:52, and is provided hereinbelow with reference to the sequence listing part.

[25169] GAM152 precursor RNA folds onto itself, forming GAM152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25170] GAM152 precursor RNA folds onto itself, forming GAM152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25171] Nucleotide sequence of GAM152 precursor RNA, designated SEQ-ID: 52, and a schematic representation of a predicted secondary folding of GAM152 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25172] An enzyme complex designated DICER COMPLEX, `dices` the GAM152 folded precursor RNA into GAM152 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM152 RNA is designated SEQ ID:378, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25173] GAM152 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM152 target RNA, herein designated GAM TARGET RNA. GAM152 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25174] GAM152 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM152 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM152 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated

that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM152 RNA may have a different number of target binding sites in untranslated regions of a GAM152 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25175] The complementary binding of GAM152 RNA, herein designated GAM RNA, to target binding sites on GAM152 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM152 target RNA into GAM152 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25176] It is appreciated that GAM152 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM152 target genes. The mRNA of each one of this plurality of GAM152 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM152 RNA, herein designated GAM RNA, and which when bound by

GAM152 RNA causes inhibition of translation of respective one or more GAM152 target proteins.

[25177] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM152 gene, herein designated GAM GENE, on one or more GAM152 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25178] It is appreciated that specific functions and accordingly utilities of GAM152 correlate with, and may be deduced from, the identity of the target genes which GAM152 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25179]

[25180]

[25181] Annexin a7 (ANXA7, Accession NM_001156.2) is a GAM152 target gene, herein designated TARGET GENE. ANXA7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ANXA7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANXA7 BINDING SITE, designated SEQ ID:7738, to the nucleotide sequence of GAM152 RNA, herein designated GAM RNA, also designated SEQ ID:378.

[25182] A function of GAM152 is therefore inhibition of Annexin a7 (ANXA7, Accession NM_001156.2), a gene which promotes membrane fusion and is involved in exocytosis. and therefore may be associated with Prostate cancer. Accordingly, utilities of GAM152 include diagnosis, prevention and treatment of Prostate cancer, and of other diseases and clinical conditions associated with ANXA7.

[25183] The function of ANXA7 has been established by previous studies. The ANX7 gene is located on chromosome 10q21, a site long hypothesized to harbor a tumor sup-

pressor gene or genes associated with prostate and other cancers. To test this hypothesis, Srivastava et al. (2001) analyzed the action of the ANX7 gene on colony formation by human tumor cell lines. They also examined the expression of the ANX7 protein in a large number of prostate cancers using tumor tissue microarray technology. Finally, they tested a panel of primary and metastatic prostate cancers for evidence of loss of heterozygosity (LOH). They found that human tumor cell proliferation and colony formation were markedly reduced when the wild-type ANX7 gene was transfected into 2 prostate tumor cell lines. Consistently, analysis of ANX7 protein expression in human prostate tumor microarrays revealed a significantly higher rate of loss of ANX7 expression in metastatic and local recurrences of hormone refractory prostate cancer as compared with primary tumors ($P = 0.0001$). Using 4 microsatellite markers at or near the ANX7 locus and laser capture microdissected tumor cells, 35% of 20 primary prostate tumors showed LOH. The microsatellite marker closest to the ANX7 locus showed the highest rate of LOH, including 1 homozygous deletion. Srivastava et al. (2001) concluded that the ANX7 gene exhibits many biologic and genetic properties expected of a tumor suppressor gene

and may play a role in prostate cancer progression.

[25184] Animal model experiments lend further support to the function of ANXA7. By gene targeting, Srivastava et al. (1999) developed Anxa7- null mice. The null phenotype was lethal at embryonic day 10. Heterozygous mice were viable and fertile, but showed a defect in insulin secretion and an increased insulin content within isolated pancreatic islets. Electrooptical recordings suggested that the mutation altered Ca(2+) release by agonists of inositol trisphosphate. Using mice with a different genetic background and an alternate strategy to introduce the null mutation, Herr et al. (2001) developed Anxa7 - /- mice that were viable, fertile, and showed no obvious defects. Analysis of insulin secretion from isolated islets revealed no evidence for the involvement of Anxa7 in Ca(2+)- dependent or cAMP- mediated exocytosis. In cardiomyocytes, however, they found a functional role for Anxa7 in electromechanical coupling. Cardiomyocytes from embryonic Anxa7- null mice displayed intact Ca(2+) homeostasis and unremarkable excitation- contraction coupling; however, adult Anxa7 - /- mice exhibited a decrease in frequency- induced cell shortening.

[25185] It is appreciated that the abovementioned animal model

for ANXA7 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[25186] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25187] Srivastava, M.; Atwater, I.; Glasman, M.; Leighton, X.; Goping, G.; Caohuy, H.; Miller, G.; Pichel, J.; Westphal, H.; Mears, D.; Rojas, E.; Pollard, H. B. : Defects in inositol 1,4,5- trisphosphate receptor expression, Ca(2+) signaling, and insulin secretion in the anx7(+/-) knockout mouse. Proc. Nat. Acad. Sci. 96: 13783- 13788, 1999. ; and

[25188] Srivastava, M.; Bubendorf, L.; Srikantan, V.; Fossom, L.; Nolan, L.; Glasman, M.; Leighton, X.; Fehrle, W.; Pittaluga, S.; Raffeld, M.; Koivisto, P.; Willi, N.; Gasser, T. C.; Kononen.

[25189] Further studies establishing the function and utilities of ANXA7 are found in John Hopkins OMIM database record ID 186360, and in cited publications listed in Table 5, which are hereby incorporated by reference.Calsenilin, presenilin binding protein, ef hand transcription factor (CSEN, Accession NM_013434.3) is another GAM152 tar-

get gene, herein designated TARGET GENE. CSEN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CSEN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSEN BINDING SITE, designated SEQ ID:13661, to the nucleotide sequence of GAM152 RNA, herein designated GAM RNA, also designated SEQ ID:378.

[25190] Another function of GAM152 is therefore inhibition of Calsenilin, presenilin binding protein, ef hand transcription factor (CSEN, Accession NM_013434.3) . Accordingly, utilities of GAM152 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSEN.

[25191] Neuroligin 1 (NLGN1, Accession NM_014932.1) is another GAM152 target gene, herein designated TARGET GENE. NLGN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NLGN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NLGN1 BINDING SITE, designated SEQ ID:6771, to the

nucleotide sequence of GAM152 RNA, herein designated GAM RNA, also designated SEQ ID:378.

[25192] Another function of GAM152 is therefore inhibition of Neuroligin 1 (NLGN1, Accession NM_014932.1), a gene which may trigger the de novo formation of presynaptic structure. Accordingly, utilities of GAM152 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NLGN1.

[25193] The function of NLGN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM90.1.

[25194] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 153 (GAM153), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25195] GAM153 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM153 was detected is described hereinabove with reference to Figs. 8-15.

[25196] GAM153 gene, herein designated GAM GENE, and

GAM153 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25197] GAM153 gene encodes a GAM153 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM153 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM153 precursor RNA is designated SEQ ID:186, and is provided hereinbelow with reference to the sequence listing part.

[25198] GAM153 precursor RNA folds onto itself, forming GAM153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25199] GAM153 precursor RNA folds onto itself, forming GAM153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin struc-

ture`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25200] Nucleotide sequence of GAM153 precursor RNA, designated SEQ-ID: 186, and a schematic representation of a predicted secondary folding of GAM153 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25201] An enzyme complex designated DICER COMPLEX, `dices` the GAM153 folded precursor RNA into GAM153 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM153 RNA is designated SEQ ID:244, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25202] GAM153 target gene, herein designated TARGET GENE,

encodes a corresponding messenger RNA, GAM153 target RNA, herein designated GAM TARGET RNA. GAM153 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25203] GAM153 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM153 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM153 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM153 RNA may have a different number of target binding sites in untranslated regions of a GAM153 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25204] The complementary binding of GAM153 RNA, herein designated GAM RNA, to target binding sites on GAM153 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM153 target RNA into GAM153 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25205] It is appreciated that GAM153 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM153 target genes. The mRNA of each one of this plurality of GAM153 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM153 RNA, herein designated GAM RNA, and which when bound by GAM153 RNA causes inhibition of translation of respective one or more GAM153 target proteins.

[25206] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM153 gene, herein designated GAM GENE, on one or more GAM153 target genes, herein collectively designated

TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25207] It is appreciated that specific functions and accordingly utilities of GAM153 correlate with, and may be deduced from, the identity of the target genes which GAM153 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25208]

[25209]

[25210] Dna-damage-inducible transcript 3 (DDIT3, Accession NM_004083.2) is a GAM153 target gene, herein designated TARGET GENE. DDIT3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA en-

coded by DDIT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDIT3 BINDING SITE, designated SEQ ID:6855, to the nucleotide sequence of GAM153 RNA, herein designated GAM RNA, also designated SEQ ID:244.

[25211] A function of GAM153 is therefore inhibition of Dna-damage-inducible transcript 3 (DDIT3, Accession NM_004083.2), a gene which May be a transcription factor and inhibits the DNA- binding activity of C/EBP and LAP and therefore may be associated with Myxoid liposarcoma . Accordingly, utilities of GAM153 include diagnosis, prevention and treatment of Myxoid liposarcoma ., and of other diseases and clinical conditions associated with DDIT3.

[25212] The function of DDIT3 has been established by previous studies. CHOP is consistently rearranged in myxoid liposarcomas (Aman et al., 1992). In the characteristic chromosomal translocation t(12;16)(q13;p11), Crozat et al. (1993) showed that the CHOP gene is fused with a gene on chromosome 16 provisionally designated TLS (for 'translocated in liposarcoma'). The same gene was called FUS by Rabbitts et al. (1993); see 137070. The TLS gene

was found to be a novel nuclear RNA- binding protein with extensive sequence similarity to EWS (OMIM Ref. No. 133450), the product of a gene commonly translocated in Ewing sarcoma. In TLS- CHOP, the RNA- binding domain of TLS is replaced by the DNA- binding and leucine zipper dimerization domain of CHOP. Targeting of a conserved effector domain of RNA- binding proteins to DNA may play a role in tumor formation. In an analysis of peripheral blood samples from 19 patients with myxoid liposarcoma due to t(12;16) and in 1 patient with myxoid liposarcoma due to t(12;22;20), resulting in the fusion of the CHOP and EWS genes, Panagopoulos et al. (1996) found FUS/ CHOP hybrid fragments in 3 patients with t(12;16) and a EWS/CHOP hybrid in the patient with the latter translocation.

[25213]

[25214] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25215] Crozat, A.; Aman, P.; Mandahl, N.; Ron, D. : Fusion of CHOP to a novel RNA- binding protein in human myxoid liposarcoma. Nature 363: 640- 644, 1993. ; and

[25216] Panagopoulos, I.; Aman, P.; Mertens, F.; Mandahl, N.; Ryd-

holm, A.; Bauer, H. F. C.; Mitelman, F. : Genomic PCR detects tumor cells in peripheral blood from patients with myxoid liposarco.

[25217] Further studies establishing the function and utilities of DDIT3 are found in John Hopkins OMIM database record ID 126337, and in cited publications listed in Table 5, which are hereby incorporated by reference.

[25218] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 154 (GAM154), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25219] GAM154 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM154 was detected is described hereinabove with reference to Figs. 8-15.

[25220] GAM154 gene, herein designated GAM GENE, and GAM154 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25221] GAM154 gene encodes a GAM154 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM154 precur-

sor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM154 precursor RNA is designated SEQ ID:176, and is provided hereinbelow with reference to the sequence listing part.

[25222] GAM154 precursor RNA folds onto itself, forming GAM154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25223] GAM154 precursor RNA folds onto itself, forming GAM154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25224] Nucleotide sequence of GAM154 precursor RNA, designated SEQ-ID: 176, and a schematic representation of a predicted secondary folding of GAM154 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25225] An enzyme complex designated DICER COMPLEX, `dices` the GAM154 folded precursor RNA into GAM154 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM154 RNA is designated SEQ ID:228, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25226] GAM154 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM154 target RNA, herein designated GAM TARGET RNA. GAM154 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[25227] GAM154 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM154 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM154 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM154 RNA may have a different number of target binding sites in untranslated regions of a GAM154 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25228] The complementary binding of GAM154 RNA, herein designated GAM RNA, to target binding sites on GAM154 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM154 target RNA into GAM154 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25229] It is appreciated that GAM154 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM154 target genes. The mRNA of each one of this plurality of GAM154 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM154 RNA, herein designated GAM RNA, and which when bound by GAM154 RNA causes inhibition of translation of respective one or more GAM154 target proteins.

[25230] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM154 gene, herein designated GAM GENE, on one or more GAM154 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25231] It is appreciated that specific functions and accordingly utilities of GAM154 correlate with, and may be deduced from, the identity of the target genes which GAM154 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25232]

[25233]

[25234] HSZFP36 (Accession XM_290868.1) is a GAM154 target gene, herein designated TARGET GENE. HSZFP36 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HSZFP36, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSZFP36 BINDING SITE, designated SEQ ID:3168, to the nucleotide sequence of GAM154 RNA, herein designated GAM RNA,

also designated SEQ ID:228.

[25235] A function of GAM154 is therefore inhibition of HSZFP36 (Accession XM_290868.1) . Accordingly, utilities of GAM154 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSZFP36.

[25236] LOC257541 (Accession) is another GAM154 target gene, herein designated TARGET GENE. LOC257541 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC257541, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC257541 BINDING SITE, designated SEQ ID:9823, to the nucleotide sequence of GAM154 RNA, herein designated GAM RNA, also designated SEQ ID:228.

[25237] Another function of GAM154 is therefore inhibition of LOC257541 (Accession) . Accordingly, utilities of GAM154 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257541.

[25238]

[25239] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, re-

ferred to here as Genomic Address Messenger 155 (GAM155), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25240] GAM155 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM155 was detected is described hereinabove with reference to Figs. 8-15.

[25241] GAM155 gene, herein designated GAM GENE, and GAM155 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25242] GAM155 gene encodes a GAM155 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM155 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM155 precursor RNA is designated SEQ ID:26, and is provided hereinbelow with reference to the sequence listing part.

[25243] GAM155 precursor RNA folds onto itself, forming GAM155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin struc-

ture`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25244] GAM155 precursor RNA folds onto itself, forming GAM155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25245] Nucleotide sequence of GAM155 precursor RNA, designated SEQ-ID: 26, and a schematic representation of a predicted secondary folding of GAM155 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25246] An enzyme complex designated DICER COMPLEX, `dices` the GAM155 folded precursor RNA into GAM155 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM155 RNA is designated SEQ ID:207, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25247] GAM155 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM155 target RNA, herein designated GAM TARGET RNA. GAM155 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25248] GAM155 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM155 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM155 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such

target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM155 RNA may have a different number of target binding sites in untranslated regions of a GAM155 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25249] The complementary binding of GAM155 RNA, herein designated GAM RNA, to target binding sites on GAM155 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM155 target RNA into GAM155 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25250] It is appreciated that GAM155 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM155 target genes. The mRNA of each one of this plurality of GAM155 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM155 RNA, herein designated GAM RNA, and which when bound by GAM155 RNA causes inhibition of translation of respective one or more GAM155 target proteins.

[25251] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM155 gene, herein designated GAM GENE, on one or more GAM155 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25252] It is appreciated that specific functions and accordingly utilities of GAM155 correlate with, and may be deduced from, the identity of the target genes which GAM155

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25253]

[25254]

[25255] DKFZp761O17121 (Accession) is a GAM155 target gene, herein designated TARGET GENE. DKFZp761O17121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761O17121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761O17121 BINDING SITE, designated SEQ ID:18570, to the nucleotide sequence of GAM155 RNA, herein designated GAM RNA, also designated SEQ ID:207.

[25256] A function of GAM155 is therefore inhibition of DKFZp761O17121 (Accession) . Accordingly, utilities of GAM155 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761O17121.

[25257] KIAA0564 (Accession XM_038664.6) is another GAM155 target gene, herein designated TARGET GENE. KIAA0564

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0564, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0564 BINDING SITE, designated SEQ ID:18220, to the nucleotide sequence of GAM155 RNA, herein designated GAM RNA, also designated SEQ ID:207.

[25258] Another function of GAM155 is therefore inhibition of KIAA0564 (Accession XM_038664.6) . Accordingly, utilities of GAM155 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0564.

[25259] LOC152941 (Accession) is another GAM155 target gene, herein designated TARGET GENE. LOC152941 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152941, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152941 BINDING SITE, designated SEQ ID:8587, to the nucleotide sequence of GAM155 RNA, herein designated GAM RNA, also designated SEQ ID:207.

[25260] Another function of GAM155 is therefore inhibition of LOC152941 (Accession) . Accordingly, utilities of GAM155 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152941.

[25261] Prostaglandin-endoperoxide synthase 1 (prostaglandin g/h synthase and cyclooxygenase) (PTGS1, Accession NM_000962.2) is another GAM155 target gene, herein designated TARGET GENE. PTGS1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTGS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGS1 BINDING SITE, designated SEQ ID:19654, to the nucleotide sequence of GAM155 RNA, herein designated GAM RNA, also designated SEQ ID:207.

[25262] Another function of GAM155 is therefore inhibition of Prostaglandin-endoperoxide synthase 1 (prostaglandin g/h synthase and cyclooxygenase) (PTGS1, Accession NM_000962.2), a gene which may play an important role in regulating or promoting cell proliferation in some normal and neoplastically transformed cells. Accordingly,

utilities of GAM155 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGS1.

[25263] The function of PTGS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.

[25264] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 156 (GAM156), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25265] GAM156 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM156 was detected is described hereinabove with reference to Figs. 8-15.

[25266] GAM156 gene, herein designated GAM GENE, and GAM156 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25267] GAM156 gene encodes a GAM156 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM156 precur-

sor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM156 precursor RNA is designated SEQ ID:54, and is provided hereinbelow with reference to the sequence listing part.

[25268] GAM156 precursor RNA folds onto itself, forming GAM156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25269] GAM156 precursor RNA folds onto itself, forming GAM156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25270] Nucleotide sequence of GAM156 precursor RNA, designated SEQ-ID: 54, and a schematic representation of a predicted secondary folding of GAM156 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25271] An enzyme complex designated DICER COMPLEX, `dices` the GAM156 folded precursor RNA into GAM156 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM156 RNA is designated SEQ ID:262, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25272] GAM156 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM156 target RNA, herein designated GAM TARGET RNA. GAM156 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[25273] GAM156 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM156 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM156 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM156 RNA may have a different number of target binding sites in untranslated regions of a GAM156 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25274] The complementary binding of GAM156 RNA, herein designated GAM RNA, to target binding sites on GAM156 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM156 target RNA into GAM156 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25275] It is appreciated that GAM156 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM156 target genes. The mRNA of each one of this plurality of GAM156 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM156 RNA, herein designated GAM RNA, and which when bound by GAM156 RNA causes inhibition of translation of respective one or more GAM156 target proteins.

[25276] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM156 gene, herein designated GAM GENE, on one or more GAM156 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25277] It is appreciated that specific functions and accordingly utilities of GAM156 correlate with, and may be deduced from, the identity of the target genes which GAM156 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25278]

[25279]

[25280] Clathrin, heavy polypeptide-like 1 (CLTCL1, Accession NM_001835.1) is a GAM156 target gene, herein designated TARGET GENE. CLTCL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLTCL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLTCL1 BINDING SITE, designated SEQ ID:6732, to the nu-

cleotide sequence of GAM156 RNA, herein designated GAM RNA, also designated SEQ ID:262.

[25281] A function of GAM156 is therefore inhibition of Clathrin, heavy polypeptide-like 1 (CLTCL1, Accession NM_001835.1), a gene which is involved in vesicle budding. and therefore may be associated with The velocardiofacial syndrome. Accordingly, utilities of GAM156 include diagnosis, prevention and treatment of The velocardiofacial syndrome, and of other diseases and clinical conditions associated with CLTCL1.

[25282] The function of CLTCL1 has been established by previous studies. Clathrin is the main structural component of the lattice covering the cytoplasmic face of the coated pits and coated vesicles in which specific macromolecules are entrapped in the process of receptor- mediated endocytosis. Clathrin is a large, soluble protein composed of heavy chains (molecular size, about 192 kD) and light chains (molecular size, about 32- 38 kD). Two major classes of clathrin light chains, referred to as LCA and LCB, have been identified. (The gene is also symbolized CLTA.) The structure of these light chains was studied by Kirchhausen et al. (1987). The clathrin unit that assembles into coats had 3 extended legs, 500 angstroms in length,

splayed out in a pinwheel- like structure (triskelion). Each of the legs is built from a single heavy chain, with a light chain bound to each proximal segment. At least 4 distinct forms of clathrin light chains are found in mammalian cells. This molecular variability derives from tissue- specific patterns of expression of LCA and LCB genes (Jackson et al., 1987). Brodsky et al. (1987) identified that part of the light- chain sequence that mediates heavy- chain binding and is the region of strongest homology with intermediate filament proteins. Sequence analysis shows an overall homology of 60% between LCA and LCB and the presence of brain- specific insertion sequences. LCA and LCB (OMIM Ref. No. 118970) are coded by distinct genes. Jackson and Parham (1988) compared cDNAs encoding the brain and nonbrain forms of human LCA and LCB with their homologs in cow and rat. The significant differences that distinguish LCA from LCB and the brain from the nonbrain forms show remarkable preservation in all 3 species. Each clathrin triskelion consists of 3 heavy chains and 3 light chains. In the brain, tissue- specific mRNA splicing yields larger forms of LCA and LCB, containing additional insertion sequences of 30 and 18 amino acids, respectively By Southern blot analysis on genomic DNA

extracted from a panel of mouse- human somatic cell hybrids and by isotopic in situ hybridization, Ponnambalam et al. (1994) assigned the CLTA gene to human 12q23-q24

[25283]

[25284] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25285] Sirotkin, H.; Morrow, B.; DasGupta, R.; Goldberg, R.; Patanjali, S. R.; Shi, G.; Cannizzaro, L.; Shprintzen, R.; Weissman, S. M.; Kucherlapati, R. : Isolation of a new clathrin heavy chain gene with muscle- specific expression from the region commonly deleted in velo- cardio-facial syndrome. Hum. Molec. Genet. 5: 617- 624, 1996. ; and

[25286] Long, K. R.; Trofatter, J. A.; Ramesh, V.; McCormick, M. K.; Buckler, A. J. : Cloning and characterization of a novel human clathrin heavy chain gene (CLTCL). Genomics 35: 466- 472, 1996.

[25287] Further studies establishing the function and utilities of CLTCL1 are found in John Hopkins OMIM database record ID 601273, and in cited publications listed in Table 5, which are hereby incorporated by reference.Dishevelled

associated activator of morphogenesis 2 (DAAM2, Accession XM_166434.3) is another GAM156 target gene, herein designated TARGET GENE. DAAM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DAAM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DAAM2 BINDING SITE, designated SEQ ID:4578, to the nucleotide sequence of GAM156 RNA, herein designated GAM RNA, also designated SEQ ID:262.

[25288] Another function of GAM156 is therefore inhibition of Dishevelled associated activator of morphogenesis 2 (DAAM2, Accession XM_166434.3), a gene which controls cell polarity and movement during development. Accordingly, utilities of GAM156 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAAM2.

[25289] The function of DAAM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.DKFZP434P0111 (Accession XM_041116.4) is another GAM156 target gene, herein designated TARGET

GENE. DKFZP434P0111 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434P0111, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434P0111 BINDING SITE, designated SEQ ID:16713, to the nucleotide sequence of GAM156 RNA, herein designated GAM RNA, also designated SEQ ID:262.

[25290] Another function of GAM156 is therefore inhibition of DKFZP434P0111 (Accession XM_041116.4) . Accordingly, utilities of GAM156 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434P0111.

[25291] FLJ10759 (Accession NM_018207.1) is another GAM156 target gene, herein designated TARGET GENE. FLJ10759 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10759, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10759 BINDING SITE, designated SEQ ID:6060, to the nucleotide sequence of GAM156 RNA, herein designated

GAM RNA, also designated SEQ ID:262.

[25292] Another function of GAM156 is therefore inhibition of FLJ10759 (Accession NM_018207.1) . Accordingly, utilities of GAM156 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10759.

[25293] KIAA0802 (Accession XM_031357.4) is another GAM156 target gene, herein designated TARGET GENE. KIAA0802 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0802, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0802 BINDING SITE, designated SEQ ID:15745, to the nucleotide sequence of GAM156 RNA, herein designated GAM RNA, also designated SEQ ID:262.

[25294] Another function of GAM156 is therefore inhibition of KIAA0802 (Accession XM_031357.4) . Accordingly, utilities of GAM156 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0802.

[25295] LOC148894 (Accession XM_097542.2) is another GAM156 target gene, herein designated TARGET GENE. LOC148894

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148894 BINDING SITE, designated SEQ ID:8056, to the nucleotide sequence of GAM156 RNA, herein designated GAM RNA, also designated SEQ ID:262.

[25296] Another function of GAM156 is therefore inhibition of LOC148894 (Accession XM_097542.2) . Accordingly, utilities of GAM156 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148894.

[25297] LOC199988 (Accession XM_117166.1) is another GAM156 target gene, herein designated TARGET GENE. LOC199988 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC199988, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199988 BINDING SITE, designated SEQ ID:3088, to the nucleotide sequence of GAM156 RNA, herein designated GAM RNA, also designated SEQ ID:262.

[25298] Another function of GAM156 is therefore inhibition of LOC199988 (Accession XM_117166.1) . Accordingly, utilities of GAM156 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199988.

[25299] Signal-regulatory protein beta 1 (SIRPB1, Accession NM_006065.1) is another GAM156 target gene, herein designated TARGET GENE. SIRPB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIRPB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIRPB1 BINDING SITE, designated SEQ ID:16696, to the nucleotide sequence of GAM156 RNA, herein designated GAM RNA, also designated SEQ ID:262.

[25300] Another function of GAM156 is therefore inhibition of Signal-regulatory protein beta 1 (SIRPB1, Accession NM_006065.1) . Accordingly, utilities of GAM156 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIRPB1.

[25301] Tripartite motif-containing 37 (TRIM37, Accession NM_015294.1) is another GAM156 target gene, herein

designated TARGET GENE. TRIM37 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRIM37, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM37 BINDING SITE, designated SEQ ID:19960, to the nucleotide sequence of GAM156 RNA, herein designated GAM RNA, also designated SEQ ID:262.

[25302] Another function of GAM156 is therefore inhibition of Tripartite motif-containing 37 (TRIM37, Accession NM_015294.1) . Accordingly, utilities of GAM156 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM37.

[25303]

[25304] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 157 (GAM157), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25305] GAM157 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM157 was detected is described hereinabove with reference to Figs. 8-15.

[25306] GAM157 gene, herein designated GAM GENE, and GAM157 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25307] GAM157 gene encodes a GAM157 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM157 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM157 precursor RNA is designated SEQ ID:193, and is provided hereinbelow with reference to the sequence listing part.

[25308] GAM157 precursor RNA folds onto itself, forming GAM157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25309] GAM157 precursor RNA folds onto itself, forming GAM157

folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25310] Nucleotide sequence of GAM157 precursor RNA, designated SEQ-ID: 193, and a schematic representation of a predicted secondary folding of GAM157 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25311] An enzyme complex designated DICER COMPLEX, `dices` the GAM157 folded precursor RNA into GAM157 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM157 RNA is designated SEQ ID:225, and is provided hereinbelow with refer-

ences to the sequence listing part and Table 3, hereby incorporated by reference.

[25312] GAM157 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM157 target RNA, herein designated GAM TARGET RNA. GAM157 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25313] GAM157 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM157 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM157 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM157 RNA may have a different number of target binding sites in untranslated regions of a GAM157 target

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25314] The complementary binding of GAM157 RNA, herein designated GAM RNA, to target binding sites on GAM157 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM157 target RNA into GAM157 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25315] It is appreciated that GAM157 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM157 target genes. The mRNA of each one of this plurality of GAM157 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM157 RNA, herein designated GAM RNA, and which when bound by GAM157 RNA causes inhibition of translation of respective one or more GAM157 target proteins.

[25316] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM157 gene, herein designated GAM GENE, on one or more GAM157 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25317] It is appreciated that specific functions and accordingly utilities of GAM157 correlate with, and may be deduced from, the identity of the target genes which GAM157 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25318]

[25319]

[25320] Angiomotin (AMOT, Accession NM_133265.1) is a

GAM157 target gene, herein designated TARGET GENE. AMOT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AMOT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMOT BINDING SITE, designated SEQ ID:1662, to the nucleotide sequence of GAM157 RNA, herein designated GAM RNA, also designated SEQ ID:225.

[25321] A function of GAM157 is therefore inhibition of Angiomotin (AMOT, Accession NM_133265.1) . Accordingly, utilities of GAM157 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMOT.

[25322] Chromatin assembly factor 1, subunit b (p60) (CHAF1B, Accession NM_005441.1) is another GAM157 target gene, herein designated TARGET GENE. CHAF1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHAF1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHAF1B BINDING SITE, designated SEQ ID:17720, to the nucleotide se-

quence of GAM157 RNA, herein designated GAM RNA, also designated SEQ ID:225.

[25323] Another function of GAM157 is therefore inhibition of Chromatin assembly factor 1, subunit b (p60) (CHAF1B, Accession NM_005441.1) . Accordingly, utilities of GAM157 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHAF1B.

[25324] D123 (Accession) is another GAM157 target gene, herein designated TARGET GENE. D123 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by D123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of D123 BINDING SITE, designated SEQ ID:2735, to the nucleotide sequence of GAM157 RNA, herein designated GAM RNA, also designated SEQ ID:225.

[25325] Another function of GAM157 is therefore inhibition of D123 (Accession) . Accordingly, utilities of GAM157 include diagnosis, prevention and treatment of diseases and clinical conditions associated with D123.

[25326] LOC149935 (Accession) is another GAM157 target gene, herein designated TARGET GENE. LOC149935 BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by LOC149935, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149935 BINDING SITE, designated SEQ ID:1436, to the nucleotide sequence of GAM157 RNA, herein designated GAM RNA, also designated SEQ ID:225.

[25327] Another function of GAM157 is therefore inhibition of LOC149935 (Accession) . Accordingly, utilities of GAM157 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149935.

[25328] LOC221491 (Accession XM_166344.3) is another GAM157 target gene, herein designated TARGET GENE. LOC221491 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221491, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221491 BINDING SITE, designated SEQ ID:9737, to the nucleotide sequence of GAM157 RNA, herein designated GAM RNA, also designated SEQ ID:225.

[25329] Another function of GAM157 is therefore inhibition of

LOC221491 (Accession XM_166344.3) . Accordingly, utilities of GAM157 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221491.

[25330]

[25331] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 158 (GAM158), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25332] GAM158 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM158 was detected is described hereinabove with reference to Figs. 8-15.

[25333] GAM158 gene, herein designated GAM GENE, and GAM158 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25334] GAM158 gene encodes a GAM158 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM158 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of

GAM158 precursor RNA is designated SEQ ID:47, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:47 is located at position 112174058 relative to chromosome 1.

[25335] GAM158 precursor RNA folds onto itself, forming GAM158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25336] GAM158 precursor RNA folds onto itself, forming GAM158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25337] Nucleotide sequence of GAM158 precursor RNA, desig-

nated SEQ-ID: 47, and a schematic representation of a predicted secondary folding of GAM158 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25338] An enzyme complex designated DICER COMPLEX, `dices` the GAM158 folded precursor RNA into GAM158 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM158 RNA is designated SEQ ID:383, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25339] GAM158 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM158 target RNA, herein designated GAM TARGET RNA. GAM158 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25340] GAM158 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM158 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM158 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM158 RNA may have a different number of target binding sites in untranslated regions of a GAM158 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25341] The complementary binding of GAM158 RNA, herein designated GAM RNA, to target binding sites on GAM158 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM158 target RNA into GAM158 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25342] It is appreciated that GAM158 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM158 target genes. The mRNA of each one of this plurality of GAM158 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM158 RNA, herein designated GAM RNA, and which when bound by GAM158 RNA causes inhibition of translation of respective one or more GAM158 target proteins.

[25343] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM158 gene, herein designated GAM GENE, on one or more GAM158 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25344] It is appreciated that specific functions and accordingly utilities of GAM158 correlate with, and may be deduced from, the identity of the target genes which GAM158 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25345]

[25346]

[25347] KIAA0237 (Accession NM_014747.1) is a GAM158 target gene, herein designated TARGET GENE. KIAA0237 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0237, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0237 BINDING SITE, designated SEQ ID:13040, to the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, also designated SEQ ID:383.

[25348] A function of GAM158 is therefore inhibition of KIAA0237 (Accession NM_014747.1) . Accordingly, utilities of GAM158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0237.

[25349] KIAA1045 (Accession XM_048592.2) is another GAM158 target gene, herein designated TARGET GENE. KIAA1045 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1045 BINDING SITE, designated SEQ ID:19310, to the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, also designated SEQ ID:383.

[25350] Another function of GAM158 is therefore inhibition of KIAA1045 (Accession XM_048592.2) . Accordingly, utilities of GAM158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1045.

[25351] KIAA1110 (Accession) is another GAM158 target gene, herein designated TARGET GENE. KIAA1110 BINDING SITE is a target binding site found in the 3` untranslated re-

gion of mRNA encoded by KIAA1110, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1110 BINDING SITE, designated SEQ ID:1213, to the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, also designated SEQ ID:383.

[25352] Another function of GAM158 is therefore inhibition of KIAA1110 (Accession) . Accordingly, utilities of GAM158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1110.

[25353] LOC124602 (Accession) is another GAM158 target gene, herein designated TARGET GENE. LOC124602 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC124602, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC124602 BINDING SITE, designated SEQ ID:1663, to the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, also designated SEQ ID:383.

[25354] Another function of GAM158 is therefore inhibition of LOC124602 (Accession) . Accordingly, utilities of

GAM158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124602.

[25355] LOC253866 (Accession) is another GAM158 target gene, herein designated TARGET GENE. LOC253866 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253866, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253866 BINDING SITE, designated SEQ ID:11918, to the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, also designated SEQ ID:383.

[25356] Another function of GAM158 is therefore inhibition of LOC253866 (Accession) . Accordingly, utilities of GAM158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253866.

[25357] LOC92305 (Accession NM_138385.1) is another GAM158 target gene, herein designated TARGET GENE. LOC92305 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92305, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92305 BINDING SITE, designated SEQ ID:16687, to the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, also designated SEQ ID:383.

[25358] Another function of GAM158 is therefore inhibition of LOC92305 (Accession NM_138385.1) . Accordingly, utilities of GAM158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92305.

[25359] Rab9b, member ras oncogene family (RAB9B, Accession NM_016370.1) is another GAM158 target gene, herein designated TARGET GENE. RAB9B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAB9B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB9B BINDING SITE, designated SEQ ID:12877, to the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, also designated SEQ ID:383.

[25360] Another function of GAM158 is therefore inhibition of Rab9b, member ras oncogene family (RAB9B, Accession

NM_016370.1) . Accordingly, utilities of GAM158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB9B.

[25361] Syntaxin 1a (brain) (STX1A, Accession NM_004603.1) is another GAM158 target gene, herein designated TARGET GENE. STX1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STX1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STX1A BINDING SITE, designated SEQ ID:18630, to the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, also designated SEQ ID:383.

[25362] Another function of GAM158 is therefore inhibition of Syntaxin 1a (brain) (STX1A, Accession NM_004603.1), a gene which may play a critical role in neurotransmitter exocytosis. Accordingly, utilities of GAM158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STX1A.

[25363] The function of STX1A has been established by previous studies. Synaptic vesicles store neurotransmitters that are released during calcium- regulated exocytosis. The specificity of neurotransmitter release requires the localization

of both synaptic vesicles and calcium channels to the presynaptic active zone. Syntaxins function in this vesicle fusion process. Syntaxins also serve as a substrate for botulinum neurotoxin type C, a metalloprotease that blocks exocytosis and has high affinity for a molecular complex that includes the alpha- latrotoxin receptor (OMIM Ref. No. 600565) which produces explosive exocytosis (Zhang et al., 1995). Bennett et al. (1992) identified two 35- kD proteins (p35 or syntaxins) that interact with synaptic vesicle protein p65 (synaptotagmin; 185605). The p35 proteins are expressed only in the nervous system. The 2 proteins are 84% identical, include C- terminal membrane anchors, and are concentrated on the plasma membrane at synaptic sites. The authors speculated that the p35 proteins may function in docking synaptic vesicles near calcium channels at presynaptic active zones.

[25364]

[25365] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25366] Bennett, M. K.; Calakos, N.; Scheller, R. H. : Syntaxin: a synaptic protein implicated in docking of synaptic vesicles at presynaptic active zones. Science 257: 255- 259, 1992.

; and

[25367] Zhang, R.; Maksymowych, A. B.; Simpson, L. L. : Cloning and sequence analysis of a cDNA encoding human syntaxin 1A, a polypeptide essential for exocytosis. Gene 159: 293- 294, 1995.

[25368] Further studies establishing the function and utilities of STX1A are found in John Hopkins OMIM database record ID 186590, and in cited publications listed in Table 5, which are hereby incorporated by reference.SUN1 (Accession) is another GAM158 target gene, herein designated TARGET GENE. SUN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SUN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SUN1 BINDING SITE, designated SEQ ID:9645, to the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, also designated SEQ ID:383.

[25369] Another function of GAM158 is therefore inhibition of SUN1 (Accession) . Accordingly, utilities of GAM158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUN1.

[25370]

[25371] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 159 (GAM159), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25372] GAM159 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM159 was detected is described hereinabove with reference to Figs. 8-15.

[25373] GAM159 gene, herein designated GAM GENE, and GAM159 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25374] GAM159 gene encodes a GAM159 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM159 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM159 precursor RNA is designated SEQ ID:109, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:109 is located at position 125133292 relative to chromosome 9.

[25375] GAM159 precursor RNA folds onto itself, forming GAM159

folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25376] GAM159 precursor RNA folds onto itself, forming GAM159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25377] Nucleotide sequence of GAM159 precursor RNA, designated SEQ-ID: 109, and a schematic representation of a predicted secondary folding of GAM159 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25378] An enzyme complex designated DICER COMPLEX, `dices`

the GAM159 folded precursor RNA into GAM159 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: B) nucleotide sequence of GAM159 RNA is designated SEQ ID:230, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25379] GAM159 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM159 target RNA, herein designated GAM TARGET RNA. GAM159 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25380] GAM159 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM159 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM159

RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM159 RNA may have a different number of target binding sites in untranslated regions of a GAM159 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25381] The complementary binding of GAM159 RNA, herein designated GAM RNA, to target binding sites on GAM159 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM159 target RNA into GAM159 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25382] It is appreciated that GAM159 target gene, herein designated TARGET GENE, in fact represents a plurality of

GAM159 target genes. The mRNA of each one of this plurality of GAM159 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM159 RNA, herein designated GAM RNA, and which when bound by GAM159 RNA causes inhibition of translation of respective one or more GAM159 target proteins.

[25383] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM159 gene, herein designated GAM GENE, on one or more GAM159 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25384] It is appreciated that specific functions and accordingly utilities of GAM159 correlate with, and may be deduced from, the identity of the target genes which GAM159 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25385]

[25386]

[25387] AF5Q31 (Accession NM_014423.1) is a GAM159 target gene, herein designated TARGET GENE. AF5Q31 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AF5Q31, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AF5Q31 BINDING SITE, designated SEQ ID:13598, to the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, also designated SEQ ID:230.

[25388] A function of GAM159 is therefore inhibition of AF5Q31 (Accession NM_014423.1) . Accordingly, utilities of GAM159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AF5Q31.

[25389] APPD (Accession) is another GAM159 target gene, herein

designated TARGET GENE. APPD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APPD BINDING SITE, designated SEQ ID:14424, to the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, also designated SEQ ID:230.

[25390] Another function of GAM159 is therefore inhibition of APPD (Accession) . Accordingly, utilities of GAM159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APPD.

[25391] Digeorge syndrome critical region gene 6 (DGCR6, Accession NM_005675.2) is another GAM159 target gene, herein designated TARGET GENE. DGCR6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DGCR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DGCR6 BINDING SITE, designated SEQ ID:10368, to the nucleotide sequence of GAM159 RNA, herein designated GAM RNA,

also designated SEQ ID:230.

[25392] Another function of GAM159 is therefore inhibition of Di-george syndrome critical region gene 6 (DGCR6, Accession NM_005675.2) . Accordingly, utilities of GAM159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGCR6.

[25393] FLJ13710 (Accession NM_024817.1) is another GAM159 target gene, herein designated TARGET GENE. FLJ13710 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13710, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13710 BINDING SITE, designated SEQ ID:19395, to the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, also designated SEQ ID:230.

[25394] Another function of GAM159 is therefore inhibition of FLJ13710 (Accession NM_024817.1) . Accordingly, utilities of GAM159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13710.

[25395] Gata binding protein 2 (GATA2, Accession) is another GAM159 target gene, herein designated TARGET GENE.

GATA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GATA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GATA2 BINDING SITE, designated SEQ ID:13334, to the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, also designated SEQ ID:230.

[25396] Another function of GAM159 is therefore inhibition of Gata binding protein 2 (GATA2, Accession) . Accordingly, utilities of GAM159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GATA2.

[25397] Huntingtin (huntington disease) (HD, Accession NM_002111.3) is another GAM159 target gene, herein designated TARGET GENE. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HD BINDING SITE, designated SEQ ID:15165, to the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, also designated SEQ ID:230.

[25398] Another function of GAM159 is therefore inhibition of Huntingtin (huntington disease) (HD, Accession NM_002111.3) . Accordingly, utilities of GAM159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HD.

[25399] KIAA0953 (Accession XM_039733.2) is another GAM159 target gene, herein designated TARGET GENE. KIAA0953 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0953, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0953 BINDING SITE, designated SEQ ID:11636, to the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, also designated SEQ ID:230.

[25400] Another function of GAM159 is therefore inhibition of KIAA0953 (Accession XM_039733.2) . Accordingly, utilities of GAM159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0953.

[25401] LOC151438 (Accession XM_098060.1) is another GAM159 target gene, herein designated TARGET GENE. LOC151438 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC151438, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151438 BINDING SITE, designated SEQ ID:18291, to the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, also designated SEQ ID:230.

[25402] Another function of GAM159 is therefore inhibition of LOC151438 (Accession XM_098060.1) . Accordingly, utilities of GAM159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151438.

[25403] LOC91748 (Accession) is another GAM159 target gene, herein designated TARGET GENE. LOC91748 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91748, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91748 BINDING SITE, designated SEQ ID:1274, to the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, also designated SEQ ID:230.

[25404] Another function of GAM159 is therefore inhibition of

LOC91748 (Accession) . Accordingly, utilities of GAM159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91748.

[25405] SDR1 (Accession NM_004753.1) is another GAM159 target gene, herein designated TARGET GENE. SDR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SDR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SDR1 BINDING SITE, designated SEQ ID:19713, to the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, also designated SEQ ID:230.

[25406] Another function of GAM159 is therefore inhibition of SDR1 (Accession NM_004753.1) . Accordingly, utilities of GAM159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDR1.

[25407]

[25408] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 160 (GAM160), which modulates expression of respective target genes thereof, the function and utility of which target

genes is known in the art.

[25409] GAM160 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM160 was detected is described hereinabove with reference to Figs. 8-15.

[25410] GAM160 gene, herein designated GAM GENE, and GAM160 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25411] GAM160 gene encodes a GAM160 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM160 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM160 precursor RNA is designated SEQ ID:174, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:174 is located at position 150162171 relative to chromosome 3.

[25412] GAM160 precursor RNA folds onto itself, forming GAM160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25413] GAM160 precursor RNA folds onto itself, forming GAM160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25414] Nucleotide sequence of GAM160 precursor RNA, designated SEQ-ID: 174, and a schematic representation of a predicted secondary folding of GAM160 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25415] An enzyme complex designated DICER COMPLEX, `dices` the GAM160 folded precursor RNA into GAM160 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM160 RNA is designated SEQ ID:343, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25416] GAM160 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM160 target RNA, herein designated GAM TARGET RNA. GAM160 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25417] GAM160 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM160 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM160 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated

that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM160 RNA may have a different number of target binding sites in untranslated regions of a GAM160 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25418] The complementary binding of GAM160 RNA, herein designated GAM RNA, to target binding sites on GAM160 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM160 target RNA into GAM160 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25419] It is appreciated that GAM160 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM160 target genes. The mRNA of each one of this plurality of GAM160 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM160 RNA, herein designated GAM RNA, and which when bound by

GAM160 RNA causes inhibition of translation of respective one or more GAM160 target proteins.

[25420] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM160 gene, herein designated GAM GENE, on one or more GAM160 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25421] It is appreciated that specific functions and accordingly utilities of GAM160 correlate with, and may be deduced from, the identity of the target genes which GAM160 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25422]

[25423]

[25424] LOC132235 (Accession XM_072302.2) is a GAM160 target gene, herein designated TARGET GENE. LOC132235 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC132235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC132235 BINDING SITE, designated SEQ ID:13188, to the nucleotide sequence of GAM160 RNA, herein designated GAM RNA, also designated SEQ ID:343.

[25425] A function of GAM160 is therefore inhibition of LOC132235 (Accession XM_072302.2) . Accordingly, utilities of GAM160 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132235.

[25426] Tnf receptor-associated factor 3 (TRAF3, Accession NM_145725.1) is another GAM160 target gene, herein designated TARGET GENE. TRAF3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TRAF3, correspond-

ing to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF3 BINDING SITE, designated SEQ ID:9111, to the nucleotide sequence of GAM160 RNA, herein designated GAM RNA, also designated SEQ ID:343.

[25427] Another function of GAM160 is therefore inhibition of Tnf receptor-associated factor 3 (TRAF3, Accession NM_145725.1) . Accordingly, utilities of GAM160 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF3.

[25428]

[25429] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 161 (GAM161), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25430] GAM161 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM161 was detected is described hereinabove with reference to Figs. 8-15.

[25431] GAM161 gene, herein designated GAM GENE, and

GAM161 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25432] GAM161 gene encodes a GAM161 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM161 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM161 precursor RNA is designated SEQ ID:24, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:24 is located at position 3119977 relative to chromosome 1.

[25433] GAM161 precursor RNA folds onto itself, forming GAM161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25434] GAM161 precursor RNA folds onto itself, forming GAM161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25435] Nucleotide sequence of GAM161 precursor RNA, designated SEQ-ID: 24, and a schematic representation of a predicted secondary folding of GAM161 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25436] An enzyme complex designated DICER COMPLEX, `dices` the GAM161 folded precursor RNA into GAM161 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM161 RNA is designated SEQ ID:304, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25437] GAM161 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM161 target RNA, herein designated GAM TARGET RNA. GAM161 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25438] GAM161 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM161 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM161 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM161 RNA may have a different number of target binding sites in untranslated regions of a GAM161 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an

example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25439] The complementary binding of GAM161 RNA, herein designated GAM RNA, to target binding sites on GAM161 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM161 target RNA into GAM161 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25440] It is appreciated that GAM161 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM161 target genes. The mRNA of each one of this plurality of GAM161 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM161 RNA, herein designated GAM RNA, and which when bound by GAM161 RNA causes inhibition of translation of respective one or more GAM161 target proteins.

[25441] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM161 gene, herein designated GAM GENE, on one or

more GAM161 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25442] It is appreciated that specific functions and accordingly utilities of GAM161 correlate with, and may be deduced from, the identity of the target genes which GAM161 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25443]

[25444]

[25445] APM1 (Accession NM_004797.1) is a GAM161 target gene, herein designated TARGET GENE. APM1 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by APM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APM1 BINDING SITE, designated SEQ ID:9908, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25446] A function of GAM161 is therefore inhibition of APM1 (Accession NM_004797.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1.

[25447] B-cell cll/lymphoma 10 (BCL10, Accession NM_003921.2) is another GAM161 target gene, herein designated TARGET GENE. BCL10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCL10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCL10 BINDING SITE, designated SEQ ID:8318, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25448] Another function of GAM161 is therefore inhibition of B-cell cll/lymphoma 10 (BCL10, Accession NM_003921.2), a

gene which is a positive regulator of lymphocyte proliferation, NF- kappaB activator. and therefore may be associated with Malt lymphoma, follicular lymphoma. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of Malt lymphoma, follicular lymphoma, and of other diseases and clinical conditions associated with BCL10.

[25449] The function of BCL10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Chromosome 13 open reading frame 1 (C13orf1, Accession NM_020456.1) is another GAM161 target gene, herein designated TARGET GENE. C13orf1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C13orf1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C13orf1 BINDING SITE, designated SEQ ID:12864, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25450] Another function of GAM161 is therefore inhibition of Chromosome 13 open reading frame 1 (C13orf1, Acces-

sion NM_020456.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C13orf1.

[25451] Chromosome 21 open reading frame 67 (C21orf67, Accession NM_058188.1) is another GAM161 target gene, herein designated TARGET GENE. C21orf67 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C21orf67, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C21orf67 BINDING SITE, designated SEQ ID:12444, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25452] Another function of GAM161 is therefore inhibition of Chromosome 21 open reading frame 67 (C21orf67, Accession NM_058188.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf67.

[25453] Chromosome 6 open reading frame 33 (C6orf33, Accession NM_133367.1) is another GAM161 target gene, herein designated TARGET GENE. C6orf33 BINDING SITE is a target binding site found in the 3` untranslated region

of mRNA encoded by C6orf33, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf33 BINDING SITE, designated SEQ ID:14623, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25454] Another function of GAM161 is therefore inhibition of Chromosome 6 open reading frame 33 (C6orf33, Accession NM_133367.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf33.

[25455] Chromosome 9 open reading frame 9 (C9orf9, Accession NM_018956.2) is another GAM161 target gene, herein designated TARGET GENE. C9orf9 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C9orf9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C9orf9 BINDING SITE, designated SEQ ID:10257, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25456] Another function of GAM161 is therefore inhibition of Chromosome 9 open reading frame 9 (C9orf9, Accession NM_018956.2) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf9.

[25457] Cadherin 17, li cadherin (liver-intestine) (CDH17, Accession NM_004063.2) is another GAM161 target gene, herein designated TARGET GENE. CDH17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDH17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH17 BINDING SITE, designated SEQ ID:1297, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25458] Another function of GAM161 is therefore inhibition of Cadherin 17, li cadherin (liver-intestine) (CDH17, Accession NM_004063.2), a gene which may have a role in the morphological organization of liver and intestine and involved in intestinal peptide transport. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH17.

[25459] The function of CDH17 has been established by previous studies. The first step in oral absorption of many medically important peptide- based drugs, such as beta- lactam antibiotics, is mediated by an intestinal proton- dependent peptide transporter. Dantzig et al. (1994) identified a monoclonal antibody that blocked uptake of the beta- lactam cephalexin by human cells. By screening an expression library with this antibody, the authors isolated cDNAs encoding a protein that they designated 'human peptide transporter- 1,' or HPT1. Sequence analysis revealed that the predicted 832- amino acid protein shares several structural features with the cadherin superfamily of calcium- dependent cell- cell adhesion proteins. See 603006. Like the cadherins, HPT1 contains an extracellular region with conserved motifs and a transmembrane domain. However, HPT1 lacks the cytoplasmic domain found in other cadherins. Using immunohistochemical staining, Dantzig et al. (1994) localized HPT1 along the gastrointestinal tract and the pancreatic ducts, but not in kidney, lung, or several other tissues. Mammalian cells expressing HPT1 showed consistently higher cephalexin uptake activity than controls. Uptake was dependent on an inwardly directed proton gradient.

[25460]

[25461] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25462] Dantzig, A. H.; Hoskins, J.; Tabas, L. B.; Bright, S.; Shepard, R. L.; Jenkins, I. L.; Duckworth, D. C.; Sportsman, J. R.; Mackensen, D.; Rosteck, P. R., Jr.; Skatrud, P. L. : Association of intestinal peptide transport with a protein related to the cadherin superfamily. Science 264: 430- 433, 1994. ; and

[25463] Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias, J.; Callen, D. F. : Localization of human cadherin genes to chromosome regions exhibiting cancer- related loss of heteroz.

[25464] Further studies establishing the function and utilities of CDH17 are found in John Hopkins OMIM database record ID 603017, and in cited publications listed in Table 5, which are hereby incorporated by reference.Fc fragment of iga, receptor for (FCAR, Accession NM_002000.2) is another GAM161 target gene, herein designated TARGET GENE. FCAR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FCAR, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE, designated SEQ ID:8313, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25465] Another function of GAM161 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NM_002000.2), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[25466] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fasciculation and elongation protein zeta 1 (zygin i) (FEZ1, Accession NM_005103.3) is another GAM161 target gene, herein designated TARGET GENE. FEZ1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA en-

coded by FEZ1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FEZ1 BINDING SITE, designated SEQ ID:8241, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25467] Another function of GAM161 is therefore inhibition of Fasciculation and elongation protein zeta 1 (zygin i) (FEZ1, Accession NM_005103.3), a gene which Zygin 1; may have a role in axonal outgrowth; has similarity to C. elegans UNC- 76. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEZ1.

[25468] The function of FEZ1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.FLJ10232 (Accession NM_018033.1) is another GAM161 target gene, herein designated TARGET GENE. FLJ10232 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10232, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of FLJ10232 BINDING SITE, designated SEQ ID:12255, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25469] Another function of GAM161 is therefore inhibition of FLJ10232 (Accession NM_018033.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10232.

[25470] FLJ12787 (Accession NM_032175.1) is another GAM161 target gene, herein designated TARGET GENE. FLJ12787 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12787, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12787 BINDING SITE, designated SEQ ID:7408, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25471] Another function of GAM161 is therefore inhibition of FLJ12787 (Accession NM_032175.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ12787.

[25472] FLJ13114 (Accession NM_024541.1) is another GAM161 target gene, herein designated TARGET GENE. FLJ13114 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13114 BINDING SITE, designated SEQ ID:930, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25473] Another function of GAM161 is therefore inhibition of FLJ13114 (Accession NM_024541.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13114.

[25474] FLJ13188 (Accession NM_022063.1) is another GAM161 target gene, herein designated TARGET GENE. FLJ13188 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13188, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ13188 BINDING SITE, designated SEQ ID:3353, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25475] Another function of GAM161 is therefore inhibition of FLJ13188 (Accession NM_022063.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13188.

[25476] FLJ13456 (Accession XM_038291.5) is another GAM161 target gene, herein designated TARGET GENE. FLJ13456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13456 BINDING SITE, designated SEQ ID:12949, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25477] Another function of GAM161 is therefore inhibition of FLJ13456 (Accession XM_038291.5) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13456.

[25478] FLJ20136 (Accession NM_017684.1) is another GAM161 target gene, herein designated TARGET GENE. FLJ20136 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20136 BINDING SITE, designated SEQ ID:8713, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25479] Another function of GAM161 is therefore inhibition of FLJ20136 (Accession NM_017684.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20136.

[25480] FLJ20507 (Accession NM_017849.1) is another GAM161 target gene, herein designated TARGET GENE. FLJ20507 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20507 BINDING SITE, designated SEQ ID:19171, to the

nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25481] Another function of GAM161 is therefore inhibition of FLJ20507 (Accession NM_017849.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20507.

[25482] FLJ31153 (Accession NM_144600.1) is another GAM161 target gene, herein designated TARGET GENE. FLJ31153 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ31153, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31153 BINDING SITE, designated SEQ ID:1064, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25483] Another function of GAM161 is therefore inhibition of FLJ31153 (Accession NM_144600.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31153.

[25484] FLJ32865 (Accession NM_144613.1) is another GAM161

target gene, herein designated TARGET GENE. FLJ32865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32865 BINDING SITE, designated SEQ ID:15270, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25485] Another function of GAM161 is therefore inhibition of FLJ32865 (Accession NM_144613.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865.

[25486] GR6 (Accession NM_007354.1) is another GAM161 target gene, herein designated TARGET GENE. GR6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GR6 BINDING SITE, designated SEQ ID:11991, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA,

also designated SEQ ID:304.

[25487] Another function of GAM161 is therefore inhibition of GR6 (Accession NM_007354.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GR6.

[25488] H2AV (Accession NM_138635.1) is another GAM161 target gene, herein designated TARGET GENE. H2AV BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H2AV, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H2AV BINDING SITE, designated SEQ ID:4146, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25489] Another function of GAM161 is therefore inhibition of H2AV (Accession NM_138635.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H2AV.

[25490] HCA4 (Accession) is another GAM161 target gene, herein designated TARGET GENE. HCA4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HCA4, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HCA4 BINDING SITE, designated SEQ ID:18806, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25491] Another function of GAM161 is therefore inhibition of HCA4 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCA4.

[25492] Histamine receptor h4 (HRH4, Accession NM_021624.2) is another GAM161 target gene, herein designated TARGET GENE. HRH4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HRH4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HRH4 BINDING SITE, designated SEQ ID:18713, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25493] Another function of GAM161 is therefore inhibition of Histamine receptor h4 (HRH4, Accession NM_021624.2) . Accordingly, utilities of GAM161 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with HRH4.

[25494] 5-hydroxytryptamine (serotonin) receptor 1e (HTR1E, Accession NM_000865.1) is another GAM161 target gene, herein designated TARGET GENE. HTR1E BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR1E, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR1E BINDING SITE, designated SEQ ID:3407, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25495] Another function of GAM161 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 1e (HTR1E, Accession NM_000865.1), a gene which belongs to g- protein coupled receptors. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR1E.

[25496] The function of HTR1E has been established by previous studies. Serotonin (5- hydroxytryptamine; 5- HT) is a neurotransmitter thought to play a role in various cognitive and behavioral functions including feeding, sleep, pain, depression, and learning. Serotonin receptors have been divided into 4 classes designated 5- HT- 1- like, 5- HT- 2 (OMIM Ref. No. 182135), 5- HT- 3 (OMIM Ref. No. 182139), and 5- HT- 4 (OMIM Ref. No. 602128), depending on their ligand binding and effector- coupling properties. McAllister et al. (1992) stated the 5- HT- 1 receptor family can be further subdivided into 4 subtypes, 5- HT- 1A to 5- HT- 1D. McAllister et al. (1992) described the cloning and characterization of a 5- HT- 1E receptor. The excellent correlation observed between the pharmacology of the expressed receptor and the human brain 5- HT- 1E binding site confirmed that their clone encodes a 5- HT- 1E receptor and establishes a fifth 5- HT- 1- like receptor subtype. Using 2 independent polymerase chain reactions on a panel of human- hamster somatic cell hybrid genomic DNA, Levy et al. (1994) showed that the 5- hydroxytryptamine- 1E serotonin receptor gene is located on human chromosome 6. Furthermore, by means of in situ hybridization to human metaphase chromosomes using the

cloned gene as a probe (Levy et al., 1992), they demonstrated that the gene is located on 6q14- q15. HTR1E is found mainly in cerebral cortex, and the precise chromosomal assignment of the gene may help evaluate this locus as a candidate for mutations in neurologic and psychiatric diseases.

[25497]

[25498] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25499] Levy, F. O.; Holtgreve- Grez, H.; Tasken, K.; Solberg, R.; Ried, T.; Gudermann, T. : Assignment of the gene encoding the 5- HT- 1E serotonin receptor (S31) (locus HTR1E) to human chromosome 6q14- q15. Genomics 22: 637-640, 1994. ; and

[25500] McAllister, G.; Charlesworth, A.; Snodin, C.; Beer, M. S.; Noble, A. J.; Middlemiss, D. N.; Iversen, L. L.; Whiting, P. : Molecular cloning of a serotonin receptor from human brain (5HT.

[25501] Further studies establishing the function and utilities of HTR1E are found in John Hopkins OMIM database record ID 182132, and in cited publications listed in Table 5, which are hereby incorporated by reference.Interferon

(alpha, beta and omega) receptor 2 (IFNAR2, Accession NM_000874.2) is another GAM161 target gene, herein designated TARGET GENE. IFNAR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IFNAR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IFNAR2 BINDING SITE, designated SEQ ID:8000, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25502] Another function of GAM161 is therefore inhibition of Interferon (alpha, beta and omega) receptor 2 (IFNAR2, Accession NM_000874.2), a gene which is a receptor for interferons alpha and beta. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IFNAR2.

[25503] The function of IFNAR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.KIAA0161 (Accession) is another GAM161 target gene, herein designated TARGET GENE. KIAA0161 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0161, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0161 BINDING SITE, designated SEQ ID:17542, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25504] Another function of GAM161 is therefore inhibition of KIAA0161 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0161.

[25505] KIAA0599 (Accession XM_085127.6) is another GAM161 target gene, herein designated TARGET GENE. KIAA0599 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0599, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0599 BINDING SITE, designated SEQ ID:6311, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25506] Another function of GAM161 is therefore inhibition of KIAA0599 (Accession XM_085127.6) . Accordingly, utilities of GAM161 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0599.

[25507] KIAA1028 (Accession) is another GAM161 target gene, herein designated TARGET GENE. KIAA1028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1028 BINDING SITE, designated SEQ ID:4329, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25508] Another function of GAM161 is therefore inhibition of KIAA1028 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1028.

[25509] KIAA1456 (Accession XM_040100.4) is another GAM161 target gene, herein designated TARGET GENE. KIAA1456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1456 BINDING SITE, designated SEQ ID:6378, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25510] Another function of GAM161 is therefore inhibition of KIAA1456 (Accession XM_040100.4) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1456.

[25511] KIAA1508 (Accession XM_290952.1) is another GAM161 target gene, herein designated TARGET GENE. KIAA1508 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1508, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1508 BINDING SITE, designated SEQ ID:2567, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25512] Another function of GAM161 is therefore inhibition of KIAA1508 (Accession XM_290952.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1508.

[25513] KIAA1655 (Accession) is another GAM161 target gene, herein designated TARGET GENE. KIAA1655 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1655, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1655 BINDING SITE, designated SEQ ID:19930, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25514] Another function of GAM161 is therefore inhibition of KIAA1655 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1655.

[25515] KIAA1877 (Accession) is another GAM161 target gene, herein designated TARGET GENE. KIAA1877 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1877, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1877 BINDING SITE, designated SEQ ID:4810, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA,

also designated SEQ ID:304.

[25516] Another function of GAM161 is therefore inhibition of KIAA1877 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1877.

[25517] LOC126133 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC126133 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC126133, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126133 BINDING SITE, designated SEQ ID:13929, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25518] Another function of GAM161 is therefore inhibition of LOC126133 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126133.

[25519] LOC128077 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC128077 BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by LOC128077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC128077 BINDING SITE, designated SEQ ID:12251, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25520] Another function of GAM161 is therefore inhibition of LOC128077 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128077.

[25521] LOC130813 (Accession XM_065904.2) is another GAM161 target gene, herein designated TARGET GENE. LOC130813 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC130813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:18432, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25522] Another function of GAM161 is therefore inhibition of

LOC130813 (Accession XM_065904.2) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813.

[25523] LOC144317 (Accession XM_084813.4) is another GAM161 target gene, herein designated TARGET GENE. LOC144317 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144317, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144317 BINDING SITE, designated SEQ ID:12865, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25524] Another function of GAM161 is therefore inhibition of LOC144317 (Accession XM_084813.4) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144317.

[25525] LOC146455 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC146455 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146455, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146455 BINDING SITE, designated SEQ ID:12181, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25526] Another function of GAM161 is therefore inhibition of LOC146455 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146455.

[25527] LOC148137 (Accession NM_144692.1) is another GAM161 target gene, herein designated TARGET GENE. LOC148137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148137 BINDING SITE, designated SEQ ID:14101, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25528] Another function of GAM161 is therefore inhibition of LOC148137 (Accession NM_144692.1) . Accordingly, utili-

ties of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148137.

[25529] LOC151201 (Accession XM_098021.1) is another GAM161 target gene, herein designated TARGET GENE. LOC151201 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE, designated SEQ ID:19905, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25530] Another function of GAM161 is therefore inhibition of LOC151201 (Accession XM_098021.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151201.

[25531] LOC151701 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC151701 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151701, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151701 BINDING SITE, designated SEQ ID:2777, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25532] Another function of GAM161 is therefore inhibition of LOC151701 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151701.

[25533] LOC152245 (Accession XM_098182.1) is another GAM161 target gene, herein designated TARGET GENE. LOC152245 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152245, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152245 BINDING SITE, designated SEQ ID:6203, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25534] Another function of GAM161 is therefore inhibition of LOC152245 (Accession XM_098182.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC152245.

[25535] LOC153077 (Accession XM_098307.1) is another GAM161 target gene, herein designated TARGET GENE. LOC153077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153077 BINDING SITE, designated SEQ ID:11568, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25536] Another function of GAM161 is therefore inhibition of LOC153077 (Accession XM_098307.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153077.

[25537] LOC153688 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC153688 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153688, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of LOC153688 BINDING SITE, designated SEQ ID:12866, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25538] Another function of GAM161 is therefore inhibition of LOC153688 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153688.

[25539] LOC153811 (Accession XM_087779.2) is another GAM161 target gene, herein designated TARGET GENE. LOC153811 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153811, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153811 BINDING SITE, designated SEQ ID:16081, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25540] Another function of GAM161 is therefore inhibition of LOC153811 (Accession XM_087779.2) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC153811.

[25541] LOC158310 (Accession XM_098919.1) is another GAM161 target gene, herein designated TARGET GENE. LOC158310 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158310, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158310 BINDING SITE, designated SEQ ID:8794, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25542] Another function of GAM161 is therefore inhibition of LOC158310 (Accession XM_098919.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158310.

[25543] LOC196047 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC196047 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC196047, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

LOC196047 BINDING SITE, designated SEQ ID:1349, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25544] Another function of GAM161 is therefore inhibition of LOC196047 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196047.

[25545] LOC199786 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC199786 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC199786, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199786 BINDING SITE, designated SEQ ID:11992, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25546] Another function of GAM161 is therefore inhibition of LOC199786 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199786.

[25547] LOC200301 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC200301 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC200301, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200301 BINDING SITE, designated SEQ ID:15098, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25548] Another function of GAM161 is therefore inhibition of LOC200301 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200301.

[25549] LOC200316 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC200316 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200316, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200316 BINDING SITE, designated SEQ ID:19042, to

the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25550] Another function of GAM161 is therefore inhibition of LOC200316 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200316.

[25551] LOC220575 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC220575 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC220575, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220575 BINDING SITE, designated SEQ ID:18968, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25552] Another function of GAM161 is therefore inhibition of LOC220575 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220575.

[25553] LOC221271 (Accession) is another GAM161 target gene,

herein designated TARGET GENE. LOC221271 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221271, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221271 BINDING SITE, designated SEQ ID:6488, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25554] Another function of GAM161 is therefore inhibition of LOC221271 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221271.

[25555] LOC245771 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC245771 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC245771, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC245771 BINDING SITE, designated SEQ ID:14795, to the nucleotide sequence of GAM161 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:304.

[25556] Another function of GAM161 is therefore inhibition of LOC245771 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC245771.

[25557] LOC254082 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC254082 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC254082, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254082 BINDING SITE, designated SEQ ID:2709, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25558] Another function of GAM161 is therefore inhibition of LOC254082 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254082.

[25559] LOC256306 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC256306 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC256306, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256306 BINDING SITE, designated SEQ ID:19369, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25560] Another function of GAM161 is therefore inhibition of LOC256306 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256306.

[25561] LOC51696 (Accession) is another GAM161 target gene, herein designated TARGET GENE. LOC51696 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51696, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51696 BINDING SITE, designated SEQ ID:6670, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25562] Another function of GAM161 is therefore inhibition of LOC51696 (Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51696.

[25563] Mediterranean fever (MEFV, Accession NM_000243.1) is another GAM161 target gene, herein designated TARGET GENE. MEFV BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MEFV, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MEFV BINDING SITE, designated SEQ ID:8754, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25564] Another function of GAM161 is therefore inhibition of Mediterranean fever (MEFV, Accession NM_000243.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEFV.

[25565] MGC10818 (Accession NM_030568.2) is another GAM161 target gene, herein designated TARGET GENE. MGC10818 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10818, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10818 BINDING SITE, designated SEQ ID:4141, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25566] Another function of GAM161 is therefore inhibition of MGC10818 (Accession NM_030568.2) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10818.

[25567] MGC13138 (Accession NM_033410.1) is another GAM161 target gene, herein designated TARGET GENE. MGC13138 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13138 BINDING SITE, designated SEQ ID:5265, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25568] Another function of GAM161 is therefore inhibition of MGC13138 (Accession NM_033410.1) . Accordingly, utili-

ties of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13138.

[25569] MGC29891 (Accession NM_144618.1) is another GAM161 target gene, herein designated TARGET GENE. MGC29891 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC29891, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC29891 BINDING SITE, designated SEQ ID:19764, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25570] Another function of GAM161 is therefore inhibition of MGC29891 (Accession NM_144618.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29891.

[25571] Matrix metalloproteinase-like 1 (MMPL1, Accession) is another GAM161 target gene, herein designated TARGET GENE. MMPL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MMPL1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MMPL1 BINDING SITE, designated SEQ ID:11792, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25572] Another function of GAM161 is therefore inhibition of Matrix metalloproteinase-like 1 (MMPL1, Accession) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMPL1.

[25573] Mitochondrial ribosomal protein l44 (MRPL44, Accession NM_022915.2) is another GAM161 target gene, herein designated TARGET GENE. MRPL44 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPL44, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL44 BINDING SITE, designated SEQ ID:17368, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25574] Another function of GAM161 is therefore inhibition of Mi-

tochondrial ribosomal protein l44 (MRPL44, Accession NM_022915.2) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL44.

[25575] V-myc myelocytomatosis viral oncogene homolog 2 (avian) (MYCL2, Accession NM_005377.1) is another GAM161 target gene, herein designated TARGET GENE. MYCL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYCL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYCL2 BINDING SITE, designated SEQ ID:8793, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25576] Another function of GAM161 is therefore inhibition of V-myc myelocytomatosis viral oncogene homolog 2 (avian) (MYCL2, Accession NM_005377.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYCL2.

[25577] Nuclear receptor coactivator 6 (NCOA6, Accession NM_014071.1) is another GAM161 target gene, herein designated TARGET GENE. NCOA6 BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by NCOA6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE, designated SEQ ID:19170, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25578] Another function of GAM161 is therefore inhibition of Nuclear receptor coactivator 6 (NCOA6, Accession NM_014071.1), a gene which activates gene transcription through ligand- dependent association with coactivators. and therefore may be associated with Breast cancer. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of Breast cancer., and of other diseases and clinical conditions associated with NCOA6.

[25579] The function of NCOA6 has been established by previous studies. Using the ligand- binding domain of the retinoid X receptor as bait in a yeast 2- hybrid screen to identify potential transcriptional coactivators of nuclear receptors, Lee et al. (1999) isolated a cDNA encoding a nuclear protein- activating signal cointegrator, which they designated ASC2. Sequence analysis of the 2,063 amino acid protein

predicted an N- terminal acidic domain, 2 glutamine- rich domains, and a C- terminal serine/threonine- rich domain as well as 2 separate basic potential nuclear localization signal domains and 2 copies of LXXLL motifs that function in ligand- dependent interaction with the AF2 domain of nuclear receptors. Analyzing tissue microarrays by FISH, Lee et al. (1999) found increased ASC2 copy number in 10% of breast cancer specimens and in all breast cancer cell lines. SDS- PAGE analysis showed that amino acids 586- 860, which do not include the LXXLL motifs, are the minimum interaction domain with the AF2 domain of numerous nuclear receptors. N- terminal subregions of ASC2, either alone or in conjunction with CBP (OMIM Ref. No. 600140) and SRC1 (NCOA1; 602691), stimulate ligand- dependent transactivation by wildtype nuclear receptors. Microinjection of anti- ASC2 into cells demonstrated abrogation of the transactivation function. Caira et al. (2000) and Mahajan and Samuels (2000) isolated cDNAs encoding a protein identical to ASC2, which they termed nuclear receptor- activating protein 250 kD (OMIM Ref. No. RAP250) and nuclear receptor coregulator (NRC), respectively. Northern blot analysis revealed widespread expression of an approximately 7.5- kb transcript, with a

4.5- kb splice variant detected in testis. Analysis of the testis sequence indicated that it encodes a 1,070 amino acid protein that lacks residues 972- 1964 of the full-length sequence (Caira et al., 2000). ASC2 was also found to be widely expressed during ontogeny in rat embryos. Using GST pull- down assays, Caira et al. (2000) determined that the first LXXLL motif (LVNLL, contained in residues 819- 1096) but not the second (LSQLL, residues 1491- 1495) interacted strongly with nuclear receptors. Mahajan and Samuels (2000) also found that only the first LXXLL domain is functional and that mutation of this sequence abolished transcriptional enhancement.

[25580]

[25581] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25582] Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.; Jung, Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa, D.; Jhun, B.- H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J. W. : A nuclear factor, ASC- 2, as a cancer- amplified transcriptional coactivator essential for ligand- dependent transactivation by nuclear receptors in vivo. J. Biol. Chem. 274: 34283- 34293, 1999. ; and

[25583] Mahajan, M. A.; Samuels, H. H : A new family of nuclear receptor coregulators that integrate nuclear receptor signaling through CREB- binding protein. Molec. Cell. Biol. 20: 5048- 5063.

[25584] Further studies establishing the function and utilities of NCOA6 are found in John Hopkins OMIM database record ID 605299, and in cited publications listed in Table 5, which are hereby incorporated by reference.Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NM_024831.5) is another GAM161 target gene, herein designated TARGET GENE. NCOA6IP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCOA6IP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6IP BINDING SITE, designated SEQ ID:4013, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25585] Another function of GAM161 is therefore inhibition of Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NM_024831.5) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with NCOA6IP.

[25586] Oral-facial-digital syndrome 1 (OFD1, Accession NM_003611.1) is another GAM161 target gene, herein designated TARGET GENE. OFD1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by OFD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OFD1 BINDING SITE, designated SEQ ID:10775, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25587] Another function of GAM161 is therefore inhibition of Oral-facial-digital syndrome 1 (OFD1, Accession NM_003611.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OFD1.

[25588] Phosducin-like (PDCL, Accession NM_005388.2) is another GAM161 target gene, herein designated TARGET GENE. PDCL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDCL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of PDCL BINDING SITE, designated SEQ ID:848, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25589] Another function of GAM161 is therefore inhibition of Phosducin-like (PDCL, Accession NM_005388.2), a gene which may regulate G- protein signaling and similar to phosducins. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDCL.

[25590] The function of PDCL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Phosphodiesterase 6b, cgmp-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NM_000283.1) is another GAM161 target gene, herein designated TARGET GENE. PDE6B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDE6B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDE6B BINDING SITE, designated SEQ ID:16553, to the

nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25591] Another function of GAM161 is therefore inhibition of Phosphodiesterase 6b, cgmp-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NM_000283.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE6B.

[25592] Polymeric immunoglobulin receptor (PIGR, Accession NM_002644.1) is another GAM161 target gene, herein designated TARGET GENE. PIGR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIGR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIGR BINDING SITE, designated SEQ ID:3992, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25593] Another function of GAM161 is therefore inhibition of Polymeric immunoglobulin receptor (PIGR, Accession NM_002644.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PIGR.

[25594] Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession NM_005038.1) is another GAM161 target gene, herein designated TARGET GENE. PPID BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PPID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPID BINDING SITE, designated SEQ ID:9646, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25595] Another function of GAM161 is therefore inhibition of Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession NM_005038.1), a gene which catalyzes the cis- trans isomerization of proline imidic peptide bonds in oligopeptides. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPID.

[25596] The function of PPID and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Protein kinase, interferon-inducible double stranded rna dependent (PRKR, Accession NM_002759.1)

is another GAM161 target gene, herein designated TARGET GENE. PRKR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKR BINDING SITE, designated SEQ ID:5680, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25597] Another function of GAM161 is therefore inhibition of Protein kinase, interferon-inducible double stranded rna dependent (PRKR, Accession NM_002759.1), a gene which catalyze the phosphorylation of the alpha subunit of eif2. and therefore may be associated with Huntington's disease. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of Huntington's disease, and of other diseases and clinical conditions associated with PRKR.

[25598] The function of PRKR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.PRO0902 (Accession NM_053057.2) is another GAM161 target gene, herein designated TARGET

GENE. PRO0902 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0902, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0902 BINDING SITE, designated SEQ ID:6546, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25599] Another function of GAM161 is therefore inhibition of PRO0902 (Accession NM_053057.2) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0902.

[25600] Rab39, member ras oncogene family (RAB39, Accession XM_084662.2) is another GAM161 target gene, herein designated TARGET GENE. RAB39 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAB39, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB39 BINDING SITE, designated SEQ ID:10258, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ

ID:304.

[25601] Another function of GAM161 is therefore inhibition of Rab39, member ras oncogene family (RAB39, Accession XM_084662.2) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB39.

[25602] RAP140 (Accession NM_015224.1) is another GAM161 target gene, herein designated TARGET GENE. RAP140 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAP140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAP140 BINDING SITE, designated SEQ ID:2756, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25603] Another function of GAM161 is therefore inhibition of RAP140 (Accession NM_015224.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP140.

[25604] Rhesus blood group, d antigen (RHD, Accession NM_016225.2) is another GAM161 target gene, herein

designated TARGET GENE. RHD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RHD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE, designated SEQ ID:10256, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25605] Another function of GAM161 is therefore inhibition of Rhesus blood group, d antigen (RHD, Accession NM_016225.2), a gene which Major antigen of the RH system. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[25606] The function of RHD has been established by previous studies. Bennett et al. (1993) demonstrated that DNA testing can be used to determine RhD type in chorionic villus samples or amniotic cells. An RhD- negative woman whose partner is heterozygous may have preexisting anti-RhD antibodies that may or may not affect a subsequent fetus, depending on whether it is heterozygous. A safe method of determining fetal RhD type early in pregnancy

would eliminate the risks to an RhD- negative fetus of fetal blood sampling or serial amniocenteses. Levine et al. (1941) showed that hemolytic disease of the fetus occurs in an RhD- positive fetus carried by an RhD- negative woman who has been immunized by transplacental passage of RhD- positive red cells during a previous pregnancy. When the father of the fetus being carried by a sensitized RhD- negative woman is heterozygous for RhD, as more than 50% of people are, half the fetuses will be RhD- negative and therefore require no treatment to avoid erythroblastosis fetalis. The others will be RhD- positive and require sophisticated investigative measures and treatments. Lo et al. (1998) described a noninvasive method of determining fetal RhD status by analyzing maternal plasma. Using a fluorescent- based PCR assay that was sensitive enough to detect the amount of RhD DNA found in a single cell, they determined the RhD status of singleton fetuses from 57 RhD- negative women whose partners were heterozygous for the RhD gene. This method correctly identified the RhD status of 10 of 12 fetuses whose mothers were in their first trimester of pregnancy, that of all 30 fetuses whose mothers were in their second trimester, and that of all 15 fetuses whose moth-

ers were in their third trimester. The method they described was rapid, providing results within 1 day, and represented a major advance in RhD genotyping.

[25607]

[25608] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25609] Bennett, P. R.; Le Van Kim, C.; Colin, Y.; Warwick, R. M.; Cherif- Zahar, B.; Fisk, N. M.; Cartron, J.- P. : Prenatal determination of fetal RhD type by DNA amplification. New Eng. J. Med. 329: 607- 610, 1993. ; and

[25610] Lo, Y. M. D.; Hjelm, N. M.; Fidler, C.; Sargent, I. L.; Murphy, M. F.; Chamberlain, P. F.; Poon, P. M. K.; Redman, C. W. G.; Wainscoat, J. S. : Prenatal diagnosis of fetal RhD status by mol.

[25611] Further studies establishing the function and utilities of RHD are found in John Hopkins OMIM database record ID 111680, and in cited publications listed in Table 5, which are hereby incorporated by reference.Sh3-domain binding protein 2 (SH3BP2, Accession NM_003023.2) is another GAM161 target gene, herein designated TARGET GENE. SH3BP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SH3BP2, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SH3BP2 BINDING SITE, designated SEQ ID:12256, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25612] Another function of GAM161 is therefore inhibition of Sh3-domain binding protein 2 (SH3BP2, Accession NM_003023.2) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BP2.

[25613] Short stature homeobox (SHOX, Accession) is another GAM161 target gene, herein designated TARGET GENE. SHOX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SHOX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SHOX BINDING SITE, designated SEQ ID:4418, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25614] Another function of GAM161 is therefore inhibition of Short stature homeobox (SHOX, Accession) . Accordingly,

utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHOX.

[25615] Synaptosomal-associated protein, 23kda (SNAP23, Accession NM_003825.2) is another GAM161 target gene, herein designated TARGET GENE. SNAP23 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNAP23, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP23 BINDING SITE, designated SEQ ID:5601, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25616] Another function of GAM161 is therefore inhibition of Synaptosomal-associated protein, 23kda (SNAP23, Accession NM_003825.2), a gene which is essential component of the high affinity receptor for the general membrane fusion machinery. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP23.

[25617] The function of SNAP23 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM30.1.Sorting nexin 15 (SNX15, Accession NM_013306.2) is another GAM161 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:19041, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25618] Another function of GAM161 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NM_013306.2) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15.

[25619] STAF65(gamma) (Accession NM_014860.1) is another GAM161 target gene, herein designated TARGET GENE. STAF65(gamma) BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STAF65(gamma), corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAF65(gamma) BINDING SITE, designated SEQ ID:18839, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25620] Another function of GAM161 is therefore inhibition of STAF65(gamma) (Accession NM_014860.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAF65(gamma).

[25621] Tap binding protein (tapasin) (TAPBP, Accession NM_003190.3) is another GAM161 target gene, herein designated TARGET GENE. TAPBP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TAPBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAPBP BINDING SITE, designated SEQ ID:9641, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25622] Another function of GAM161 is therefore inhibition of Tap binding protein (tapasin) (TAPBP, Accession

NM_003190.3), a gene which is involved in MHC class I-restricted antigen processing. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAPBP.

[25623] The function of TAPBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Transcription factor 2, hepatic; lf-b3; variant hepatic nuclear factor (TCF2, Accession NM_000458.1) is another GAM161 target gene, herein designated TARGET GENE. TCF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TCF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCF2 BINDING SITE, designated SEQ ID:4621, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25624] Another function of GAM161 is therefore inhibition of Transcription factor 2, hepatic; lf-b3; variant hepatic nuclear factor (TCF2, Accession NM_000458.1), a gene which probably binds to the inverted palindrome 5'- gttaatnat-

taac- 3'. and therefore is associated with Maturity- onset diabetes of the young type 5 (mody5), familial hypoplastic glomerulocystic kidney disease (gckd). Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of Maturity- onset diabetes of the young type 5 (mody5), familial hypoplastic glomerulocystic kidney disease (gckd), and of other diseases and clinical conditions associated with TCF2.

[25625] The function of TCF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.Teratocarcinoma-derived growth factor 1 (TDGF1, Accession NM_003212.1) is another GAM161 target gene, herein designated TARGET GENE. TDGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TDGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TDGF1 BINDING SITE, designated SEQ ID:2312, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25626] Another function of GAM161 is therefore inhibition of

Teratocarcinoma-derived growth factor 1 (TDGF1, Accession NM_003212.1), a gene which can play a role in the determination of the epiblastic cells that subsequently give rise to the mesoderm. and therefore may be associated with Forebrain defects. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of Forebrain defects, and of other diseases and clinical conditions associated with TDGF1.

[25627] The function of TDGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NM_021809.2) is another GAM161 target gene, herein designated TARGET GENE. TGIF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGIF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGIF2 BINDING SITE, designated SEQ ID:14237, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25628] Another function of GAM161 is therefore inhibition of

Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NM_021809.2) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGIF2.

[25629] Tnf receptor-associated factor 5 (TRAF5, Accession NM_004619.2) is another GAM161 target gene, herein designated TARGET GENE. TRAF5 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TRAF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:1063, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25630] Another function of GAM161 is therefore inhibition of Tnf receptor-associated factor 5 (TRAF5, Accession NM_004619.2), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5.

[25631] The function of TRAF5 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Transient receptor potential cation channel, subfamily m, member 6 (TRPM6, Accession NM_017662.3) is another GAM161 target gene, herein designated TARGET GENE. TRPM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPM6 BINDING SITE, designated SEQ ID:12681, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25632] Another function of GAM161 is therefore inhibition of Transient receptor potential cation channel, subfamily m, member 6 (TRPM6, Accession NM_017662.3), a gene which contains a predicted ion channel domain and a protein kinase domain. and therefore is associated with Hypomagnesemia with secondary hypocalcemia. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of Hypomagnesemia with secondary hypocalcemia, and of other diseases and clinical condi-

tions associated with TRPM6.

[25633] The function of TRPM6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Vent-like homeobox 2 (VENTX2, Accession NM_014468.1) is another GAM161 target gene, herein designated TARGET GENE. VENTX2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VENTX2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VENTX2 BINDING SITE, designated SEQ ID:17401, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25634] Another function of GAM161 is therefore inhibition of Vent-like homeobox 2 (VENTX2, Accession NM_014468.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VENTX2.

[25635] Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NM_133332.1) is another GAM161 target gene, herein designated TARGET GENE. WHSC1 BINDING SITE is a

target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WHSC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE, designated SEQ ID:18202, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25636] Another function of GAM161 is therefore inhibition of Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NM_133332.1), a gene which binds covalently to and repairs g/t mismatches. and therefore may be associated with Wolf- hirschhorn syndrome. Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of Wolf- hirschhorn syndrome, and of other diseases and clinical conditions associated with WHSC1.

[25637] The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Zinc finger protein 253 (ZNF253, Accession NM_021047.1) is another GAM161 target gene, herein designated TARGET GENE. ZNF253 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by ZNF253, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF253 BINDING SITE, designated SEQ ID:12566, to the nucleotide sequence of GAM161 RNA, herein designated GAM RNA, also designated SEQ ID:304.

[25638] Another function of GAM161 is therefore inhibition of Zinc finger protein 253 (ZNF253, Accession NM_021047.1) . Accordingly, utilities of GAM161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF253.

[25639]

[25640] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 162 (GAM162), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25641] GAM162 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM162 was detected is described hereinabove with reference to Figs. 8-15.

[25642] GAM162 gene, herein designated GAM GENE, and GAM162 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25643] GAM162 gene encodes a GAM162 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM162 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM162 precursor RNA is designated SEQ ID:58, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:58 is located at position 76562126 relative to chromosome 17.

[25644] GAM162 precursor RNA folds onto itself, forming GAM162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25645] GAM162 precursor RNA folds onto itself, forming GAM162 folded precursor RNA, herein designated GAM FOLDED

PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25646] Nucleotide sequence of GAM162 precursor RNA, designated SEQ-ID: 58, and a schematic representation of a predicted secondary folding of GAM162 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25647] An enzyme complex designated DICER COMPLEX, `dices` the GAM162 folded precursor RNA into GAM162 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM162 RNA is designated SEQ ID:376, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby in-

corporated by reference.

[25648] GAM162 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM162 target RNA, herein designated GAM TARGET RNA. GAM162 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25649] GAM162 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM162 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM162 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM162 RNA may have a different number of target binding sites in untranslated regions of a GAM162 target RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25650] The complementary binding of GAM162 RNA, herein designated GAM RNA, to target binding sites on GAM162 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM162 target RNA into GAM162 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25651] It is appreciated that GAM162 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM162 target genes. The mRNA of each one of this plurality of GAM162 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM162 RNA, herein designated GAM RNA, and which when bound by GAM162 RNA causes inhibition of translation of respective one or more GAM162 target proteins.

[25652] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM162 gene, herein designated GAM GENE, on one or more GAM162 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25653] It is appreciated that specific functions and accordingly utilities of GAM162 correlate with, and may be deduced from, the identity of the target genes which GAM162 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25654]

[25655]

[25656] KIAA1582 (Accession XM_037262.4) is a GAM162 target gene, herein designated TARGET GENE. KIAA1582 BIND-

ING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1582, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1582 BINDING SITE, designated SEQ ID:12216, to the nucleotide sequence of GAM162 RNA, herein designated GAM RNA, also designated SEQ ID:376.

[25657] A function of GAM162 is therefore inhibition of KIAA1582 (Accession XM_037262.4) . Accordingly, utilities of GAM162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1582.

[25658] VRP (Accession NM_007063.1) is another GAM162 target gene, herein designated TARGET GENE. VRP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VRP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VRP BINDING SITE, designated SEQ ID:11972, to the nucleotide sequence of GAM162 RNA, herein designated GAM RNA, also designated SEQ ID:376.

[25659] Another function of GAM162 is therefore inhibition of VRP (Accession NM_007063.1) . Accordingly, utilities of GAM162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VRP.

[25660]

[25661] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 163 (GAM163), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25662] GAM163 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM163 was detected is described hereinabove with reference to Figs. 8-15.

[25663] GAM163 gene, herein designated GAM GENE, and GAM163 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25664] GAM163 gene encodes a GAM163 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM163 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of

GAM163 precursor RNA is designated SEQ ID:84, and is provided hereinbelow with reference to the sequence listing part.

[25665] GAM163 precursor RNA folds onto itself, forming GAM163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25666] GAM163 precursor RNA folds onto itself, forming GAM163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25667] Nucleotide sequence of GAM163 precursor RNA, designated SEQ-ID: 84, and a schematic representation of a

predicted secondary folding of GAM163 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25668] An enzyme complex designated DICER COMPLEX, `dices` the GAM163 folded precursor RNA into GAM163 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM163 RNA is designated SEQ ID:249, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25669] GAM163 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM163 target RNA, herein designated GAM TARGET RNA. GAM163 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25670] GAM163 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM163 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM163 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM163 RNA may have a different number of target binding sites in untranslated regions of a GAM163 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25671] The complementary binding of GAM163 RNA, herein designated GAM RNA, to target binding sites on GAM163 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM163 target RNA into GAM163 tar-

get protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25672] It is appreciated that GAM163 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM163 target genes. The mRNA of each one of this plurality of GAM163 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM163 RNA, herein designated GAM RNA, and which when bound by GAM163 RNA causes inhibition of translation of respective one or more GAM163 target proteins.

[25673] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM163 gene, herein designated GAM GENE, on one or more GAM163 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25674] It is appreciated that specific functions and accordingly utilities of GAM163 correlate with, and may be deduced from, the identity of the target genes which GAM163 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25675]

[25676]

[25677] Endothelial differentiation, g-protein-coupled receptor 6 (EDG6, Accession NM_003775.1) is a GAM163 target gene, herein designated TARGET GENE. EDG6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EDG6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDG6 BINDING SITE, designated SEQ ID:859, to the nucleotide sequence of GAM163 RNA, herein designated GAM RNA, also designated SEQ ID:249.

[25678] A function of GAM163 is therefore inhibition of Endothelial differentiation, g-protein-coupled receptor 6 (EDG6, Accession NM_003775.1), a gene which may act as a receptor for a trophic factor and is involved in the survival of brain cells. Accordingly, utilities of GAM163 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDG6.

[25679] The function of EDG6 has been established by previous studies. By PCR with degenerate oligonucleotides derived from regions conserved among GPCRs, Graler et al. (1998) cloned differentiated dendritic cell cDNAs encoding EDG6. The predicted 384- amino acid EDG6 protein has 7 transmembrane domains. The EDG6 protein shares 82% sequence identity with mouse Edg6, 46% identity with human EDG3 (OMIM Ref. No. 601965), 44% identity with human EDG1, 39% identity with human EDG4 (OMIM Ref. No. 605110), and 37% identity with human EDG2. Northern blot analysis indicated that EDG6 is expressed as a 1.7-kb transcript in fetal and adult lymphoid and hematopoietic tissues, lung, and Burkitt lymphoma cell lines. Graler et al. (1998) noted that the 3- prime end of their EDG6 cDNA is identical to a short sequence encompassing the dinucleotide repeat polymorphism D19S120 (GenBank

X65642), which was assigned to 19p13.3 by Jedlicka et al. (1994). By PCR of human genomic DNA using a gene-specific primer to EDG6 and a primer to the D19S120 amplicon, Graler et al. (1998) localized the EDG6 gene to 19p13.3.

[25680]

[25681] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25682] Graler, M. H.; Bernhardt, G.; Lipp, M. : EDG6, a novel G-protein- coupled receptor related to receptors for bioactive lysophospholipids, is specifically expressed in lymphoid tissue. Genomics 53: 164- 169, 1998. ; and

[25683] Jedlicka, A. E.; Taylor, E. W.; Meyers, D. A.; Liu, Z.; Levitt, R. C. : Localization of the highly polymorphic locus D19S120 to 19p13.3 by linkage. Cytogenet. Cell. Genet. 65: 140 only.

[25684] Further studies establishing the function and utilities of EDG6 are found in John Hopkins OMIM database record ID 603751, and in cited publications listed in Table 5, which are hereby incorporated by reference.LOC112868 (Accession XM_053402.4) is another GAM163 target gene, herein designated TARGET GENE. LOC112868 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112868, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112868 BINDING SITE, designated SEQ ID:17580, to the nucleotide sequence of GAM163 RNA, herein designated GAM RNA, also designated SEQ ID:249.

[25685] Another function of GAM163 is therefore inhibition of LOC112868 (Accession XM_053402.4) . Accordingly, utilities of GAM163 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112868.

[25686] Oligodendrocyte lineage transcription factor 2 (OLIG2, Accession NM_005806.1) is another GAM163 target gene, herein designated TARGET GENE. OLIG2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLIG2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OLIG2 BINDING SITE, designated SEQ ID:18460, to the nucleotide sequence of GAM163 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:249.

[25687] Another function of GAM163 is therefore inhibition of Oligodendrocyte lineage transcription factor 2 (OLIG2, Accession NM_005806.1), a gene which may bind DNA and contains a helix- loop- helix DNA- binding domain. Accordingly, utilities of GAM163 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OLIG2.

[25688] The function of OLIG2 has been established by previous studies. The oligodendrocyte lineage transcription factors OLIG1 (OMIM Ref. No. 606385) and OLIG2, originally identified in rodents, encode basic helix- loop- helix transcription factors. In the rodent central nervous system, they are expressed exclusively in oligodendrocytes and oligodendrocyte precursors (Lu et al., 2000; Zhou et al., 2000). Pursuing the suggestion that novel molecular markers might be found among factors that have roles in glial development (Raff et al., 1983), Lu et al. (2001) found that the human OLIG1/2 genes are expressed strongly in oligodendroglioma, contrasting absent or low expression in astrocytoma. Their study provided evidence that neoplastic cells of oligodendroglioma resemble oligodendrocytes or their progenitor cells and may derive

from cells of this lineage.

[25689] Animal model experiments lend further support to the function of OLIG2. In Olig1/2 double- mutant mice, Zhou and Anderson (2002) found that motoneurons were largely eliminated, and oligodendrocyte differentiation was abolished. Lineage tracing data suggested that Olig1/2 - /- pMN progenitors instead generated V2 interneurons and then astrocytes. This apparent conversion likely reflects independent roles for OLIG1/2 in specifying motoneuron and oligodendrocyte fates. OLIG genes therefore couple neuronal and glial subtype specification, unlike proneural bHLH factors that control the neuron versus glia decision. The authors concluded that, in the spinal cord, OLIG and proneural genes comprise a combinatorial code for the specification of neurons, astrocytes, and oligodendrocytes, the 3 fundamental cell types of the central nervous system.

[25690] It is appreciated that the abovementioned animal model for OLIG2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[25691] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[25692] Lu, Q. R.; Park, J. K.; Noll, E.; Chan, J. A.; Alberta, J.; Yuk, D.; Alzamora, M. G.; Louis, D. N.; Stiles, C. D.; Rowitch, D. H.; Black, P. M. : Oligodendrocyte lineage genes (OLIG) as molecular markers for human glial brain tumors. Proc. Nat. Acad. Sci. 98: 10851- 10856, 2001. ; and

[25693] Zhou, Q.; Anderson, D. J. : The bHLH transcription factors OLIG2 and OLIG1 couple neuronal and glial subtype specification. Cell 109: 61- 73, 2002.

[25694] Further studies establishing the function and utilities of OLIG2 are found in John Hopkins OMIM database record ID 606386, and in cited publications listed in Table 5, which are hereby incorporated by reference.Phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN, Accession NM_000314.1) is another GAM163 target gene, herein designated TARGET GENE. PTEN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTEN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTEN BINDING SITE, designated SEQ ID:2919, to the nucleotide sequence of GAM163 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:249.

[25695] Another function of GAM163 is therefore inhibition of Phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN, Accession NM_000314.1) . Accordingly, utilities of GAM163 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTEN.

[25696]

[25697] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 164 (GAM164), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25698] GAM164 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM164 was detected is described hereinabove with reference to Figs. 8-15.

[25699] GAM164 gene, herein designated GAM GENE, and GAM164 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25700] GAM164 gene encodes a GAM164 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA

genes, and unlike most ordinary genes, GAM164 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM164 precursor RNA is designated SEQ ID:66, and is provided hereinbelow with reference to the sequence listing part.

[25701] GAM164 precursor RNA folds onto itself, forming GAM164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25702] GAM164 precursor RNA folds onto itself, forming GAM164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nu-

cleotide sequence of the second half thereof.

[25703] Nucleotide sequence of GAM164 precursor RNA, designated SEQ-ID: 66, and a schematic representation of a predicted secondary folding of GAM164 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25704] An enzyme complex designated DICER COMPLEX, `dices` the GAM164 folded precursor RNA into GAM164 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM164 RNA is designated SEQ ID:322, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25705] GAM164 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM164 target RNA, herein designated GAM TARGET RNA. GAM164 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein

coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25706] GAM164 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM164 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM164 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM164 RNA may have a different number of target binding sites in untranslated regions of a GAM164 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25707] The complementary binding of GAM164 RNA, herein designated GAM RNA, to target binding sites on GAM164 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM164 target RNA into GAM164 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25708] It is appreciated that GAM164 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM164 target genes. The mRNA of each one of this plurality of GAM164 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM164 RNA, herein designated GAM RNA, and which when bound by GAM164 RNA causes inhibition of translation of respective one or more GAM164 target proteins.

[25709] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM164 gene, herein designated GAM GENE, on one or more GAM164 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25710] It is appreciated that specific functions and accordingly utilities of GAM164 correlate with, and may be deduced from, the identity of the target genes which GAM164 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25711]

[25712]

[25713] FLJ21986 (Accession NM_024913.1) is a GAM164 target gene, herein designated TARGET GENE. FLJ21986 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ21986, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21986 BINDING SITE, designated SEQ ID:11076, to the nucleotide

sequence of GAM164 RNA, herein designated GAM RNA, also designated SEQ ID:322.

[25714] A function of GAM164 is therefore inhibition of FLJ21986 (Accession NM_024913.1) . Accordingly, utilities of GAM164 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21986.

[25715] Lipase, member i (LIPI, Accession) is another GAM164 target gene, herein designated TARGET GENE. LIPI BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LIPI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LIPI BINDING SITE, designated SEQ ID:15797, to the nucleotide sequence of GAM164 RNA, herein designated GAM RNA, also designated SEQ ID:322.

[25716] Another function of GAM164 is therefore inhibition of Lipase, member i (LIPI, Accession) . Accordingly, utilities of GAM164 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIPI.

[25717]

[25718] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, re-

ferred to here as Genomic Address Messenger 165 (GAM165), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25719] GAM165 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM165 was detected is described hereinabove with reference to Figs. 8-15.

[25720] GAM165 gene, herein designated GAM GENE, and GAM165 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25721] GAM165 gene encodes a GAM165 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM165 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM165 precursor RNA is designated SEQ ID:134, and is provided hereinbelow with reference to the sequence listing part.

[25722] GAM165 precursor RNA folds onto itself, forming GAM165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin struc-

ture`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25723] GAM165 precursor RNA folds onto itself, forming GAM165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25724] Nucleotide sequence of GAM165 precursor RNA, designated SEQ-ID: 134, and a schematic representation of a predicted secondary folding of GAM165 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25725] An enzyme complex designated DICER COMPLEX, `dices` the GAM165 folded precursor RNA into GAM165 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM165 RNA is designated SEQ ID:270, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25726] GAM165 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM165 target RNA, herein designated GAM TARGET RNA. GAM165 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25727] GAM165 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM165 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM165 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such

target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM165 RNA may have a different number of target binding sites in untranslated regions of a GAM165 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25728] The complementary binding of GAM165 RNA, herein designated GAM RNA, to target binding sites on GAM165 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM165 target RNA into GAM165 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25729] It is appreciated that GAM165 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM165 target genes. The mRNA of each one of this plurality of GAM165 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM165 RNA, herein designated GAM RNA, and which when bound by GAM165 RNA causes inhibition of translation of respective one or more GAM165 target proteins.

[25730] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM165 gene, herein designated GAM GENE, on one or more GAM165 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25731] It is appreciated that specific functions and accordingly utilities of GAM165 correlate with, and may be deduced from, the identity of the target genes which GAM165

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25732]

[25733]

[25734] Ras homolog gene family, member c (ARHC, Accession NM_175744.1) is a GAM165 target gene, herein designated TARGET GENE. ARHC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ARHC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHC BINDING SITE, designated SEQ ID:15644, to the nucleotide sequence of GAM165 RNA, herein designated GAM RNA, also designated SEQ ID:270.

[25735] A function of GAM165 is therefore inhibition of Ras homolog gene family, member c (ARHC, Accession NM_175744.1), a gene which remodels of the actin cytoskeleton during cell morphogenesis and motility. and therefore may be associated with Metastatic melanoma. Accordingly, utilities of GAM165 include diagnosis, prevention and treatment of Metastatic melanoma., and of

other diseases and clinical conditions associated with ARHC.

[25736] The function of ARHC has been established by previous studies. The small guanosine triphosphatase Rho regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility. In their Figure 3C, Maekawa et al. (1999) diagrammed proposed signaling pathways for Rho- induced remodeling of the actin cytoskeleton. They demonstrated that active Rho signals to its downstream effector ROCK (OMIM Ref. No. 601702), which phosphorylates and activates LIM kinase (see OMIM Ref. No. 601329). LIM kinase, in turn, phosphorylates cofilin (OMIM Ref. No. 601442), inhibiting its actin- depolymerizing activity. Clark et al. (2000) used an in vivo selection scheme to select highly metastatic melanoma cells. By analyzing these cells on DNA arrays, they defined a pattern of gene expression that correlates with progression to a metastatic phenotype. In particular, Clark et al. (2000) showed enhanced expression of several genes involved in extracellular matrix assembly and of a second set of genes that regulate, either directly or indirectly, the actin-based cytoskeleton. Clark et al. (2000) found that RhoC enhances metastasis when overexpressed, whereas a

dominant- negative Rho inhibits metastasis. Analysis of the phenotype of cells expressing dominant- negative Rho or RhoC indicates that RhoC is important in tumor cell invasion. The genomic approach allowed Clark et al. (2000) to identify families of genes involved in a process, not just single genes, and could indicate which molecular and cellular events might be important in complex biologic processes such as metastasis.

[25737]

[25738] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25739] Clark, E. A.; Golub, T. R.; Lander, E. S.; Hynes, R. O. : Genomic analysis of metastasis reveals an essential role for RhoC. Nature 406: 532- 535, 2000. ; and

[25740] Maekawa, M.; Ishizaki, T.; Boku, S.; Watanabe, N.; Fujita, A.; Iwamatsu, A.; Obinata, T.; Ohashi, K.; Mizuno, K.; Narumiya, S. : Signaling from Rho to the actin cytoskeleton through pro.

[25741] Further studies establishing the function and utilities of ARHC are found in John Hopkins OMIM database record ID 165380, and in cited publications listed in Table 5, which are hereby incorporated by reference.BNIP-S (Accession

NM_138278.1) is another GAM165 target gene, herein designated TARGET GENE. BNIP-S BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BNIP-S, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BNIP-S BINDING SITE, designated SEQ ID:1814, to the nucleotide sequence of GAM165 RNA, herein designated GAM RNA, also designated SEQ ID:270.

[25742] Another function of GAM165 is therefore inhibition of BNIP-S (Accession NM_138278.1) . Accordingly, utilities of GAM165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BNIP-S.

[25743] DKFZp434M0331 (Accession NM_017600.1) is another GAM165 target gene, herein designated TARGET GENE. DKFZp434M0331 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp434M0331, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434M0331 BINDING SITE, designated SEQ ID:8421, to the nucleotide sequence of

GAM165 RNA, herein designated GAM RNA, also designated SEQ ID:270.

[25744] Another function of GAM165 is therefore inhibition of DKFZp434M0331 (Accession NM_017600.1) . Accordingly, utilities of GAM165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434M0331.

[25745] FLJ14728 (Accession) is another GAM165 target gene, herein designated TARGET GENE. FLJ14728 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ14728, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14728 BINDING SITE, designated SEQ ID:9157, to the nucleotide sequence of GAM165 RNA, herein designated GAM RNA, also designated SEQ ID:270.

[25746] Another function of GAM165 is therefore inhibition of FLJ14728 (Accession) . Accordingly, utilities of GAM165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14728.

[25747] KIAA1969 (Accession) is another GAM165 target gene, herein designated TARGET GENE. KIAA1969 BINDING SITE

is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1969, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1969 BINDING SITE, designated SEQ ID:12294, to the nucleotide sequence of GAM165 RNA, herein designated GAM RNA, also designated SEQ ID:270.

[25748] Another function of GAM165 is therefore inhibition of KIAA1969 (Accession) . Accordingly, utilities of GAM165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1969.

[25749] LOC199777 (Accession NM_145297.1) is another GAM165 target gene, herein designated TARGET GENE. LOC199777 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC199777, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199777 BINDING SITE, designated SEQ ID:16714, to the nucleotide sequence of GAM165 RNA, herein designated GAM RNA, also designated SEQ ID:270.

[25750] Another function of GAM165 is therefore inhibition of

LOC199777 (Accession NM_145297.1) . Accordingly, utilities of GAM165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199777.

[25751] LOC199906 (Accession XM_114052.1) is another GAM165 target gene, herein designated TARGET GENE. LOC199906 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC199906, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199906 BINDING SITE, designated SEQ ID:18302, to the nucleotide sequence of GAM165 RNA, herein designated GAM RNA, also designated SEQ ID:270.

[25752] Another function of GAM165 is therefore inhibition of LOC199906 (Accession XM_114052.1) . Accordingly, utilities of GAM165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199906.

[25753] MGC20460 (Accession NM_053043.1) is another GAM165 target gene, herein designated TARGET GENE. MGC20460 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC20460, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC20460 BINDING SITE, designated SEQ ID:17732, to the nucleotide sequence of GAM165 RNA, herein designated GAM RNA, also designated SEQ ID:270.

[25754] Another function of GAM165 is therefore inhibition of MGC20460 (Accession NM_053043.1) . Accordingly, utilities of GAM165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC20460.

[25755] Transducin (beta)-like 1x-linked (TBL1X, Accession NM_005647.2) is another GAM165 target gene, herein designated TARGET GENE. TBL1X BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TBL1X, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TBL1X BINDING SITE, designated SEQ ID:11582, to the nucleotide sequence of GAM165 RNA, herein designated GAM RNA, also designated SEQ ID:270.

[25756] Another function of GAM165 is therefore inhibition of

Transducin (beta)-like 1x-linked (TBL1X, Accession NM_005647.2), a gene which activates latent HDAC3 activity. Accordingly, utilities of GAM165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBL1X.

[25757] The function of TBL1X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM28.1.

[25758] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 166 (GAM166), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25759] GAM166 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM166 was detected is described hereinabove with reference to Figs. 8-15.

[25760] GAM166 gene, herein designated GAM GENE, and GAM166 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25761] GAM166 gene encodes a GAM166 precursor RNA, herein

designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM166 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM166 precursor RNA is designated SEQ ID:161, and is provided hereinbelow with reference to the sequence listing part.

[25762] GAM166 precursor RNA folds onto itself, forming GAM166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25763] GAM166 precursor RNA folds onto itself, forming GAM166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate

or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25764] Nucleotide sequence of GAM166 precursor RNA, designated SEQ-ID: 161, and a schematic representation of a predicted secondary folding of GAM166 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25765] An enzyme complex designated DICER COMPLEX, `dices` the GAM166 folded precursor RNA into GAM166 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM166 RNA is designated SEQ ID:232, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25766] GAM166 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM166 target RNA, herein designated GAM TARGET RNA. GAM166 target RNA comprises three regions, as is typical of mRNA of

a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25767] GAM166 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM166 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM166 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM166 RNA may have a different number of target binding sites in untranslated regions of a GAM166 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25768] The complementary binding of GAM166 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM166 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM166 target RNA into GAM166 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25769] It is appreciated that GAM166 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM166 target genes. The mRNA of each one of this plurality of GAM166 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM166 RNA, herein designated GAM RNA, and which when bound by GAM166 RNA causes inhibition of translation of respective one or more GAM166 target proteins.

[25770] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM166 gene, herein designated GAM GENE, on one or more GAM166 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary bind-

ing site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25771] It is appreciated that specific functions and accordingly utilities of GAM166 correlate with, and may be deduced from, the identity of the target genes which GAM166 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25772]

[25773]

[25774] MGC13198 (Accession) is a GAM166 target gene, herein designated TARGET GENE. MGC13198 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13198, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13198

BINDING SITE, designated SEQ ID:1875, to the nucleotide sequence of GAM166 RNA, herein designated GAM RNA, also designated SEQ ID:232.

[25775] A function of GAM166 is therefore inhibition of MGC13198 (Accession) . Accordingly, utilities of GAM166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13198.

[25776] NEBL (Accession NM_006393.1) is another GAM166 target gene, herein designated TARGET GENE. NEBL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NEBL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEBL BINDING SITE, designated SEQ ID:6830, to the nucleotide sequence of GAM166 RNA, herein designated GAM RNA, also designated SEQ ID:232.

[25777] Another function of GAM166 is therefore inhibition of NEBL (Accession NM_006393.1) . Accordingly, utilities of GAM166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEBL.

[25778]

[25779] Fig. 8 further provides a conceptual description of a novel

bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 167 (GAM167), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25780] GAM167 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM167 was detected is described hereinabove with reference to Figs. 8-15.

[25781] GAM167 gene, herein designated GAM GENE, and GAM167 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25782] GAM167 gene encodes a GAM167 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM167 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM167 precursor RNA is designated SEQ ID:140, and is provided hereinbelow with reference to the sequence listing part.

[25783] GAM167 precursor RNA folds onto itself, forming GAM167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25784] GAM167 precursor RNA folds onto itself, forming GAM167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25785] Nucleotide sequence of GAM167 precursor RNA, designated SEQ-ID: 140, and a schematic representation of a predicted secondary folding of GAM167 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25786] An enzyme complex designated DICER COMPLEX, `dices` the GAM167 folded precursor RNA into GAM167 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM167 RNA is designated SEQ ID:236, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25787] GAM167 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM167 target RNA, herein designated GAM TARGET RNA. GAM167 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25788] GAM167 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM167 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM167 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target

binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM167 RNA may have a different number of target binding sites in untranslated regions of a GAM167 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25789] The complementary binding of GAM167 RNA, herein designated GAM RNA, to target binding sites on GAM167 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM167 target RNA into GAM167 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25790] It is appreciated that GAM167 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM167 target genes. The mRNA of each one of this plurality of GAM167 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM167 RNA, herein designated GAM RNA, and which when bound by GAM167 RNA causes inhibition of translation of respective one or more GAM167 target proteins.

[25791] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM167 gene, herein designated GAM GENE, on one or more GAM167 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25792] It is appreciated that specific functions and accordingly utilities of GAM167 correlate with, and may be deduced

from, the identity of the target genes which GAM167 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25793]

[25794]

[25795] Kruppel-like factor 12 (KLF12, Accession NM_007249.3) is a GAM167 target gene, herein designated TARGET GENE. KLF12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLF12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLF12 BINDING SITE, designated SEQ ID:14666, to the nucleotide sequence of GAM167 RNA, herein designated GAM RNA, also designated SEQ ID:236.

[25796] A function of GAM167 is therefore inhibition of Kruppel-like factor 12 (KLF12, Accession NM_007249.3) . Accordingly, utilities of GAM167 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF12.

[25797] LOC131873 (Accession XM_067585.7) is another GAM167

target gene, herein designated TARGET GENE. LOC131873 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC131873, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC131873 BINDING SITE, designated SEQ ID:11445, to the nucleotide sequence of GAM167 RNA, herein designated GAM RNA, also designated SEQ ID:236.

[25798] Another function of GAM167 is therefore inhibition of LOC131873 (Accession XM_067585.7) . Accordingly, utilities of GAM167 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC131873.

[25799] LOC63929 (Accession NM_022098.1) is another GAM167 target gene, herein designated TARGET GENE. LOC63929 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC63929, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC63929 BINDING SITE, designated SEQ ID:17904, to the nucleotide sequence of GAM167 RNA, herein designated

GAM RNA, also designated SEQ ID:236.

[25800] Another function of GAM167 is therefore inhibition of LOC63929 (Accession NM_022098.1) . Accordingly, utilities of GAM167 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC63929.

[25801] VIT1 (Accession) is another GAM167 target gene, herein designated TARGET GENE. VIT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VIT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VIT1 BINDING SITE, designated SEQ ID:16317, to the nucleotide sequence of GAM167 RNA, herein designated GAM RNA, also designated SEQ ID:236.

[25802] Another function of GAM167 is therefore inhibition of VIT1 (Accession) . Accordingly, utilities of GAM167 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIT1.

[25803]

[25804] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, re-

ferred to here as Genomic Address Messenger 168 (GAM168), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25805] GAM168 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM168 was detected is described hereinabove with reference to Figs. 8-15.

[25806] GAM168 gene, herein designated GAM GENE, and GAM168 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25807] GAM168 gene encodes a GAM168 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM168 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM168 precursor RNA is designated SEQ ID:97, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:97 is located at position 48046908 relative to chromosome 19.

[25808] GAM168 precursor RNA folds onto itself, forming GAM168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25809] GAM168 precursor RNA folds onto itself, forming GAM168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25810] Nucleotide sequence of GAM168 precursor RNA, designated SEQ-ID: 97, and a schematic representation of a predicted secondary folding of GAM168 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25811] An enzyme complex designated DICER COMPLEX, `dices` the GAM168 folded precursor RNA into GAM168 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM168 RNA is designated SEQ ID:217, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25812] GAM168 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM168 target RNA, herein designated GAM TARGET RNA. GAM168 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25813] GAM168 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM168 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM168 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target

binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM168 RNA may have a different number of target binding sites in untranslated regions of a GAM168 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25814] The complementary binding of GAM168 RNA, herein designated GAM RNA, to target binding sites on GAM168 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM168 target RNA into GAM168 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25815] It is appreciated that GAM168 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM168 target genes. The mRNA of each one of this plurality of GAM168 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM168 RNA, herein designated GAM RNA, and which when bound by GAM168 RNA causes inhibition of translation of respective one or more GAM168 target proteins.

[25816] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM168 gene, herein designated GAM GENE, on one or more GAM168 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25817] It is appreciated that specific functions and accordingly utilities of GAM168 correlate with, and may be deduced

from, the identity of the target genes which GAM168 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25818]

[25819]

[25820] LOC220930 (Accession XM_167624.3) is a GAM168 target gene, herein designated TARGET GENE. LOC220930 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC220930, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220930 BINDING SITE, designated SEQ ID:3451, to the nucleotide sequence of GAM168 RNA, herein designated GAM RNA, also designated SEQ ID:217.

[25821] A function of GAM168 is therefore inhibition of LOC220930 (Accession XM_167624.3) . Accordingly, utilities of GAM168 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220930.

[25822] PIR51 (Accession NM_006479.2) is another GAM168 target gene, herein designated TARGET GENE. PIR51 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIR51, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIR51 BINDING SITE, designated SEQ ID:14378, to the nucleotide sequence of GAM168 RNA, herein designated GAM RNA, also designated SEQ ID:217.

[25823] Another function of GAM168 is therefore inhibition of PIR51 (Accession NM_006479.2), a gene which interacts with the RAD51 recombinase protein and is involved in DNA recombination and repair. Accordingly, utilities of GAM168 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIR51.

[25824] The function of PIR51 has been established by previous studies. RAD51 (OMIM Ref. No. 179617), a eukaryotic homolog of the bacterial RecA recombinase, plays a role in a variety of recombination events in the eukaryotic cell. Using a yeast 2- hybrid screen with human RAD51 as the bait, Mizuta et al. (1997) isolated mouse cDNAs corresponding to a gene that they designated Rab22. The Rab22 protein interacted with RAD51 in vitro and colocalized with RAD51 in large nuclear foci in hamster cells. Ko-

valenko et al. (1997) also used a yeast 2- hybrid screen with RAD51 as the bait and isolated a HeLa cell cDNA encoding a protein that they called PIR51 for 'protein interacting with Rad51'. The predicted PIR51 protein has 335 amino acids and a calculated pI of 9.95. The authors suggested that PIR51 is the human homolog of mouse Rab22 since the 2 proteins share 63% sequence identity. Northern blot analysis revealed that PIR51 is expressed as a 2.4- kb mRNA in human testis and thymus, and at lower levels, in colon and small intestine. Recombinant PIR51 bound RNA and single- and double- stranded DNA, and was capable of aggregating DNA. Kovalenko et al. (1997) stated that PIR51 may represent a new member of the multiprotein complexes thought to carry out homologous recombination and DNA repair in mammalian cells. By analysis of an interspecific backcross, Mizuta et al. (1997) mapped the Rab22 gene to the distal region of mouse chromosome 6. Using fluorescence in situ hybridization, Kovalenko et al. (1997) mapped the PIR51 gene to 12p13.2- p13.1, a region that shows homology of synteny with the mouse chromosome 6 segment containing the Rab22 gene.

[25825]

[25826] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25827] Kovalenko, O. V.; Golub, E. I.; Bray- Ward, P.; Ward, D. C.; Radding, C. M. : A novel nucleic acid- binding protein that interacts with human Rad51 recombinase. Nucleic Acids Res. 25: 4946- 4953, 1997. ; and

[25828] Mizuta, R.; LaSalle, J. M.; Cheng, H.- L.; Shinohara, A.; Ogawa, H.; Copeland, N.; Jenkins, N. A.; Lalande, M.; Alt, F. W. : RAB22 and RAB163/mouse BRCA2: proteins that specifically inte.

[25829] Further studies establishing the function and utilities of PIR51 are found in John Hopkins OMIM database record ID 603070, and in cited publications listed in Table 5, which are hereby incorporated by reference.Pregnancy specific beta-1-glycoprotein 4 (PSG4, Accession NM_002780.1) is another GAM168 target gene, herein designated TARGET GENE. PSG4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se- quences of PSG4 BINDING SITE, designated SEQ ID:12119,

to the nucleotide sequence of GAM168 RNA, herein designated GAM RNA, also designated SEQ ID:217.

[25830] Another function of GAM168 is therefore inhibition of Pregnancy specific beta-1-glycoprotein 4 (PSG4, Accession NM_002780.1), a gene which is a member of the pregnancy- specific glycoprotein (PSG) and CEA families. Accordingly, utilities of GAM168 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSG4.

[25831] The function of PSG4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.1.Pregnancy specific beta-1-glycoprotein 7 (PSG7, Accession NM_002783.1) is another GAM168 target gene, herein designated TARGET GENE. PSG7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSG7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSG7 BINDING SITE, designated SEQ ID:2562, to the nucleotide sequence of GAM168 RNA, herein designated GAM RNA, also designated SEQ ID:217.

[25832] Another function of GAM168 is therefore inhibition of Pregnancy specific beta-1-glycoprotein 7 (PSG7, Accession NM_002783.1), a gene which function still unknown. Accordingly, utilities of GAM168 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSG7.

[25833] The function of PSG7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.

[25834] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 169 (GAM169), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25835] GAM169 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM169 was detected is described hereinabove with reference to Figs. 8-15.

[25836] GAM169 gene, herein designated GAM GENE, and GAM169 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25837] GAM169 gene encodes a GAM169 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM169 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM169 precursor RNA is designated SEQ ID:55, and is provided hereinbelow with reference to the sequence listing part.

[25838] GAM169 precursor RNA folds onto itself, forming GAM169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25839] GAM169 precursor RNA folds onto itself, forming GAM169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25840] Nucleotide sequence of GAM169 precursor RNA, designated SEQ-ID: 55, and a schematic representation of a predicted secondary folding of GAM169 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25841] An enzyme complex designated DICER COMPLEX, `dices` the GAM169 folded precursor RNA into GAM169 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM169 RNA is designated SEQ ID:365, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25842] GAM169 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM169 target RNA, herein designated GAM TARGET RNA. GAM169 tar-

get RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25843] GAM169 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM169 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM169 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM169 RNA may have a different number of target binding sites in untranslated regions of a GAM169 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25844] The complementary binding of GAM169 RNA, herein designated GAM RNA, to target binding sites on GAM169 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM169 target RNA into GAM169 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25845] It is appreciated that GAM169 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM169 target genes. The mRNA of each one of this plurality of GAM169 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM169 RNA, herein designated GAM RNA, and which when bound by GAM169 RNA causes inhibition of translation of respective one or more GAM169 target proteins.

[25846] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM169 gene, herein designated GAM GENE, on one or more GAM169 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the back-

ground section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25847] It is appreciated that specific functions and accordingly utilities of GAM169 correlate with, and may be deduced from, the identity of the target genes which GAM169 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25848]

[25849]

[25850] B29 (Accession NM_031939.2) is a GAM169 target gene, herein designated TARGET GENE. B29 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B29, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of B29 BINDING SITE, designated SEQ ID:9748, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25851] A function of GAM169 is therefore inhibition of B29 (Accession NM_031939.2) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B29.

[25852] BCMP1 (Accession NM_031442.1) is another GAM169 target gene, herein designated TARGET GENE. BCMP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCMP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCMP1 BINDING SITE, designated SEQ ID:8815, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25853] Another function of GAM169 is therefore inhibition of BCMP1 (Accession NM_031442.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCMP1.

[25854] Cyclin m4 (CNNM4, Accession NM_020184.1) is another GAM169 target gene, herein designated TARGET GENE.

CNNM4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNNM4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNNM4 BINDING SITE, designated SEQ ID:18090, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25855] Another function of GAM169 is therefore inhibition of Cyclin m4 (CNNM4, Accession NM_020184.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNNM4.

[25856] Collagen, type i, alpha 1 (COL1A1, Accession NM_000088.2) is another GAM169 target gene, herein designated TARGET GENE. COL1A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by COL1A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL1A1 BINDING SITE, designated SEQ ID:16271, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA,

also designated SEQ ID:365.

[25857] Another function of GAM169 is therefore inhibition of Collagen, type i, alpha 1 (COL1A1, Accession NM_000088.2) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL1A1.

[25858] Ferrochelatase (protoporphyria) (FECH, Accession NM_000140.1) is another GAM169 target gene, herein designated TARGET GENE. FECH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FECH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FECH BINDING SITE, designated SEQ ID:2667, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25859] Another function of GAM169 is therefore inhibition of Ferrochelatase (protoporphyria) (FECH, Accession NM_000140.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FECH.

[25860] FLJ11160 (Accession) is another GAM169 target gene, herein designated TARGET GENE. FLJ11160 BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11160, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11160 BINDING SITE, designated SEQ ID:409, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25861] Another function of GAM169 is therefore inhibition of FLJ11160 (Accession) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11160.

[25862] FLJ14950 (Accession) is another GAM169 target gene, herein designated TARGET GENE. FLJ14950 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14950, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14950 BINDING SITE, designated SEQ ID:12773, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25863] Another function of GAM169 is therefore inhibition of

FLJ14950 (Accession) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14950.

[25864] Glucose-6-phosphatase, catalytic (glycogen storage disease type i, von gierke disease) (G6PC, Accession NM_000151.1) is another GAM169 target gene, herein designated TARGET GENE. G6PC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G6PC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G6PC BINDING SITE, designated SEQ ID:19886, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25865] Another function of GAM169 is therefore inhibition of Glucose-6-phosphatase, catalytic (glycogen storage disease type i, von gierke disease) (G6PC, Accession NM_000151.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G6PC.

[25866] HRLP5 (Accession NM_054108.1) is another GAM169 target gene, herein designated TARGET GENE. HRLP5 BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HRLP5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HRLP5 BINDING SITE, designated SEQ ID:7902, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25867] Another function of GAM169 is therefore inhibition of HRLP5 (Accession NM_054108.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRLP5.

[25868] 5-hydroxytryptamine (serotonin) receptor 3a (HTR3A, Accession NM_000869.1) is another GAM169 target gene, herein designated TARGET GENE. HTR3A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR3A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR3A BINDING SITE, designated SEQ ID:7644, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25869] Another function of GAM169 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 3a (HTR3A, Accession NM_000869.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR3A.

[25870] Iduronate 2-sulfatase (hunter syndrome) (IDS, Accession NM_000202.2) is another GAM169 target gene, herein designated TARGET GENE. IDS BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IDS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IDS BINDING SITE, designated SEQ ID:2619, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25871] Another function of GAM169 is therefore inhibition of Iduronate 2-sulfatase (hunter syndrome) (IDS, Accession NM_000202.2) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IDS.

[25872] Potassium channel, subfamily k, member 7 (KCNK7, Accession NM_033347.1) is another GAM169 target gene,

herein designated TARGET GENE. KCNK7 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by KCNK7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNK7 BINDING SITE, designated SEQ ID:10339, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25873] Another function of GAM169 is therefore inhibition of Potassium channel, subfamily k, member 7 (KCNK7, Accession NM_033347.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK7.

[25874] KIAA0630 (Accession) is another GAM169 target gene, herein designated TARGET GENE. KIAA0630 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0630, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0630 BINDING SITE, designated SEQ ID:19492, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA,

also designated SEQ ID:365.

[25875] Another function of GAM169 is therefore inhibition of KIAA0630 (Accession) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0630.

[25876] KIAA1061 (Accession XM_048786.5) is another GAM169 target gene, herein designated TARGET GENE. KIAA1061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1061 BINDING SITE, designated SEQ ID:14654, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25877] Another function of GAM169 is therefore inhibition of KIAA1061 (Accession XM_048786.5) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1061.

[25878] KIAA1577 (Accession XM_035299.2) is another GAM169 target gene, herein designated TARGET GENE. KIAA1577 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1577, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1577 BINDING SITE, designated SEQ ID:4142, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25879] Another function of GAM169 is therefore inhibition of KIAA1577 (Accession XM_035299.2) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1577.

[25880] Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NM_003679.1) is another GAM169 target gene, herein designated TARGET GENE. KMO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KMO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KMO BINDING SITE, designated SEQ ID:6772, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25881] Another function of GAM169 is therefore inhibition of Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NM_003679.1), a gene which may play a role in encephalic photoreception. Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KMO.

[25882] The function of KMO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Left-right determination, factor b (LEFTB, Accession NM_020997.2) is another GAM169 target gene, herein designated TARGET GENE. LEFTB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LEFTB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LEFTB BINDING SITE, designated SEQ ID:1639, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25883] Another function of GAM169 is therefore inhibition of Left-right determination, factor b (LEFTB, Accession

NM_020997.2) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LEFTB.

[25884] LOC116211 (Accession NM_138461.1) is another GAM169 target gene, herein designated TARGET GENE. LOC116211 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC116211, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC116211 BINDING SITE, designated SEQ ID:18253, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25885] Another function of GAM169 is therefore inhibition of LOC116211 (Accession NM_138461.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116211.

[25886] LOC145757 (Accession XM_085227.1) is another GAM169 target gene, herein designated TARGET GENE. LOC145757 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145757, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145757 BINDING SITE, designated SEQ ID:897, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25887] Another function of GAM169 is therefore inhibition of LOC145757 (Accession XM_085227.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145757.

[25888] LOC146512 (Accession) is another GAM169 target gene, herein designated TARGET GENE. LOC146512 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146512, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146512 BINDING SITE, designated SEQ ID:9963, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25889] Another function of GAM169 is therefore inhibition of LOC146512 (Accession) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with LOC146512.

[25890] LOC151124 (Accession XM_098006.2) is another GAM169 target gene, herein designated TARGET GENE. LOC151124 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151124, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151124 BINDING SITE, designated SEQ ID:13174, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25891] Another function of GAM169 is therefore inhibition of LOC151124 (Accession XM_098006.2) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151124.

[25892] LOC151723 (Accession XM_093395.6) is another GAM169 target gene, herein designated TARGET GENE. LOC151723 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151723, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC151723 BINDING SITE, designated SEQ ID:11154, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25893] Another function of GAM169 is therefore inhibition of LOC151723 (Accession XM_093395.6) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151723.

[25894] LOC157931 (Accession XM_098845.1) is another GAM169 target gene, herein designated TARGET GENE. LOC157931 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC157931, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157931 BINDING SITE, designated SEQ ID:8404, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25895] Another function of GAM169 is therefore inhibition of LOC157931 (Accession XM_098845.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC157931.

[25896] LOC197259 (Accession) is another GAM169 target gene, herein designated TARGET GENE. LOC197259 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC197259, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC197259 BINDING SITE, designated SEQ ID:18112, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25897] Another function of GAM169 is therefore inhibition of LOC197259 (Accession) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197259.

[25898] LOC220763 (Accession XM_055551.4) is another GAM169 target gene, herein designated TARGET GENE. LOC220763 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC220763, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC220763 BINDING SITE, designated SEQ ID:7258, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25899] Another function of GAM169 is therefore inhibition of LOC220763 (Accession XM_055551.4) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220763.

[25900] LOC222068 (Accession XM_166556.3) is another GAM169 target gene, herein designated TARGET GENE. LOC222068 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC222068, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222068 BINDING SITE, designated SEQ ID:15325, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25901] Another function of GAM169 is therefore inhibition of LOC222068 (Accession XM_166556.3) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222068.

[25902] LOC257486 (Accession) is another GAM169 target gene, herein designated TARGET GENE. LOC257486 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC257486, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC257486 BINDING SITE, designated SEQ ID:10209, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25903] Another function of GAM169 is therefore inhibition of LOC257486 (Accession) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257486.

[25904] Leucine-rich repeat protein, neuronal 3 (LRRN3, Accession) is another GAM169 target gene, herein designated TARGET GENE. LRRN3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LRRN3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LRRN3 BINDING SITE, designated

SEQ ID:11257, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25905] Another function of GAM169 is therefore inhibition of Leucine-rich repeat protein, neuronal 3 (LRRN3, Accession) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRRN3.

[25906] MGC5466 (Accession NM_030922.1) is another GAM169 target gene, herein designated TARGET GENE. MGC5466 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC5466, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC5466 BINDING SITE, designated SEQ ID:9839, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25907] Another function of GAM169 is therefore inhibition of MGC5466 (Accession NM_030922.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5466.

[25908] MTCH1 (Accession NM_014341.1) is another GAM169 target gene, herein designated TARGET GENE. MTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTCH1 BINDING SITE, designated SEQ ID:5849, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25909] Another function of GAM169 is therefore inhibition of MTCH1 (Accession NM_014341.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTCH1.

[25910] Natriuretic peptide receptor a/guanylate cyclase a (atrionatriuretic peptide receptor a) (NPR1, Accession NM_000906.1) is another GAM169 target gene, herein designated TARGET GENE. NPR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of NPR1 BINDING SITE, designated SEQ ID:2666, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25911] Another function of GAM169 is therefore inhibition of Na-triuretic peptide receptor a/guanylate cyclase a (atrionatriuretic peptide receptor a) (NPR1, Accession NM_000906.1), a gene which has guanylate cyclase activity on binding of anf. Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPR1.

[25912] The function of NPR1 has been established by previous studies. The precursor of atrial natriuretic peptide (ANP; 108780) is produced and stored mainly in the right atrium of the heart (see OMIM Ref. No. Oliver et al., 1997). ANP formed from this precursor is released in response to atrial stretch. Once in the circulation, ANP binds to the natriuretic peptide receptor A (ANPRA, or NPR1), also known as guanylate cyclase A (or GC- A), mainly in the kidney, vascular tissue, and adrenal gland. This binding induces an increase in intracellular cGMP and initiates natriuresis, diuresis, and vasodilation, all of which contribute to lowering blood pressure. 'B- type' natriuretic peptide, a structurally related peptide formed mainly in the cardiac

ventricles, also acts through ANPRA and has effects similar to ANP. Lowe et al. (1990) assigned the ANPRA gene to 1q12- qter by PCR analysis of genomic DNA from somatic cell hybrids. By in situ hybridization, the gene was further localized to 1q21- q22.

[25913] Animal model experiments lend further support to the function of NPR1. To study the role of NPRA in the regulation of blood pressure and in the cardiovascular response to sustained hypertension, Oliver et al. (1997) made mice completely lacking this receptor. They found that mice lacking a functional Npr1 gene coding for NPRA had elevated blood pressures and heart exhibiting marked hypertrophy with interstitial fibrosis resembling that seen in human hypertensive heart disease. Echocardiographic evaluation of the mice demonstrated a compensated state of systemic hypertension in which cardiac hypertrophy and dilatation were evident but with no reduction in ventricular performance. Nevertheless, sudden death, with morphologic evidence indicative in some animals of congestive heart failure and in others of aortic dissection, occurred in all 15 male mice lacking Npr1 before 6 months of age, and in 1 of 16 females in this study.

[25914] It is appreciated that the abovementioned animal model

for NPR1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[25915] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25916] Lowe, D. G.; Klisak, I.; Sparkes, R. S.; Mohandas, T.; Goeddel, D. V. : Chromosomal distribution of three members of the human natriuretic peptide receptor/guanylyl cyclase gene family. Genomics 8: 304- 312, 1990. ; and

[25917] Oliver, P. M.; Fox, J. E.; Kim, R.; Rockman, H. A.; Kim, H.-S.; Reddick, R. L.; Pandey, K. N.; Milgram, S. L.; Smithies, O.; Maeda, N. : Hypertension, cardiac hypertrophy, and sudden dea.

[25918] Further studies establishing the function and utilities of NPR1 are found in John Hopkins OMIM database record ID 108960, and in cited publications listed in Table 5, which are hereby incorporated by reference.phorbolin-1 (Accession) is another GAM169 target gene, herein designated TARGET GENE. phorbolin-1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by phorbolin-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of phorbolin-1 BINDING SITE, designated SEQ ID:1815, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25919] Another function of GAM169 is therefore inhibition of phorbolin-1 (Accession) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with phorbolin-1.

[25920] PP1665 (Accession NM_030792.2) is another GAM169 target gene, herein designated TARGET GENE. PP1665 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PP1665, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP1665 BINDING SITE, designated SEQ ID:5088, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25921] Another function of GAM169 is therefore inhibition of PP1665 (Accession NM_030792.2) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PP1665.

[25922] Peroxisome proliferative activated receptor, gamma, coactivator 1 (PPARGC1, Accession NM_013261.2) is another GAM169 target gene, herein designated TARGET GENE. PPARGC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPARGC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPARGC1 BINDING SITE, designated SEQ ID:16406, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25923] Another function of GAM169 is therefore inhibition of Peroxisome proliferative activated receptor, gamma, coactivator 1 (PPARGC1, Accession NM_013261.2), a gene which may play a role in insulin sensitivity and thermogenesis and therefore may be associated with Familial partial lipodystrophy and type ii diabetes. Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of Familial partial lipodystrophy and type ii diabetes, and of other diseases and clinical conditions associated with

PPARGC1.

[25924] The function of PPARGC1 has been established by previous studies. Adaptive thermogenesis is an important component of energy homeostasis and a metabolic defense against obesity, which is characterized by a chronic imbalance between energy intake and expenditure. Part of energy expenditure results from a leaking of protons across the mitochondrial inner membrane which leads to energy dissipation because of uncoupling of oxygen consumption to ATP synthesis. Three mitochondrial uncoupling proteins, UCP1 (OMIM Ref. No. 113730), UCP2 (OMIM Ref. No. 601693), and UCP3 (OMIM Ref. No. 602044), are candidates to explain the proton leak. The most compelling evidence for a direct role of uncoupling proteins in the proton leak comes from data on brown fat- specific UCP1. During cold exposure, energy dissipation is increased through brown adipose tissue (BAT) hypertrophy, biogenesis of mitochondria, and increased expression and activation of UCP1. Data pointed to peroxisome proliferator- activated receptor- gamma (PPARG; 601487) as a transcriptional regulator of uncoupling protein expression. PPAR- gamma is a nuclear receptor activated by fatty acids and eicosanoids which plays a major

role in adipocyte differentiation. In brown fat cells, PPARG activates an enhancer of the UCP1 gene promoter. Puigserver et al. (1998) cloned a novel transcription coactivator of nuclear receptors, termed Pgc1, from a mouse brown fat cDNA library. Pgc1 mRNA expression was dramatically elevated upon cold exposure of mice in both brown fat and skeletal muscle, key thermogenic tissues. Pgc1 greatly increased the transcriptional activity of Ppar-gamma (OMIM Ref. No. 601487) and thyroid hormone receptor (see OMIM Ref. No. 190120) on the uncoupling protein Ucp1 (OMIM Ref. No. 113730) promoter. Ectopic expression of Pgc1 in white adipose cells activated expression of Ucp1 and key mitochondrial enzymes of the respiratory chain, and increased the cellular content of mitochondrial DNA. Puigserver et al. (1998) suggested that PGC1 plays a key role in linking nuclear receptors to the transcriptional program of adaptive thermogenesis.

[25925] Animal model experiments lend further support to the function of PPARGC1. Herzig et al. (2001) demonstrated that mice carrying a targeted disruption of the cAMP response element- binding (CREB) protein gene (OMIM Ref. No. 123810), or overexpressing a dominant- negative CREB inhibitor, exhibit fasting hyperglycemia and reduced

expression of gluconeogenic enzymes. CREB was found to induce expression of the gluconeogenic program through the nuclear receptor coactivator PGC1, which was demonstrated to be a direct target for CREB regulation in vivo. Overexpression of PGC1 in CREB- deficient mice restored glucose homeostasis and rescued the expression of gluconeogenic genes. In transient assays, PGC1 potentiated glucocorticoid induction of the gene for PEPCK, the rate-limiting enzyme in gluconeogenesis. PGC1 promotes cooperativity between cAMP and glucocorticoid signaling pathways during hepatic gluconeogenesis. Fasting hyperglycemia is strongly correlated with type II diabetes (OMIM Ref. No. 125853), so Herzig et al. (2001) concluded that the activation of PGC1 by CREB in liver contributes importantly to the pathogenesis of this disease.

[25926] It is appreciated that the abovementioned animal model for PPARGC1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[25927] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25928] Puigserver, P.; Wu, Z.; Park, C. W.; Graves, R.; Wright, M.;

Spiegelman, B. M. : A cold- inducible coactivator of nuclear receptors linked to adaptive thermogenesis. Cell 92: 829- 839, 1998. ; and

[25929] Herzig, S.; Long, F.; Jhala, U. S.; Hedrick, S.; Quinn, R.; Bauer, A.; Rudolph, D.; Schutz, G.; Yoon, C.; Puigserver, P.; Spiegelman, B.; Montminy, M. : CREB regulates hepatic gluconeoge.

[25930] Further studies establishing the function and utilities of PPARGC1 are found in John Hopkins OMIM database record ID 604517, and in cited publications listed in Table 5, which are hereby incorporated by reference.Regulator of g-protein signalling 19 interacting protein 1 (RGS19IP1, Accession NM_005716.1) is another GAM169 target gene, herein designated TARGET GENE. RGS19IP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RGS19IP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RGS19IP1 BINDING SITE, designated SEQ ID:5745, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25931] Another function of GAM169 is therefore inhibition of

Regulator of g-protein signalling 19 interacting protein 1 (RGS19IP1, Accession NM_005716.1), a gene which is involved in g protein- linked signaling. Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS19IP1.

[25932] The function of RGS19IP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM129.1.RPF-1 (Accession NM_007252.1) is another GAM169 target gene, herein designated TARGET GENE. RPF-1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RPF-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RPF-1 BINDING SITE, designated SEQ ID:12622, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25933] Another function of GAM169 is therefore inhibition of RPF-1 (Accession NM_007252.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPF-1.

[25934] Src-like-adaptor (SLA, Accession NM_006748.1) is another GAM169 target gene, herein designated TARGET GENE. SLA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLA BINDING SITE, designated SEQ ID:4672, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25935] Another function of GAM169 is therefore inhibition of Src-like-adaptor (SLA, Accession NM_006748.1), a gene which is a negative regulator of T- cell receptor signaling. Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA.

[25936] The function of SLA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK, Accession NM_004598.2) is another GAM169 target gene, herein designated TARGET GENE. SPOCK BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by SPOCK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPOCK BINDING SITE, designated SEQ ID:16266, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25937] Another function of GAM169 is therefore inhibition of Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK, Accession NM_004598.2) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPOCK.

[25938] Ubiquitin-conjugating enzyme e2l 3 (UBE2L3, Accession NM_003347.1) is another GAM169 target gene, herein designated TARGET GENE. UBE2L3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBE2L3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBE2L3 BINDING SITE, designated SEQ ID:9338, to the nucleotide sequence of

GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25939] Another function of GAM169 is therefore inhibition of Ubiquitin-conjugating enzyme e2l 3 (UBE2L3, Accession NM_003347.1), a gene which catalyzes the covalent attachment of ubiquitin to other proteins. and therefore may be associated with Parkinson disease. Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of Parkinson disease, and of other diseases and clinical conditions associated with UBE2L3.

[25940] The function of UBE2L3 has been established by previous studies. Shimura et al. (2001) hypothesized that alpha-synuclein (OMIM Ref. No. 163890) and parkin (OMIM Ref. No. 602544) interact functionally, namely, that parkin ubiquitinates alpha- synuclein normally and that this process is altered in autosomal recessive Parkinson disease (OMIM Ref. No. 600116). Shimura et al. (2001) identified a protein complex in normal human brain that includes parkin as the E3 ubiquitin ligase, UBCH7 as its associated E2 ubiquitin- conjugating enzyme, and a novel 22- kD glycosylated form of alpha- synuclein (alpha- Sp22) as its substrate. In contrast to normal parkin, mutant parkin associated with autosomal recessive Parkinson disease failed

to bind alpha- Sp22. In an in vitro ubiquitination assay, alpha- Sp22 was modified by normal, but not mutant, parkin into polyubiquitinated, high molecular weight species. Accordingly, alpha- Sp22 accumulated in a nonubiquitinated form in parkin- deficient Parkinson disease brains. Shimura et al. (2001) concluded that alpha- Sp22 is a substrate for parkin's ubiquitin ligase activity in normal human brain and that loss of parkin function causes pathologic accumulation of alpha- Sp22. These findings demonstrated a critical biochemical reaction between the 2 Parkinson disease- linked gene products and suggested that this reaction underlies the accumulation of ubiquitinated alpha- synuclein in conventional Parkinson disease. By RT- PCR, Moynihan et al. (1998) determined that UBE2L3 is expressed as 4 mRNAs that differ in the length of the 3- prime untranslated region (UTR). Sequence comparisons revealed that the human and mouse UBE2L3 cDNAs share 97% DNA sequence identity in the coding region and 93% identity for 287 nucleotides extending into the 3- prime UTR. The predicted mouse and human UBE2L3 proteins are identical.

[25941]

[25942] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[25943] Moynihan, T. P.; Cole, C. G.; Dunham, I.; O'Neil, L.; Markham, A. F.; Robinson, P. A. : Fine- mapping, genomic organization, and transcript analysis of the human ubiquitin- conjugating enzyme gene UBE2L3. Genomics 51: 124- 127, 1998. ; and

[25944] Shimura, H.; Schlossmacher, M. G.; Hattori, N.; Frosch, M. P.; Trockenbacher, A.; Schneider, R.; Mizuno, Y.; Kosik, K. S.; Selkoe, D. J. : Ubiquitination of a new form of alpha-synuclei.

[25945] Further studies establishing the function and utilities of UBE2L3 are found in John Hopkins OMIM database record ID 603721, and in cited publications listed in Table 5, which are hereby incorporated by reference.Wd repeat domain 7 (WDR7, Accession NM_015285.1) is another GAM169 target gene, herein designated TARGET GENE. WDR7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WDR7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WDR7 BINDING SITE, designated

SEQ ID:18603, to the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, also designated SEQ ID:365.

[25946] Another function of GAM169 is therefore inhibition of Wd repeat domain 7 (WDR7, Accession NM_015285.1) . Accordingly, utilities of GAM169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDR7.

[25947]

[25948] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 170 (GAM170), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25949] GAM170 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM170 was detected is described hereinabove with reference to Figs. 8-15.

[25950] GAM170 gene, herein designated GAM GENE, and GAM170 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25951] GAM170 gene encodes a GAM170 precursor RNA, herein

designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM170 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM170 precursor RNA is designated SEQ ID:72, and is provided hereinbelow with reference to the sequence listing part.

[25952] GAM170 precursor RNA folds onto itself, forming GAM170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25953] GAM170 precursor RNA folds onto itself, forming GAM170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate

or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25954] Nucleotide sequence of GAM170 precursor RNA, designated SEQ-ID: 72, and a schematic representation of a predicted secondary folding of GAM170 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25955] An enzyme complex designated DICER COMPLEX, `dices` the GAM170 folded precursor RNA into GAM170 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM170 RNA is designated SEQ ID:283, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25956] GAM170 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM170 target RNA, herein designated GAM TARGET RNA. GAM170 target RNA comprises three regions, as is typical of mRNA of

a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25957] GAM170 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM170 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM170 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM170 RNA may have a different number of target binding sites in untranslated regions of a GAM170 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25958] The complementary binding of GAM170 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM170 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM170 target RNA into GAM170 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25959] It is appreciated that GAM170 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM170 target genes. The mRNA of each one of this plurality of GAM170 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM170 RNA, herein designated GAM RNA, and which when bound by GAM170 RNA causes inhibition of translation of respective one or more GAM170 target proteins.

[25960] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM170 gene, herein designated GAM GENE, on one or more GAM170 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary bind-

ing site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25961] It is appreciated that specific functions and accordingly utilities of GAM170 correlate with, and may be deduced from, the identity of the target genes which GAM170 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25962]

[25963]

[25964] LOC121457 (Accession) is a GAM170 target gene, herein designated TARGET GENE. LOC121457 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC121457, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC121457

BINDING SITE, designated SEQ ID:4519, to the nucleotide sequence of GAM170 RNA, herein designated GAM RNA, also designated SEQ ID:283.

[25965] A function of GAM170 is therefore inhibition of LOC121457 (Accession) . Accordingly, utilities of GAM170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121457.

[25966] LOC145483 (Accession) is another GAM170 target gene, herein designated TARGET GENE. LOC145483 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145483, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145483 BINDING SITE, designated SEQ ID:5675, to the nucleotide sequence of GAM170 RNA, herein designated GAM RNA, also designated SEQ ID:283.

[25967] Another function of GAM170 is therefore inhibition of LOC145483 (Accession) . Accordingly, utilities of GAM170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145483.

[25968] LOC150113 (Accession) is another GAM170 target gene, herein designated TARGET GENE. LOC150113 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150113 BINDING SITE, designated SEQ ID:16990, to the nucleotide sequence of GAM170 RNA, herein designated GAM RNA, also designated SEQ ID:283.

[25969] Another function of GAM170 is therefore inhibition of LOC150113 (Accession) . Accordingly, utilities of GAM170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150113.

[25970] Pyrimidinergic receptor p2y, g-protein coupled, 6 (P2RY6, Accession NM_176796.1) is another GAM170 target gene, herein designated TARGET GENE. P2RY6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by P2RY6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

P2RY6 BINDING SITE, designated SEQ ID:2447, to the nucleotide sequence of GAM170 RNA, herein designated GAM RNA, also designated SEQ ID:283.

[25971] Another function of GAM170 is therefore inhibition of Pyrimidinergic receptor p2y, g-protein coupled, 6 (P2RY6, Accession NM_176796.1), a gene which mediates cellular responses to nucleotides. Accordingly, utilities of GAM170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RY6.

[25972] The function of P2RY6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.SRp25 (Accession) is another GAM170 target gene, herein designated TARGET GENE. SRp25 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SRp25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRp25 BINDING SITE, designated SEQ ID:1331, to the nucleotide sequence of GAM170 RNA, herein designated GAM RNA, also designated SEQ ID:283.

[25973] Another function of GAM170 is therefore inhibition of

SRp25 (Accession) . Accordingly, utilities of GAM170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRp25.

[25974]

[25975] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 171 (GAM171), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25976] GAM171 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM171 was detected is described hereinabove with reference to Figs. 8-15.

[25977] GAM171 gene, herein designated GAM GENE, and GAM171 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[25978] GAM171 gene encodes a GAM171 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM171 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM171 precursor RNA is designated SEQ ID:17, and is

provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:17 is located at position 242532302 relative to chromosome 2.

[25979] GAM171 precursor RNA folds onto itself, forming GAM171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25980] GAM171 precursor RNA folds onto itself, forming GAM171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[25981] Nucleotide sequence of GAM171 precursor RNA, designated SEQ-ID: 17, and a schematic representation of a

predicted secondary folding of GAM171 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[25982] An enzyme complex designated DICER COMPLEX, `dices` the GAM171 folded precursor RNA into GAM171 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM171 RNA is designated SEQ ID:392, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[25983] GAM171 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM171 target RNA, herein designated GAM TARGET RNA. GAM171 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[25984] GAM171 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM171 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM171 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM171 RNA may have a different number of target binding sites in untranslated regions of a GAM171 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[25985] The complementary binding of GAM171 RNA, herein designated GAM RNA, to target binding sites on GAM171 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM171 target RNA into GAM171 tar-

get protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25986] It is appreciated that GAM171 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM171 target genes. The mRNA of each one of this plurality of GAM171 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM171 RNA, herein designated GAM RNA, and which when bound by GAM171 RNA causes inhibition of translation of respective one or more GAM171 target proteins.

[25987] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM171 gene, herein designated GAM GENE, on one or more GAM171 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25988] It is appreciated that specific functions and accordingly utilities of GAM171 correlate with, and may be deduced from, the identity of the target genes which GAM171 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25989]

[25990]

[25991] Dead/h (asp-glu-ala-asp/his) box polypeptide 6 (rna helicase, 54kda) (DDX6, Accession NM_004397.3) is a GAM171 target gene, herein designated TARGET GENE. DDX6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DDX6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX6 BINDING SITE, designated SEQ ID:12093, to the nucleotide sequence of GAM171 RNA, herein designated GAM RNA, also designated SEQ ID:392.

[25992] A function of GAM171 is therefore inhibition of Dead/h (asp-glu-ala-asp/his) box polypeptide 6 (rna helicase, 54kda) (DDX6, Accession NM_004397.3), a gene which is putative RNA helicases and therefore may be associated with Hematopoietic tumors . Accordingly, utilities of GAM171 include diagnosis, prevention and treatment of Hematopoietic tumors ., and of other diseases and clinical conditions associated with DDX6.

[25993] The function of DDX6 has been established by previous studies. DEAD box proteins are putative RNA helicases that have a characteristic Asp- Glu- Ala- Asp (DEAD) box as 1 of 8 highly conserved sequence motifs. Akao et al. (1991) cloned the breakpoint of the t(11;14)(q23;q32) in B- cell lymphoma, as represented in the RC- K8 cell line, and named the locus RCK. By pulsed field gel elec- trophoresis, RCK was shown to be centromeric to the gene for porphobilinogen deaminase (OMIM Ref. No. 176000), while the breakpoints of t(11;19)(q23;p13) were detected by the CD3D gene probe (OMIM Ref. No. 186790), which is centromeric to RCK. Akao et al. (1992) did long- range mapping from the CD3 genes to the PBGD gene on 11q23 to determine the relationship between RCK and MLL- ALL1 (OMIM Ref. No. 159555). They showed that RCK and MLL

are on different NotI fragments, indicating that 2 different genes are associated with 11q23 translocations in hematopoietic tumors. Seto et al. (1995) found that the RCK/P54 gene, which had been found to encode a 472 to 483 amino acid- peptide belonging to the RNA helicase/ translation initiation factor family, is highly conserved in the mouse. The mouse cDNA showed 93.7% nucleotide identity and 97.7% predicted amino acid identity with human RCK. Lu and Yunis (1992) cloned a putative human RNA helicase, p54, from a lymphoid cell line with chromosomal breakpoint 11q23.3. The predicted amino acid sequence shared 75% identity with the female germline-specific RNA helicase ME31B gene of Drosophila. Unlike ME31B, however, the new gene expressed an abundant transcript in a large number of adult tissues and its 5-prime noncoding region was found to be split in a t(11;14)(q23.3;q32.3) cell line from a diffuse large B- cell lymphoma. Tunnacliffe et al. (1993) assigned the HLR2 gene more precisely using a panel of sequence tagged sites (STSs) representing 30 markers previously assigned to 11q23. Using fluorescence in situ hybridization, Akao and Matsuda (1996) mapped the Ddx6 gene to mouse chromosome 9.

[25994]

[25995] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[25996] Akao, Y.; Seto, M.; Yamamoto, K.; Iida, S.; Nakazawa, S.; Inazawa, J.; Abe, T.; Takahashi, T.; Ueda, R. : The RCK gene associated with t(11;14) translocation is distinct from the MLL/ALL- 1 gene with t(4;11) and t(11;19) translocations. Cancer Res. 52: 6083- 6087, 1992. ; and

[25997] Akao, Y.; Tsujimoto, Y.; Finan, J.; Nowell, P. C.; Croce, C. M. : Molecular characterization of a t(11;14)(q23;q32) chromosome translocation in a B- cell lymphoma. Cancer Res. 50: 4856- 4.

[25998] Further studies establishing the function and utilities of DDX6 are found in John Hopkins OMIM database record ID 600326, and in cited publications listed in Table 5, which are hereby incorporated by reference.Glucokinase (hexokinase 4) regulatory protein (GCKR, Accession NM_001486.1) is another GAM171 target gene, herein designated TARGET GENE. GCKR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GCKR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GCKR BINDING SITE, designated SEQ ID:12938, to the nucleotide sequence of GAM171 RNA, herein designated GAM RNA, also designated SEQ ID:392.

[25999] Another function of GAM171 is therefore inhibition of Glucokinase (hexokinase 4) regulatory protein (GCKR, Accession NM_001486.1), a gene which inhibits glucokinase by forming an inactive complex with this enzyme. and therefore may be associated with Maturity- onset diabetes of the young (mody) type ii. Accordingly, utilities of GAM171 include diagnosis, prevention and treatment of Maturity- onset diabetes of the young (mody) type ii., and of other diseases and clinical conditions associated with GCKR.

[26000] The function of GCKR has been established by previous studies. Glucokinase (GCK; 138079) in the liver and pancreatic beta cells is subject to inhibition by a regulatory protein, GCKR. The inhibitory effect of GCKR depends on the presence of fructose- 6- phosphate and is antagonized by fructose- 1- phosphate. Warner et al. (1995) noted that mutations in GCKR might be diabetogenic if they resulted in the synthesis of proteins with increased

inhibitory activity, perhaps reflecting increased sensitivity to fructose- 6- phosphate or reduced susceptibility to antagonism by fructose- 1- phosphate. Warner et al. (1995) determined the complete sequence of human GCKR cDNA, isolated YAC clones containing human GCKR, and localized them to 2p23 by fluorescence in situ hybridization. The GCKR cDNA encodes a protein of 625 amino acids. Vaxillaire et al. (1994) had previously assigned the GCKR gene to 2p23- p22.3. Given the role of glucokinase in the causation of maturity- onset diabetes of the young (MODY) type II (OMIM Ref. No. 125851), GCKR had been considered a candidate gene for a form of MODY. To further understand the role of glucokinase regulatory protein, which they symbolized GKRP, Farrelly et al. (1999) inactivated the mouse homolog. With the knockout of the mouse gene, there was a parallel loss of glucokinase protein and activity in mutant mouse liver. The loss was primarily because of posttranscriptional regulation of glucokinase, indicating a positive regulatory role for GKRP in maintaining glucokinase levels and activity. As in rat hepatocytes, both glucokinase and GKRP were localized in the nuclei of mouse hepatocytes cultured in low glucose-containing medium. In the presence of fructose or high

concentrations of glucose, conditions known to relieve glucokinase inhibition by GKRP in vitro, only glucokinase was translocated into the cytoplasm. In the GKRP- mutant hepatocytes, glucokinase was not found in the nucleus under any tested conditions. Farrelly et al. (1999) proposed that GKRP functions as an anchor to sequester and inhibit glucokinase in the hepatocyte nucleus, where it is protected from degradation. This ensures that glucose phosphorylation is minimal when the liver is in the fasting, glucose- producing phase. This also enables the hepatocytes rapidly to mobilize glucokinase into the cytoplasm to phosphorylate and store or metabolize glucose after the ingestion of dietary glucose. In GKRP- mutant mice, the disruption of this regulation and the subsequent decrease in GK activity led to altered glucose metabolism and impaired glycemic control.

[26001]

[26002] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26003] Farrelly, D.; Brown, K. S.; Tieman, A.; Ren, J.; Lira, S. A.; Hagan, D.; Gregg, R.; Mookhtiar, K. A.; Hariharan, N. : Mice mutant for glucokinase regulatory protein exhibit

decreased liver glucokinase: a sequestration mechanism in metabolic regulation. Proc. Nat. Acad. Sci. 96: 14511-14516, 1999. ; and

[26004] Vaxillaire, M.; Vionnet, N.; Vigouroux, C.; Sun, F.; Espinosa, R., III; LeBeau, M. M.; Stoffel, M.; Lehto, M.; Beckmann, J. S.; Detheux, M.; Passa, P.; Cohen, D.; Van Schaftingen, E.; V.

[26005] Further studies establishing the function and utilities of GCKR are found in John Hopkins OMIM database record ID 600842, and in cited publications listed in Table 5, which are hereby incorporated by reference.KIAA0042 (Accession) is another GAM171 target gene, herein designated TARGET GENE. KIAA0042 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0042, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0042 BINDING SITE, designated SEQ ID:5935, to the nucleotide sequence of GAM171 RNA, herein designated GAM RNA, also designated SEQ ID:392.

[26006] Another function of GAM171 is therefore inhibition of KIAA0042 (Accession) . Accordingly, utilities of GAM171

include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0042.

[26007] KIAA1030 (Accession XM_290502.1) is another GAM171 target gene, herein designated TARGET GENE. KIAA1030 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1030, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1030 BINDING SITE, designated SEQ ID:8929, to the nucleotide sequence of GAM171 RNA, herein designated GAM RNA, also designated SEQ ID:392.

[26008] Another function of GAM171 is therefore inhibition of KIAA1030 (Accession XM_290502.1) . Accordingly, utilities of GAM171 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1030.

[26009] KIAA1036 (Accession NM_014909.1) is another GAM171 target gene, herein designated TARGET GENE. KIAA1036 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1036, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA1036 BINDING SITE, designated SEQ ID:13086, to the nucleotide sequence of GAM171 RNA, herein designated GAM RNA, also designated SEQ ID:392.

[26010] Another function of GAM171 is therefore inhibition of KIAA1036 (Accession NM_014909.1) . Accordingly, utilities of GAM171 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1036.

[26011] LOC148113 (Accession) is another GAM171 target gene, herein designated TARGET GENE. LOC148113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148113 BINDING SITE, designated SEQ ID:8770, to the nucleotide sequence of GAM171 RNA, herein designated GAM RNA, also designated SEQ ID:392.

[26012] Another function of GAM171 is therefore inhibition of LOC148113 (Accession) . Accordingly, utilities of GAM171 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC148113.

[26013]

[26014] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 172 (GAM172), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26015] GAM172 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM172 was detected is described hereinabove with reference to Figs. 8-15.

[26016] GAM172 gene, herein designated GAM GENE, and GAM172 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[26017] GAM172 gene encodes a GAM172 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM172 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM172 precursor RNA is designated SEQ ID:86, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:86 is located at po-

sition 195192414 relative to chromosome 1.

[26018] GAM172 precursor RNA folds onto itself, forming GAM172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26019] GAM172 precursor RNA folds onto itself, forming GAM172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[26020] Nucleotide sequence of GAM172 precursor RNA, designated SEQ-ID: 86, and a schematic representation of a predicted secondary folding of GAM172 folded precursor RNA are further described with reference to Table 2,

hereby incorporated by reference.

[26021] An enzyme complex designated DICER COMPLEX, `dices` the GAM172 folded precursor RNA into GAM172 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM172 RNA is designated SEQ ID:253, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[26022] GAM172 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM172 target RNA, herein designated GAM TARGET RNA. GAM172 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[26023] GAM172 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM172 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM172 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM172 RNA may have a different number of target binding sites in untranslated regions of a GAM172 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[26024] The complementary binding of GAM172 RNA, herein designated GAM RNA, to target binding sites on GAM172 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM172 target RNA into GAM172 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26025] It is appreciated that GAM172 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM172 target genes. The mRNA of each one of this plurality of GAM172 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM172 RNA, herein designated GAM RNA, and which when bound by GAM172 RNA causes inhibition of translation of respective one or more GAM172 target proteins.

[26026] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM172 gene, herein designated GAM GENE, on one or more GAM172 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26027] It is appreciated that specific functions and accordingly utilities of GAM172 correlate with, and may be deduced from, the identity of the target genes which GAM172 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26028]

[26029]

[26030] Deiodinase, iodothyronine, type ii (DIO2, Accession NM_000793.2) is a GAM172 target gene, herein designated TARGET GENE. DIO2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DIO2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DIO2 BINDING SITE, designated SEQ ID:4073, to the nucleotide sequence of GAM172 RNA, herein designated GAM RNA, also designated SEQ ID:253.

[26031] A function of GAM172 is therefore inhibition of Deiodinase, iodothyronine, type ii (DIO2, Accession

NM_000793.2) . Accordingly, utilities of GAM172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIO2.

[26032] Protein tyrosine phosphatase, receptor type, c (PTPRC, Accession NM_002838.2) is another GAM172 target gene, herein designated TARGET GENE. PTPRC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTPRC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPRC BINDING SITE, designated SEQ ID:11527, to the nucleotide sequence of GAM172 RNA, herein designated GAM RNA, also designated SEQ ID:253.

[26033] Another function of GAM172 is therefore inhibition of Protein tyrosine phosphatase, receptor type, c (PTPRC, Accession NM_002838.2) . Accordingly, utilities of GAM172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRC.

[26034] Transcription factor-like 5 (basic helix-loop-helix) (TCFL5, Accession NM_006602.1) is another GAM172 target gene, herein designated TARGET GENE. TCFL5 BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by TCFL5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCFL5 BINDING SITE, designated SEQ ID:11818, to the nucleotide sequence of GAM172 RNA, herein designated GAM RNA, also designated SEQ ID:253.

[26035] Another function of GAM172 is therefore inhibition of Transcription factor-like 5 (basic helix-loop-helix) (TCFL5, Accession NM_006602.1) . Accordingly, utilities of GAM172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCFL5.

[26036]

[26037] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 173 (GAM173), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26038] GAM173 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM173 was detected is described hereinabove with reference to Figs. 8-15.

[26039] GAM173 gene, herein designated GAM GENE, and GAM173 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[26040] GAM173 gene encodes a GAM173 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM173 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM173 precursor RNA is designated SEQ ID:124, and is provided hereinbelow with reference to the sequence listing part.

[26041] GAM173 precursor RNA folds onto itself, forming GAM173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26042] GAM173 precursor RNA folds onto itself, forming GAM173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[26043] Nucleotide sequence of GAM173 precursor RNA, designated SEQ-ID: 124, and a schematic representation of a predicted secondary folding of GAM173 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[26044] An enzyme complex designated DICER COMPLEX, `dices` the GAM173 folded precursor RNA into GAM173 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM173 RNA is designated SEQ ID:208, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[26045] GAM173 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM173 target RNA, herein designated GAM TARGET RNA. GAM173 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[26046] GAM173 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM173 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM173 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM173 RNA may have a different number of target binding sites in untranslated regions of a GAM173 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an

example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[26047] The complementary binding of GAM173 RNA, herein designated GAM RNA, to target binding sites on GAM173 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM173 target RNA into GAM173 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26048] It is appreciated that GAM173 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM173 target genes. The mRNA of each one of this plurality of GAM173 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM173 RNA, herein designated GAM RNA, and which when bound by GAM173 RNA causes inhibition of translation of respective one or more GAM173 target proteins.

[26049] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM173 gene, herein designated GAM GENE, on one or

more GAM173 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26050] It is appreciated that specific functions and accordingly utilities of GAM173 correlate with, and may be deduced from, the identity of the target genes which GAM173 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26051]

[26052]

[26053] LOC149157 (Accession XM_086442.1) is a GAM173 target gene, herein designated TARGET GENE. LOC149157 BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by LOC149157, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149157 BINDING SITE, designated SEQ ID:18849, to the nucleotide sequence of GAM173 RNA, herein designated GAM RNA, also designated SEQ ID:208.

[26054] A function of GAM173 is therefore inhibition of LOC149157 (Accession XM_086442.1) . Accordingly, utilities of GAM173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149157.

[26055] Spondin 1, (f-spondin) extracellular matrix protein (SPON1, Accession NM_006108.1) is another GAM173 target gene, herein designated TARGET GENE. SPON1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPON1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPON1 BINDING SITE, designated SEQ ID:15969, to the nucleotide sequence of GAM173 RNA, herein designated GAM RNA, also designated SEQ ID:208.

[26056] Another function of GAM173 is therefore inhibition of Spondin 1, (f-spondin) extracellular matrix protein (SPON1, Accession NM_006108.1) . Accordingly, utilities of GAM173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPON1.

[26057]

[26058] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 174 (GAM174), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26059] GAM174 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM174 was detected is described hereinabove with reference to Figs. 8-15.

[26060] GAM174 gene, herein designated GAM GENE, and GAM174 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[26061] GAM174 gene encodes a GAM174 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM174 precursor RNA does not encode a protein. A nucleotide sequence

identical or highly similar to the nucleotide sequence of GAM174 precursor RNA is designated SEQ ID:16, and is provided hereinbelow with reference to the sequence listing part.

[26062] GAM174 precursor RNA folds onto itself, forming GAM174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26063] GAM174 precursor RNA folds onto itself, forming GAM174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[26064] Nucleotide sequence of GAM174 precursor RNA, desig-

nated SEQ-ID: 16, and a schematic representation of a predicted secondary folding of GAM174 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[26065] An enzyme complex designated DICER COMPLEX, `dices` the GAM174 folded precursor RNA into GAM174 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM174 RNA is designated SEQ ID:252, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[26066] GAM174 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM174 target RNA, herein designated GAM TARGET RNA. GAM174 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[26067] GAM174 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM174 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM174 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM174 RNA may have a different number of target binding sites in untranslated regions of a GAM174 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[26068] The complementary binding of GAM174 RNA, herein designated GAM RNA, to target binding sites on GAM174 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM174 target RNA into GAM174 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26069] It is appreciated that GAM174 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM174 target genes. The mRNA of each one of this plurality of GAM174 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM174 RNA, herein designated GAM RNA, and which when bound by GAM174 RNA causes inhibition of translation of respective one or more GAM174 target proteins.

[26070] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM174 gene, herein designated GAM GENE, on one or more GAM174 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26071] It is appreciated that specific functions and accordingly utilities of GAM174 correlate with, and may be deduced from, the identity of the target genes which GAM174 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26072]

[26073]

[26074] A kinase (prka) anchor protein 13 (AKAP13, Accession NM_007200.2) is a GAM174 target gene, herein designated TARGET GENE. AKAP13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AKAP13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKAP13 BINDING SITE, designated SEQ ID:2878, to the nucleotide sequence of GAM174 RNA, herein designated

GAM RNA, also designated SEQ ID:252.

[26075] A function of GAM174 is therefore inhibition of A kinase (prka) anchor protein 13 (AKAP13, Accession NM_007200.2), a gene which regulates subcellular localization of type II cAMP- dependent PKA. Accordingly, utilities of GAM174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP13.

[26076] The function of AKAP13 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM54.1.D21S2056E (Accession NM_003683.2) is another GAM174 target gene, herein designated TARGET GENE. D21S2056E BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by D21S2056E, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of D21S2056E BINDING SITE, designated SEQ ID:3842, to the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, also designated SEQ ID:252.

[26077] Another function of GAM174 is therefore inhibition of

D21S2056E (Accession NM_003683.2) . Accordingly, utilities of GAM174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with D21S2056E.

[26078] DKFZP434O047 (Accession NM_015594.1) is another GAM174 target gene, herein designated TARGET GENE. DKFZP434O047 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP434O047, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434O047 BINDING SITE, designated SEQ ID:7607, to the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, also designated SEQ ID:252.

[26079] Another function of GAM174 is therefore inhibition of DKFZP434O047 (Accession NM_015594.1) . Accordingly, utilities of GAM174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434O047.

[26080] Inhibin, beta b (activin ab beta polypeptide) (INHBB, Accession NM_002193.1) is another GAM174 target gene, herein designated TARGET GENE. INHBB BINDING SITE is a

target binding site found in the 5` untranslated region of mRNA encoded by INHBB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INHBB BINDING SITE, designated SEQ ID:4697, to the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, also designated SEQ ID:252.

[26081] Another function of GAM174 is therefore inhibition of Inhibin, beta b (activin ab beta polypeptide) (INHBB, Accession NM_002193.1), a gene which inhibins inhibit the secretion of follitropin by the pituitary gland. and therefore may be associated with Tumors. Accordingly, utilities of GAM174 include diagnosis, prevention and treatment of Tumors, and of other diseases and clinical conditions associated with INHBB.

[26082] The function of INHBB has been established by previous studies. The activins, dimers of beta- A or beta- B subunits encoded by the genes Inhba (OMIM Ref. No. 147290) and Inhbb, respectively, are TGF- beta (see OMIM Ref. No. 190180) superfamily members that have roles in reproduction and development (Brown et al., 2000). Activin ligands act as growth and differentiation factors in many

cells and tissues. Mellor et al. (2000) examined the localization of and dimerization among activin subunits. The results demonstrated that activin beta- C (see OMIM Ref. No. 601233) can form dimers with activin beta- A and beta- B in vitro, but not with the inhibin alpha subunit (OMIM Ref. No. 147380). Using a specific antibody, activin beta- C protein was localized to human liver and prostate and colocalized with beta- A and beta- B subunits to specific cell types in benign and malignant prostate tissues. The capacity to form novel activin heterodimers (but not inhibin C) appears to reside in the human liver and prostate. The authors concluded that formation of activin AC or BC heterodimers may have significant implications in the regulation of levels and/or biologic activity of other activins in these tissues. Malignancy of pheochromocytomas is difficult to estimate on the basis of histopathologic features. In a search for new markers to differentiate malignant pheochromocytomas from benign ones, Salmenkivi et al. (2001) tested the value of inhibin/activin subunit expression. Inhibins are heterodimeric glycoproteins consisting of an alpha subunit and either a beta- A or a beta- B subunit. Activins are composed of beta subunits only. Immunohistochemically, inhibin/activin beta- B

subunit was strongly positive in the normal adrenal medulla, but the cortex was negative. A striking difference was found in inhibin/activin beta- B expression between benign and malignant pheochromocytomas. The majority of benign adrenal tumors (27 of 30) showed strong or moderate immunoreactivity, whereas all 7 malignant tumors were negative or only weakly positive for inhibin/activin beta- B subunit. Salmenkivi et al. (2001) suggested that inhibin/activin beta- B subunit is expressed in normal adrenal medullary cells. Strong staining was found in most benign adrenal pheochromocytomas, whereas malignant tumors were almost negative. They concluded that loss of inhibin/activin beta- B subunit expression in pheochromocytomas may be used as an indicator of malignant potential.

[26083] Animal model experiments lend further support to the function of INHBB. Whereas mice homozygous for the Inhba- null allele demonstrate disruption of whisker, palate, and tooth development leading to neonatal lethality, homozygous Inhbb- null mice are viable, fertile, and have eye defects. To determine if these phenotypes were due to spatiotemporal expression differences of the ligands or disruption of specific ligand- receptor interactions, Brown

et al. (2000) replaced the region of Inhba encoding the mature protein with Inhbb, creating the allele designated Inhba(BK). Although the craniofacial phenotypes of the Inhba- null mutation were rescued by the Inhba(BK) allele, somatic, testicular, genital, and hair growth were grossly affected and influenced by the dosage and bioactivity of the allele. Thus, Brown et al. (2000) concluded that functional compensation within the TGF- beta superfamily can occur if the replacement gene is expressed appropriately. The novel phenotypes in these mice further illustrate the usefulness of insertion strategies for defining protein function. The structural organization of the testes of adult Inhba(BK/BK) mice was normal; however, the differentiation of the seminiferous tubules of Inhba(BK/-) mice was delayed. The testicular volumes of both Inhba(BK/BK) and Inhba(BK/-) mice were less than those of controls, and the dosage of the Inhba(BK) allele correlated positively with testicular size. Inhba(+/BK) males had normal onset of fertility, whereas Inhba(BK/BK) males had delayed onset of fertility similar to Acvr2 (OMIM Ref. No. 102581) - /- mice. Only 1 in 6 Inhba(BK/BK) females produced litters, whereas Inhba(+/BK) females were normally fertile. The ovaries of Inhba(BK/-) mice were smaller and contained

fewer large preantral follicles than those of controls. Inhba(BK/BK) and Inhba(BK/-) mice were identified by their smaller size, slower hair growth, the rough appearance of their fur, and sunken eyes. Approximately 50% of Inhba(BK/BK) mice died by 26 weeks, whereas Inhba(BK/-) mice invariably became cachectic and died between 3 and 4 weeks. The summary of phenotypic findings of Inhba(BK/-) mice includes short whiskers, normal tooth development, no cleft palate, symmetric growth deficiency (OMIM Ref. No. severe), enlargement of external genitalia, hypogonadism (OMIM Ref. No. severe), delayed hair growth (moderate), hypoglycemia (mild), decreased life expectancy (OMIM Ref. No. severe), and anemia

[26084] It is appreciated that the abovementioned animal model for INHBB is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[26085] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26086] Salmenkivi, K.; Arola, J.; Voutilainen, R.; Ilvesmaki, V.; Haglund, C.; Kahri, A. I.; Heikkila, P.; Liu, J. : Inhibin/activin beta- B- subunit expression in pheochromocytomas

favors benign diagnosis. J. Clin. Endocr. Metab. 86: 2231-2235, 2001. ; and

[26087] Brown, C. W.; Houston- Hawkins, D. E.; Woodruff, T. K.; Matzuk, M. M. : Insertion of Inhbb into the Inhba locus rescues the Inhba- null phenotype and reveals new activin functions. Nature.

[26088] Further studies establishing the function and utilities of INHBB are found in John Hopkins OMIM database record ID 147390, and in cited publications listed in Table 5, which are hereby incorporated by reference.LOC147165 (Accession XM_294884.1) is another GAM174 target gene, herein designated TARGET GENE. LOC147165 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147165, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147165 BINDING SITE, designated SEQ ID:15184, to the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, also designated SEQ ID:252.

[26089] Another function of GAM174 is therefore inhibition of LOC147165 (Accession XM_294884.1) . Accordingly, utilities of GAM174 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147165.

[26090] LOC162417 (Accession) is another GAM174 target gene, herein designated TARGET GENE. LOC162417 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC162417, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162417 BINDING SITE, designated SEQ ID:13555, to the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, also designated SEQ ID:252.

[26091] Another function of GAM174 is therefore inhibition of LOC162417 (Accession) . Accordingly, utilities of GAM174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162417.

[26092] MGC12921 (Accession NM_032728.1) is another GAM174 target gene, herein designated TARGET GENE. MGC12921 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC12921, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC12921 BINDING SITE, designated SEQ ID:2736, to the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, also designated SEQ ID:252.

[26093] Another function of GAM174 is therefore inhibition of MGC12921 (Accession NM_032728.1) . Accordingly, utilities of GAM174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12921.

[26094] MGC15504 (Accession NM_032751.1) is another GAM174 target gene, herein designated TARGET GENE. MGC15504 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC15504, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15504 BINDING SITE, designated SEQ ID:8930, to the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, also designated SEQ ID:252.

[26095] Another function of GAM174 is therefore inhibition of MGC15504 (Accession NM_032751.1) . Accordingly, utilities of GAM174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC15504.

[26096] Protein kinase, lysine deficient 2 (PRKWNK2, Accession) is another GAM174 target gene, herein designated TARGET GENE. PRKWNK2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRKWNK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKWNK2 BINDING SITE, designated SEQ ID:20003, to the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, also designated SEQ ID:252.

[26097] Another function of GAM174 is therefore inhibition of Protein kinase, lysine deficient 2 (PRKWNK2, Accession) . Accordingly, utilities of GAM174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKWNK2.

[26098] Tumor protein d52-like 2 (TPD52L2, Accession NM_003288.1) is another GAM174 target gene, herein designated TARGET GENE. TPD52L2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TPD52L2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPD52L2 BINDING SITE, designated SEQ ID:18571, to the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, also designated SEQ ID:252.

[26099] Another function of GAM174 is therefore inhibition of Tumor protein d52-like 2 (TPD52L2, Accession NM_003288.1) . Accordingly, utilities of GAM174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TPD52L2.

[26100] Ubiquitin specific protease 20 (USP20, Accession NM_006676.1) is another GAM174 target gene, herein designated TARGET GENE. USP20 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by USP20, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of USP20 BINDING SITE, designated SEQ ID:554, to the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, also designated SEQ ID:252.

[26101] Another function of GAM174 is therefore inhibition of Ubiquitin specific protease 20 (USP20, Accession NM_006676.1) . Accordingly, utilities of GAM174 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with USP20.

[26102]

[26103] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 175 (GAM175), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26104] GAM175 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM175 was detected is described hereinabove with reference to Figs. 8-15.

[26105] GAM175 gene, herein designated GAM GENE, and GAM175 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[26106] GAM175 gene encodes a GAM175 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM175 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM175 precursor RNA is designated SEQ ID:28, and is provided hereinbelow with reference to the sequence list-

ing part. Nucleotide sequence SEQ ID:28 is located at position 557 relative to chromosome X.

[26107] GAM175 precursor RNA folds onto itself, forming GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26108] GAM175 precursor RNA folds onto itself, forming GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[26109] Nucleotide sequence of GAM175 precursor RNA, designated SEQ-ID: 28, and a schematic representation of a predicted secondary folding of GAM175 folded precursor

RNA are further described with reference to Table 2, hereby incorporated by reference.

[26110] An enzyme complex designated DICER COMPLEX, `dices` the GAM175 folded precursor RNA into GAM175 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: B) nucleotide sequence of GAM175 RNA is designated SEQ ID:265, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[26111] GAM175 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM175 target RNA, herein designated GAM TARGET RNA. GAM175 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[26112] GAM175 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM175 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM175 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM175 RNA may have a different number of target binding sites in untranslated regions of a GAM175 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[26113] The complementary binding of GAM175 RNA, herein designated GAM RNA, to target binding sites on GAM175 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM175 target RNA into GAM175 target protein, herein designated GAM TARGET PROTEIN.

GAM target protein is therefore outlined by a broken line.

[26114] It is appreciated that GAM175 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM175 target genes. The mRNA of each one of this plurality of GAM175 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM175 RNA, herein designated GAM RNA, and which when bound by GAM175 RNA causes inhibition of translation of respective one or more GAM175 target proteins.

[26115] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM175 gene, herein designated GAM GENE, on one or more GAM175 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26116] It is appreciated that specific functions and accordingly utilities of GAM175 correlate with, and may be deduced from, the identity of the target genes which GAM175 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26117]

[26118]

[26119] Aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT, Accession NP_056238.2) is a GAM175 target gene, herein designated TARGET GENE. AASDHPPT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AASDHPPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AASDHPPT BINDING SITE, designated SEQ ID:16747, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26120] A function of GAM175 is therefore inhibition of Aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT, Accession NP_056238.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AASDHPPT.

[26121] Adenosine deaminase, rna-specific (ADAR, Accession NP_056655.1) is another GAM175 target gene, herein designated TARGET GENE. ADAR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAR BINDING SITE, designated SEQ ID:13257, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26122] Another function of GAM175 is therefore inhibition of Adenosine deaminase, rna-specific (ADAR, Accession NP_056655.1), a gene which converts adenosine to inosine in double- stranded RNA. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAR.

[26123] The function of ADAR has been established by previous studies. Double- stranded RNA- specific adenosine deaminase (DSRAD) was identified as a developmentally regulated dsRNA unwinding activity in early antisense experiments with Xenopus oocytes (Bass and Weintraub, 1988). The enzyme converts adenosine to inosine in dsRNA, which destabilizes the dsRNA helix. The RNA modifying activity of DSRAD is important for various functions. Among these are site- specific RNA editing of transcripts of the glutamate receptors (see OMIM Ref. No. 138248), which are channels for the neurotransmitter L- glutamate in the brain. DSRAD also functions to modify viral RNA genomes and may be responsible for hypermutation of certain negative- stranded viruses, such as measles, which may result in lethal measles inclusion body encephalitis (Weier et al., 1995). By fluorescence in situ hybridization, Weier et al. (1995) mapped the DSRAD gene to 1q21.1- q21.2, centromeric to the marker D1S1705. Wang et al. (1995) mapped the DRADA gene to 1q21 by fluorescence in situ hybridization. By FISH, Weier et al. (2000) mapped the mouse homolog (Adar) to chromosome 3F2.

[26124] Animal model experiments lend further support to the

function of ADAR. Wang et al. (2000) knocked out the Adar1 gene in mice by targeted disruption and found that heterozygosity for the Adar1 knockout causes embryonic lethality.

[26125] It is appreciated that the abovementioned animal model for ADAR is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[26126] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26127] Weier, H.- U. G.; George, C. X.; Greulich, K. M.; Samuel, C. E. : The interferon- inducible, double- stranded RNA- specific adenosine deaminase gene (DSRAD) maps to human chromosome 1q21.1- 21.2. Genomics 30: 372- 375, 1995. ; and

[26128] Wang, Q.; Khillan, J.; Gadue, P.; Nishikura, K. : Requirement of the RNA editing deaminase ADAR1 gene for embryonic erythropoiesis. Science 290: 1765- 1768, 2000.

[26129] Further studies establishing the function and utilities of ADAR are found in John Hopkins OMIM database record ID 601059, and in cited publications listed in Table 5, which are hereby incorporated by reference.Adenosine deami-

nase, rna-specific (ADAR, Accession NP_001102.1) is another GAM175 target gene, herein designated TARGET GENE. ADAR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAR BINDING SITE, designated SEQ ID:13257, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26130] Another function of GAM175 is therefore inhibition of Adenosine deaminase, rna-specific (ADAR, Accession NP_001102.1), a gene which converts adenosine to inosine in double- stranded RNA. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAR.

[26131] The function of ADAR has been established by previous studies. Double- stranded RNA- specific adenosine deaminase (DSRAD) was identified as a developmentally regulated dsRNA unwinding activity in early antisense experiments with Xenopus oocytes (Bass and Weintraub, 1988). The enzyme converts adenosine to inosine in dsRNA,

which destabilizes the dsRNA helix. The RNA modifying activity of DSRAD is important for various functions. Among these are site- specific RNA editing of transcripts of the glutamate receptors (see OMIM Ref. No. 138248), which are channels for the neurotransmitter L- glutamate in the brain. DSRAD also functions to modify viral RNA genomes and may be responsible for hypermutation of certain negative- stranded viruses, such as measles, which may result in lethal measles inclusion body encephalitis (Weier et al., 1995). By fluorescence in situ hybridization, Weier et al. (1995) mapped the DSRAD gene to 1q21.1- q21.2, centromeric to the marker D1S1705. Wang et al. (1995) mapped the DRADA gene to 1q21 by fluorescence in situ hybridization. By FISH, Weier et al. (2000) mapped the mouse homolog (Adar) to chromosome 3F2.

[26132] Animal model experiments lend further support to the function of ADAR. Wang et al. (2000) knocked out the Adar1 gene in mice by targeted disruption and found that heterozygosity for the Adar1 knockout causes embryonic lethality.

[26133] It is appreciated that the abovementioned animal model for ADAR is acknowledged by those skilled in the art as a

scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[26134] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26135] Weier, H.- U. G.; George, C. X.; Greulich, K. M.; Samuel, C. E. : The interferon- inducible, double- stranded RNA-specific adenosine deaminase gene (DSRAD) maps to human chromosome 1q21.1- 21.2. Genomics 30: 372- 375, 1995. ; and

[26136] Wang, Q.; Khillan, J.; Gadue, P.; Nishikura, K. : Requirement of the RNA editing deaminase ADAR1 gene for embryonic erythropoiesis. Science 290: 1765- 1768, 2000.

[26137] Further studies establishing the function and utilities of ADAR are found in John Hopkins OMIM database record ID 601059, and in cited publications listed in Table 5, which are hereby incorporated by reference.Adenosine deaminase, rna-specific (ADAR, Accession NP_056656.1) is another GAM175 target gene, herein designated TARGET GENE. ADAR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAR BINDING SITE, designated SEQ ID:13257, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26138] Another function of GAM175 is therefore inhibition of Adenosine deaminase, rna-specific (ADAR, Accession NP_056656.1), a gene which converts adenosine to inosine in double- stranded RNA. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAR.

[26139] The function of ADAR has been established by previous studies. Double- stranded RNA- specific adenosine deaminase (DSRAD) was identified as a developmentally regulated dsRNA unwinding activity in early antisense experiments with Xenopus oocytes (Bass and Weintraub, 1988). The enzyme converts adenosine to inosine in dsRNA, which destabilizes the dsRNA helix. The RNA modifying activity of DSRAD is important for various functions. Among these are site- specific RNA editing of transcripts of the glutamate receptors (see OMIM Ref. No. 138248), which are channels for the neurotransmitter L- glutamate in the brain. DSRAD also functions to modify viral RNA

genomes and may be responsible for hypermutation of certain negative- stranded viruses, such as measles, which may result in lethal measles inclusion body encephalitis (Weier et al., 1995). By fluorescence in situ hybridization, Weier et al. (1995) mapped the DSRAD gene to 1q21.1- q21.2, centromeric to the marker D1S1705. Wang et al. (1995) mapped the DRADA gene to 1q21 by fluorescence in situ hybridization. By FISH, Weier et al. (2000) mapped the mouse homolog (Adar) to chromosome 3F2.

[26140] Animal model experiments lend further support to the function of ADAR. Wang et al. (2000) knocked out the Adar1 gene in mice by targeted disruption and found that heterozygosity for the Adar1 knockout causes embryonic lethality.

[26141] It is appreciated that the abovementioned animal model for ADAR is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[26142] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26143] Weier, H.- U. G.; George, C. X.; Greulich, K. M.; Samuel, C.

E. : The interferon- inducible, double- stranded RNA- specific adenosine deaminase gene (DSRAD) maps to human chromosome 1q21.1- 21.2. Genomics 30: 372- 375, 1995. ; and

[26144] Wang, Q.; Khillan, J.; Gadue, P.; Nishikura, K. : Requirement of the RNA editing deaminase ADAR1 gene for embryonic erythropoiesis. Science 290: 1765- 1768, 2000.

[26145] Further studies establishing the function and utilities of ADAR are found in John Hopkins OMIM database record ID 601059, and in cited publications listed in Table 5, which are hereby incorporated by reference.AFAP (Accession NP_067651.1) is another GAM175 target gene, herein designated TARGET GENE. AFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AFAP BINDING SITE, designated SEQ ID:7185, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26146] Another function of GAM175 is therefore inhibition of AFAP (Accession NP_067651.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with AFAP.

[26147] Annexin a8 (ANXA8, Accession NP_001621.1) is another GAM175 target gene, herein designated TARGET GENE. ANXA8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ANXA8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANXA8 BINDING SITE, designated SEQ ID:15378, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26148] Another function of GAM175 is therefore inhibition of Annexin a8 (ANXA8, Accession NP_001621.1), a gene which acts as an indirect inhibitor of the thromboplastin- specific complex, which is involved in the blood coagulation cascade. and therefore may be associated with Promyelocytic leukemia locus (pml). Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Promyelocytic leukemia locus (pml), and of other diseases and clinical conditions associated with ANXA8.

[26149] The function of ANXA8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM55.2.Apoptotic protease activating factor (APAF1, Accession NP_037361.1) is another GAM175 target gene, herein designated TARGET GENE. APAF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APAF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE, designated SEQ ID:12211, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26150] Another function of GAM175 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_037361.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[26151] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apoptotic protease activating factor (APAF1,

Accession NP_001151.1) is another GAM175 target gene, herein designated TARGET GENE. APAF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APAF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE, designated SEQ ID:12211, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26152] Another function of GAM175 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_001151.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[26153] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apolipoprotein l, 1 (APOL1, Accession NP_003652.2) is another GAM175 target gene, herein

designated TARGET GENE. APOL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL1 BINDING SITE, designated SEQ ID:10954, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26154] Another function of GAM175 is therefore inhibition of Apolipoprotein l, 1 (APOL1, Accession NP_003652.2), a gene which may participate in reverse cholesterol transport from peripheral cells to the liver. and therefore may be associated with Schizophrenia. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Schizophrenia, and of other diseases and clinical conditions associated with APOL1.

[26155] The function of APOL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apolipoprotein l, 1 (APOL1, Accession NP_663319.1) is another GAM175 target gene, herein designated TARGET GENE. APOL1 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL1 BINDING SITE, designated SEQ ID:10954, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26156] Another function of GAM175 is therefore inhibition of Apolipoprotein l, 1 (APOL1, Accession NP_663319.1), a gene which may participate in reverse cholesterol transport from peripheral cells to the liver. and therefore may be associated with Schizophrenia. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Schizophrenia, and of other diseases and clinical conditions associated with APOL1.

[26157] The function of APOL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apolipoprotein l, 1 (APOL1, Accession NP_663318.1) is another GAM175 target gene, herein designated TARGET GENE. APOL1 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by APOL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL1 BINDING SITE, designated SEQ ID:10954, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26158] Another function of GAM175 is therefore inhibition of Apolipoprotein l, 1 (APOL1, Accession NP_663318.1), a gene which may participate in reverse cholesterol transport from peripheral cells to the liver. and therefore may be associated with Schizophrenia. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Schizophrenia, and of other diseases and clinical conditions associated with APOL1.

[26159] The function of APOL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Adp-ribosylation factor 4 (ARF4, Accession NP_001651.1) is another GAM175 target gene, herein designated TARGET GENE. ARF4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARF4, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARF4 BINDING SITE, designated SEQ ID:16305, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26160] Another function of GAM175 is therefore inhibition of Adp-ribosylation factor 4 (ARF4, Accession NP_001651.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARF4.

[26161] Rho/rac guanine nucleotide exchange factor (gef) 2 (ARHGEF2, Accession NP_004714.2) is another GAM175 target gene, herein designated TARGET GENE. ARHGEF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGEF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGEF2 BINDING SITE, designated SEQ ID:10786, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26162] Another function of GAM175 is therefore inhibition of

Rho/rac guanine nucleotide exchange factor (gef) 2 (ARHGEF2, Accession NP_004714.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF2.

[26163] Cdc42 guanine nucleotide exchange factor (gef) 9 (ARHGEF9, Accession NP_056000.1) is another GAM175 target gene, herein designated TARGET GENE. ARHGEF9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGEF9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGEF9 BINDING SITE, designated SEQ ID:527, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26164] Another function of GAM175 is therefore inhibition of Cdc42 guanine nucleotide exchange factor (gef) 9 (ARHGEF9, Accession NP_056000.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF9.

[26165] Aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2,

Accession NP_055677.1) is another GAM175 target gene, herein designated TARGET GENE. ARNT2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARNT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARNT2 BINDING SITE, designated SEQ ID:16746, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26166] Another function of GAM175 is therefore inhibition of Aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2, Accession NP_055677.1), a gene which specifically recognizes the xenobiotic response element (xre). Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARNT2.

[26167] The function of ARNT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.1.ART5 (Accession NP_443750.2) is another GAM175 target gene, herein designated TARGET GENE. ART5 BINDING SITE is a target binding site found in the 5`

untranslated region of mRNA encoded by ART5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ART5 BINDING SITE, designated SEQ ID:13679, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26168] Another function of GAM175 is therefore inhibition of ART5 (Accession NP_443750.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ART5.

[26169] Chromosome 10 open reading frame 2 (C10orf2, Accession NP_068602.1) is another GAM175 target gene, herein designated TARGET GENE. C10orf2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C10orf2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C10orf2 BINDING SITE, designated SEQ ID:3494, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26170] Another function of GAM175 is therefore inhibition of

Chromosome 10 open reading frame 2 (C10orf2, Accession NP_068602.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C10orf2.

[26171] Chromosome 14 open reading frame 37 (C14orf37, Accession XP_085124.2) is another GAM175 target gene, herein designated TARGET GENE. C14orf37 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf37, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf37 BINDING SITE, designated SEQ ID:18001, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26172] Another function of GAM175 is therefore inhibition of Chromosome 14 open reading frame 37 (C14orf37, Accession XP_085124.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf37.

[26173] Chromosome 1 open reading frame 34 (C1orf34, Accession XP_027172.1) is another GAM175 target gene, herein designated TARGET GENE. C1orf34 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by C1orf34, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf34 BINDING SITE, designated SEQ ID:10527, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26174] Another function of GAM175 is therefore inhibition of Chromosome 1 open reading frame 34 (C1orf34, Accession XP_027172.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf34.

[26175] Chromosome 5 open reading frame 7 (C5orf7, Accession NP_057688.1) is another GAM175 target gene, herein designated TARGET GENE. C5orf7 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C5orf7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C5orf7 BINDING SITE, designated SEQ ID:449, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26176] Another function of GAM175 is therefore inhibition of Chromosome 5 open reading frame 7 (C5orf7, Accession NP_057688.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf7.

[26177] Chemokine (c-c motif) receptor 2 (CCR2, Accession NP_000639.1) is another GAM175 target gene, herein designated TARGET GENE. CCR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CCR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCR2 BINDING SITE, designated SEQ ID:13143, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26178] Another function of GAM175 is therefore inhibition of Chemokine (c-c motif) receptor 2 (CCR2, Accession NP_000639.1), a gene which binds chemokines and transduces a signal by increasing the intracellular calcium ions level. and therefore may be associated with Hiv- 1 infection. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Hiv- 1 infection, and of other

diseases and clinical conditions associated with CCR2.

[26179] The function of CCR2 has been established by previous studies. Charo et al. (1994) isolated 2 cDNAs by degenerate PCR using primers for a conserved region in the second and third transmembrane domains of the MIP- 1- alpha/RANTES receptor (OMIM Ref. No. 601159) and IL- 8 receptors (146928, 146929). They then used PCR products to screen a human monocytic leukemia- cell library. The 2 cDNAs encoded putative chemokine receptors (termed A and B) that are identical except for their C termini and thus appear to result from alternative splicing. The 347- amino acid predicted protein from the A isoform, designated MCP1RA (and later termed CC CKR2A by Combadiere et al., 1995), is 51% identical to the MIP- 1- alpha/RANTES receptor. As are the other members of this receptor family, MCP1RA is a 7- transmembrane G protein- coupled receptor. Combadiere et al. (1995) demonstrated that the predominant agonist for CC CKR2A is MCP1, while both MCP1 and MCP3 (OMIM Ref. No. 158106) are ligands for the CC CKR2B isoform (Combadiere et al., 1995).

[26180] Animal model experiments lend further support to the function of CCR2. Peters et al. (2000) observed that after

immunization with Th1- inducing agents, Ccr2 - /- mice produced markedly less gamma- interferon (IFNG; 147570) after antigen- specific stimulation than did wild-type mice. In contrast, IL5 (OMIM Ref. No. 147850), IL10 (OMIM Ref. No. 124092), and IL13 (OMIM Ref. No. 147683) production was not impaired in Ccr2 - /- mice. Flow cytometric analysis showed that fewer antigen- presenting cells migrated to the immunization site or draining lymph nodes in the Ccr2 - /- mice. Peters et al. (2000) concluded that CCR2 is required for proper trafficking of antigen- presenting cells capable of inducing IFNG production by T cells.

[26181] It is appreciated that the abovementioned animal model for CCR2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[26182] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26183] Combadiere, C.; Ahuja, S. K.; Van Damme, J.; Tiffany, H. L.; Gao, J.- L.; Murphy, P. M. : Monocyte chemoattractant protein- 3 is a functional ligand for CC chemokine receptors 1 and 2B. J. Biol. Chem. 270: 29671- 29675, 1995. ;

and

[26184] Peters, W.; Dupuis, M.; Charo, I. F. : A mechanism for the impaired IFN- gamma production in C- C chemokine receptor 2 (CCR2) knockout mice: role of CCR2 in linking the innate and adaptive.

[26185] Further studies establishing the function and utilities of CCR2 are found in John Hopkins OMIM database record ID 601267, and in cited publications listed in Table 5, which are hereby incorporated by reference.Ccr4 carbon catabolite repression 4-like (s. cerevisiae) (CCRN4L, Accession NP_036250.2) is another GAM175 target gene, herein designated TARGET GENE. CCRN4L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCRN4L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCRN4L BINDING SITE, designated SEQ ID:708, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26186] Another function of GAM175 is therefore inhibition of Ccr4 carbon catabolite repression 4-like (s. cerevisiae) (CCRN4L, Accession NP_036250.2) . Accordingly, utilities

of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCRN4L.

[26187] CHDC1 (Accession XP_166260.1) is another GAM175 target gene, herein designated TARGET GENE. CHDC1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CHDC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHDC1 BINDING SITE, designated SEQ ID:13850, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26188] Another function of GAM175 is therefore inhibition of CHDC1 (Accession XP_166260.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHDC1.

[26189] Carbohydrate (n-acetylglucosamine 6-o) sulfotransferase 5 (CHST5, Accession NP_036258.1) is another GAM175 target gene, herein designated TARGET GENE. CHST5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CHST5, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHST5 BINDING SITE, designated SEQ ID:1259, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26190] Another function of GAM175 is therefore inhibition of Carbohydrate (n-acetylglucosamine 6-o) sulfotransferase 5 (CHST5, Accession NP_036258.1), a gene which may be involved in sulfation of glycoproteins and proteoglycans. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST5.

[26191] The function of CHST5 has been established by previous studies. The carbohydrates of glycoconjugates are highly diverse structures with variation in monosaccharide composition, glycosidic linkage positions, and branching of chains. Further diversity is added by the covalent addition of sulfate moieties to particular hydroxyl groups and amino groups of saccharides. The sulfate modifications of glycoproteins can be extensive in amount and frequently occur at high density. They can have a profound effect on the physiochemical properties of the glycoconjugates, at least in part through the addition of negative charge. Car-

bohydrate sulfation plays a critical role in many biologic processes. The GST family of sulfotransferases includes CHST1 (OMIM Ref. No. 603797), CHST2 (OMIM Ref. No. 603798), CHST3 (OMIM Ref. No. 603799), and LSST. These enzymes are 6- O- sulfotransferases, which add sulfate to C6 of galactose (Gal), N- acetylgalactosamine (OMIM Ref. No. GalNAc), or N- acetylglucosamine (OMIM Ref. No. Glc-NAc). By searching an EST database with the sequences of CHST1 and LSST, Lee et al. (1999) identified nonoverlapping ESTs encoding CHST5, which they called IGlcNAc6ST. They isolated additional CHST5 ESTs and assembled a complete CHST5 coding sequence. The deduced 390-amino acid CHST5 protein is predicted to be a type II transmembrane protein, with an N- terminal cytoplasmic tail of 9 residues and a single transmembrane domain. The extracellular domain contains 3 potential N- glycosylation sites. CHST5 shares 55% amino acid sequence identity with LSST, 35.8% identity with CHST1, and 76% identity with mouse Chst5, whose cDNA Lee et al. (1999) also cloned. Recombinant CHST5 expressed in mammalian cells catalyzed the addition of sulfate to C6 of GlcNAc. Lee et al. (1999) isolated the CHST5 genomic sequence. The CHST5 gene is intronless. Northern blot analysis of a vari-

ety of normal human tissues showed a major 2.8- kb CHST5 transcript at relatively high levels in colon and small intestine and at lower levels in fetal liver. Minor transcripts of 3.5, 4, 5, and 8 kb were also found in colon and small intestine. CHST5 expression was not detected in any of the other tissues tested. CHST5, encoding an intestinal sulfotransferase, is situated close to CHST6 (OMIM Ref. No. 605294), which encodes a corneal sulfotransferase and is mutant in cases of macular corneal dystrophy (OMIM Ref. No. 217800). By radiation hybrid analysis, Akama et al. (2000) mapped the CHST5 and CHST6 genes to 16q22, between markers D16S3326 and D16S3016

[26192]

[26193] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26194] Akama, T. O.; Nishida, K.; Nakayama, J.; Watanabe, H.; Ozaki, K.; Nakamura, T.; Dota, A.; Kawasaki, S.; Inoue, Y.; Maeda, N.; Yamamoto, S.; Fujiwara, T.; Thonar, E. J.- M. A.; Shimomura, Y.; Kinoshita, S.; Tanigami, A.; Fukuda, M. N. : Macular corneal dystrophy type I and type II are caused by distinct mutations in a new sulphotransferase gene. Nature Genet. 26: 237- 241, 2000. ; and

[26195] Lee, J. K.; Bhakta, S.; Rosen, S. D.; Hemmerich, S. : Cloning and characterization of a mammalian N- acetylglu- cosamine- 6- sulfotransferase that is highly restricted to intestinal tissue.

[26196] Further studies establishing the function and utilities of CHST5 are found in John Hopkins OMIM database record ID 604817, and in cited publications listed in Table 5, which are hereby incorporated by reference.Cop9 consti- tutive photomorphogenic homolog subunit 7a (arabidopsis) (COPS7A, Accession NP_057403.1) is an- other GAM175 target gene, herein designated TARGET GENE. COPS7A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by COPS7A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu- cleotide sequences of COPS7A BINDING SITE, designated SEQ ID:15229, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26197] Another function of GAM175 is therefore inhibition of Cop9 constitutive photomorphogenic homolog subunit 7a (arabidopsis) (COPS7A, Accession NP_057403.1) . Accord-

ingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COPS7A.

[26198] Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_803185.1) is another GAM175 target gene, herein designated TARGET GENE. CSE1L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CSE1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSE1L BINDING SITE, designated SEQ ID:17881, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26199] Another function of GAM175 is therefore inhibition of Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_803185.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE1L.

[26200] Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_001307.2) is another GAM175 target gene, herein designated TARGET GENE. CSE1L BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by CSE1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSE1L BINDING SITE, designated SEQ ID:17881, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26201] Another function of GAM175 is therefore inhibition of Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_001307.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE1L.

[26202] Catenin (cadherin-associated protein), alpha 2 (CTNNA2, Accession NP_004380.1) is another GAM175 target gene, herein designated TARGET GENE. CTNNA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNNA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTNNA2 BINDING SITE, designated SEQ ID:1392, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26203] Another function of GAM175 is therefore inhibition of Catenin (cadherin-associated protein), alpha 2 (CTNNA2, Accession NP_004380.1), a gene which is involved in the cytoplasmic anchorage of cell- cell and cell- substrate adhesion molecules. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTNNA2.

[26204] The function of CTNNA2 has been established by previous studies. Cell- cell and cell- matrix adhesions involve transmembrane glycoproteins such as cell adhesion molecules and integrins, which are thought to function via interactions of their cytoplasmic domains with proteins associated with the cytoskeleton. Vinculin (OMIM Ref. No. 193065) and talin (OMIM Ref. No. 186745) are examples. The activity of cadherins (e.g., 114020), which mediate homophilic cell- cell Ca(2+)- dependent association, depends on their anchorage to cytoskeleton via proteins termed catenins (Herrenknecht et al., 1991).

[26205] Animal model experiments lend further support to the function of CTNNA2. Mice homozygous for the 'cerebellar-deficient folia' (cdf) mutation are ataxic and have cerebellar hypoplasia and abnormal lobulation of the cerebellum (Cook et al., 1997). In the cerebella of cdf/cdf homozy-

gous mice, approximately 40% of Purkinje cells are located ectopically in the white matter and inner granule- cell layer. Many hippocampal pyramidal cells are scattered in the plexiform layers, and those that are correctly positioned are less densely packed than are cells in wildtype mice. Park et al. (2002) showed that fear conditioning and prepulse inhibition of the startle response are also disrupted in cdf/cdf mice. They identified a deletion on mouse chromosome 6 that removed approximately 150 kb of the cdf region. The deletion included part of Catna2, encoding alpha- N- catenin, a protein that links the classic cadherins to the neuronal cytoskeleton. Expression of a Catna2 transgene in cdf/cdf mice restored normal cerebellar and hippocampal morphology, prepulse inhibition, and fear conditioning. The findings suggested that catenin- cadherin cell- adhesion complexes are important in cerebellar and hippocampal lamination and in the control of startle modulation.

[26206] It is appreciated that the abovementioned animal model for CTNNA2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[26207] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[26208] Claverie, J.- M.; Hardelin, J.- P.; Legouis, R.; Levilliers, J.; Bougueleret, L.; Mattei, M.- G.; Petit, C. : Characterization and chromosomal assignment of a human cDNA encoding a protein related to the murine 102- kDa cadherin- associated protein (alpha- catenin). Genomics 15: 13- 20, 1993. ; and

[26209] Park, C.; Falls, W.; Finger, J. H.; Longo- Guess, C. M.; Ackerman, S. L. : Deletion in Catna2, encoding alpha- N-catenin, causes cerebellar and hippocampal lamination defects and impaired.

[26210] Further studies establishing the function and utilities of CTNNA2 are found in John Hopkins OMIM database record ID 114025, and in cited publications listed in Table 5, which are hereby incorporated by reference.Catenin, beta interacting protein 1 (CTNNBIP1, Accession NP_064633.1) is another GAM175 target gene, herein designated TARGET GENE. CTNNBIP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNNBIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of CTNNBIP1 BINDING SITE, designated SEQ ID:17490, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26211] Another function of GAM175 is therefore inhibition of Catenin, beta interacting protein 1 (CTNNBIP1, Accession NP_064633.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTNNBIP1.

[26212] Catenin (cadherin-associated protein), delta 1 (CTNND1, Accession NP_001322.1) is another GAM175 target gene, herein designated TARGET GENE. CTNND1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTNND1 BINDING SITE, designated SEQ ID:18658, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26213] Another function of GAM175 is therefore inhibition of Catenin (cadherin-associated protein), delta 1 (CTNND1, Accession NP_001322.1) . Accordingly, utilities of

GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTNND1.

[26214] Death-associated protein kinase 1 (DAPK1, Accession NP_004929.1) is another GAM175 target gene, herein designated TARGET GENE. DAPK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DAPK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DAPK1 BINDING SITE, designated SEQ ID:10219, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26215] Another function of GAM175 is therefore inhibition of Death-associated protein kinase 1 (DAPK1, Accession NP_004929.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAPK1.

[26216] Dna cross-link repair 1c (pso2 homolog, s. cerevisiae) (DCLRE1C, Accession NP_071932.1) is another GAM175 target gene, herein designated TARGET GENE. DCLRE1C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DCLRE1C, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCLRE1C BINDING SITE, designated SEQ ID:8700, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26217] Another function of GAM175 is therefore inhibition of Dna cross-link repair 1c (pso2 homolog, s. cerevisiae) (DCLRE1C, Accession NP_071932.1), a gene which intervenes in V(D)J recombination/DNA repair. and therefore may be associated with Severe combined immunodeficiency with sensitivity to ionizing radiation . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Severe combined immunodeficiency with sensitivity to ionizing radiation ., and of other diseases and clinical conditions associated with DCLRE1C.

[26218] The function of DCLRE1C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1) is another GAM175 target gene, herein designated TARGET GENE. DIAPH2 BINDING SITE is a target binding site found in the 3` untranslated region

of multiple transcripts of mRNA encoded by DIAPH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DIAPH2 BINDING SITE, designated SEQ ID:5513, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26219] Another function of GAM175 is therefore inhibition of Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1), a gene which may affect in oogenesis and therefore may be associated with Premature ovarian failure . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Premature ovarian failure ., and of other diseases and clinical conditions associated with DIAPH2.

[26220] The function of DIAPH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.DKFZp434G179 (Accession XP_087065.1) is another GAM175 target gene, herein designated TARGET GENE. DKFZp434G179 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434G179, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434G179 BINDING SITE, designated SEQ ID:15093, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26221] Another function of GAM175 is therefore inhibition of DKFZp434G179 (Accession XP_087065.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434G179.

[26222] DKFZP434H132 (Accession NP_056307.1) is another GAM175 target gene, herein designated TARGET GENE. DKFZP434H132 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434H132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434H132 BINDING SITE, designated SEQ ID:10923, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26223] Another function of GAM175 is therefore inhibition of DK-

FZP434H132 (Accession NP_056307.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434H132.

[26224] DKFZP434H2010 (Accession NP_115505.1) is another GAM175 target gene, herein designated TARGET GENE. DKFZP434H2010 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434H2010, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434H2010 BINDING SITE, designated SEQ ID:2795, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26225] Another function of GAM175 is therefore inhibition of DKFZP434H2010 (Accession NP_115505.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434H2010.

[26226] DKFZp434K2435 (Accession NP_115632.1) is another GAM175 target gene, herein designated TARGET GENE. DKFZp434K2435 BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by DKFZp434K2435, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434K2435 BINDING SITE, designated SEQ ID:6806, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26227] Another function of GAM175 is therefore inhibition of DKFZp434K2435 (Accession NP_115632.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434K2435.

[26228] DKFZp761G0122 (Accession NP_689874.1) is another GAM175 target gene, herein designated TARGET GENE. DKFZp761G0122 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761G0122, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761G0122 BINDING SITE, designated SEQ ID:10041, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:265.

[26229] Another function of GAM175 is therefore inhibition of DKFZp761G0122 (Accession NP_689874.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761G0122.

[26230] Ectodermal dysplasia 1, anhidrotic (ED1, Accession NP_001390.1) is another GAM175 target gene, herein designated TARGET GENE. ED1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ED1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ED1 BINDING SITE, designated SEQ ID:3738, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26231] Another function of GAM175 is therefore inhibition of Ectodermal dysplasia 1, anhidrotic (ED1, Accession NP_001390.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ED1.

[26232] Endothelial differentiation, sphingolipid g-protein-coupled receptor, 1 (EDG1, Accession NP_001391.2)

is another GAM175 target gene, herein designated TARGET GENE. EDG1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by EDG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDG1 BINDING SITE, designated SEQ ID:5089, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26233] Another function of GAM175 is therefore inhibition of Endothelial differentiation, sphingolipid g-protein-coupled receptor, 1 (EDG1, Accession NP_001391.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDG1.

[26234] Epsin 2 (EPN2, Accession NP_055779.1) is another GAM175 target gene, herein designated TARGET GENE. EPN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EPN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EPN2 BINDING SITE, designated

SEQ ID:3856, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26235] Another function of GAM175 is therefore inhibition of Epsin 2 (EPN2, Accession NP_055779.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPN2.

[26236] Epsin 2 (EPN2, Accession NP_683723.1) is another GAM175 target gene, herein designated TARGET GENE. EPN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EPN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EPN2 BINDING SITE, designated SEQ ID:3856, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26237] Another function of GAM175 is therefore inhibition of Epsin 2 (EPN2, Accession NP_683723.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPN2.

[26238] Fem-1 homolog a (c.elegans) (FEM1A, Accession

NP_061178.1) is another GAM175 target gene, herein designated TARGET GENE. FEM1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FEM1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FEM1A BINDING SITE, designated SEQ ID:18114, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26239] Another function of GAM175 is therefore inhibition of Fem-1 homolog a (c.elegans) (FEM1A, Accession NP_061178.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEM1A.

[26240] FLJ10520 (Accession NP_060594.2) is another GAM175 target gene, herein designated TARGET GENE. FLJ10520 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10520, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10520 BINDING SITE, designated SEQ ID:2136, to the

nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26241] Another function of GAM175 is therefore inhibition of FLJ10520 (Accession NP_060594.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10520.

[26242] FLJ11286 (Accession NP_060851.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ11286 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11286, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11286 BINDING SITE, designated SEQ ID:5419, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26243] Another function of GAM175 is therefore inhibition of FLJ11286 (Accession NP_060851.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11286.

[26244] FLJ11700 (Accession NP_079168.1) is another GAM175

target gene, herein designated TARGET GENE. FLJ11700 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11700, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11700 BINDING SITE, designated SEQ ID:12317, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26245] Another function of GAM175 is therefore inhibition of FLJ11700 (Accession NP_079168.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11700.

[26246] FLJ12242 (Accession NP_078957.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ12242 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12242, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12242 BINDING SITE, designated SEQ ID:6997, to the nucleotide sequence of GAM175 RNA, herein designated

GAM RNA, also designated SEQ ID:265.

[26247] Another function of GAM175 is therefore inhibition of FLJ12242 (Accession NP_078957.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12242.

[26248] FLJ13081 (Accession NP_079110.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ13081 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13081, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13081 BINDING SITE, designated SEQ ID:16448, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26249] Another function of GAM175 is therefore inhibition of FLJ13081 (Accession NP_079110.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13081.

[26250] FLJ13241 (Accession NP_079364.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ13241

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13241 BINDING SITE, designated SEQ ID:14121, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26251] Another function of GAM175 is therefore inhibition of FLJ13241 (Accession NP_079364.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13241.

[26252] FLJ13544 (Accession NP_079284.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ13544 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13544, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13544 BINDING SITE, designated SEQ ID:9579, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26253] Another function of GAM175 is therefore inhibition of FLJ13544 (Accession NP_079284.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13544.

[26254] FLJ21868 (Accession NP_073606.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ21868 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ21868, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21868 BINDING SITE, designated SEQ ID:10496, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26255] Another function of GAM175 is therefore inhibition of FLJ21868 (Accession NP_073606.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21868.

[26256] FLJ22167 (Accession NP_078809.2) is another GAM175 target gene, herein designated TARGET GENE. FLJ22167 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by FLJ22167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22167 BINDING SITE, designated SEQ ID:1259, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26257] Another function of GAM175 is therefore inhibition of FLJ22167 (Accession NP_078809.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22167.

[26258] FLJ22578 (Accession NP_079140.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ22578 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22578, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22578 BINDING SITE, designated SEQ ID:15094, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26259] Another function of GAM175 is therefore inhibition of

FLJ22578 (Accession NP_079140.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22578.

[26260] FLJ23754 (Accession NP_689888.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ23754 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23754, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23754 BINDING SITE, designated SEQ ID:543, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26261] Another function of GAM175 is therefore inhibition of FLJ23754 (Accession NP_689888.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23754.

[26262] FLJ36928 (Accession NP_775822.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ36928 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36928, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36928 BINDING SITE, designated SEQ ID:15645, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26263] Another function of GAM175 is therefore inhibition of FLJ36928 (Accession NP_775822.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36928.

[26264] FLJ39058 (Accession NP_775851.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ39058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39058 BINDING SITE, designated SEQ ID:1228, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26265] Another function of GAM175 is therefore inhibition of FLJ39058 (Accession NP_775851.1) . Accordingly, utilities

of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39058.

[26266] FLJ39501 (Accession NP_775754.1) is another GAM175 target gene, herein designated TARGET GENE. FLJ39501 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39501, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39501 BINDING SITE, designated SEQ ID:7439, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26267] Another function of GAM175 is therefore inhibition of FLJ39501 (Accession NP_775754.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39501.

[26268] Folylpolyglutamate synthase (FPGS, Accession NP_004948.2) is another GAM175 target gene, herein designated TARGET GENE. FPGS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPGS, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FPGS BINDING SITE, designated SEQ ID:7959, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26269] Another function of GAM175 is therefore inhibition of Folylpolyglutamate synthase (FPGS, Accession NP_004948.2), a gene which is involved in conversion of folates to polyglutamate derivatives. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FPGS.

[26270] The function of FPGS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM120.1.Galactose-4-epimerase, udp- (GALE, Accession NP_000394.1) is another GAM175 target gene, herein designated TARGET GENE. GALE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GALE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GALE BINDING SITE, designated SEQ ID:6061, to the nucleotide sequence of GAM175 RNA,

herein designated GAM RNA, also designated SEQ ID:265.

[26271] Another function of GAM175 is therefore inhibition of Galactose-4-epimerase, udp- (GALE, Accession NP_000394.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALE.

[26272] Glial fibrillary acidic protein (GFAP, Accession NP_002046.1) is another GAM175 target gene, herein designated TARGET GENE. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GFAP BINDING SITE, designated SEQ ID:3851, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26273] Another function of GAM175 is therefore inhibition of Glial fibrillary acidic protein (GFAP, Accession NP_002046.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFAP.

[26274] G protein-coupled receptor 44 (GPR44, Accession NP_004769.1) is another GAM175 target gene, herein

designated TARGET GENE. GPR44 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR44, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR44 BINDING SITE, designated SEQ ID:5220, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26275] Another function of GAM175 is therefore inhibition of G protein-coupled receptor 44 (GPR44, Accession NP_004769.1), a gene which mediates signals to the interior of the cell via activation of heterotrimeric G proteins . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR44.

[26276] The function of GPR44 has been established by previous studies. By PCR amplification of human genomic DNA using degenerate oligonucleotides corresponding to transmembrane domains 3 and 7 of the mouse delta- opioid receptor and somatostatin receptors, Marchese et al. (1999) isolated a partial cDNA for a novel G protein- coupled receptor, which they designated GPR44. They obtained a full- length clone by screening a lambda human

genomic library. GPR44 encodes a 472- amino acid protein that is closely related to chemoattractant receptors. Northern blot analysis revealed a 3.5- kb GPR44 transcript primarily in thalamus, frontal cortex, pons, and hippocampus and at lower levels in hypothalamus and caudate/putamen. A 3.4- kb transcript was detected in fetal liver, leukocytes, and thymus. Prostaglandin D2 (PGD2; OMIM Ref. No. 176803) and other prostanoids are synthesized by the constitutive cyclooxygenase COX1 (PTGS1; 176805) and its inducible isoform, COX2 (PTGS2; 600262). PGD2, which is implicated in allergic disease, elicits its biologic function through interaction with the DP receptor (PTGDR; 604687). Hirai et al. (2001) showed that PGD2 produced by activated mast cells uses CRTH2 to induce intracellular calcium mobilization and chemotaxis in Th2 cells in a G- alpha(i) (GNAI1; 139310)- dependent manner. In addition, they found that CRTH2 rather than DP mediates PGD2- dependent migration of blood eosinophils and basophils. Functional analysis indicated that PGD2 signaling through DP is coupled to G- alpha(s) (GNAS; 139320) and does not induce chemotaxis.

[26277]

[26278] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[26279] Hirai, H.; Tanaka, K.; Yoshie, O.; Ogawa, K.; Kenmotsu, K.; Takamori, Y.; Ichimasa, M.; Sugamura, K.; Nakamura, M.; Takano, S.; Nagata, K. : Prostaglandin D2 selectively induces chemotaxis in T helper type 2 cells, eosinophils, and basophils via seven- transmembrane receptor CRTH2. J. Exp. Med. 193: 255- 261, 2001. ; and

[26280] Marchese, A.; Sawzdargo, M.; Nguyen, T.; Cheng, R.; Heng, H. H. Q.; Nowak, T.; Im, D- S.; Lynch, K. R.; George, S. R.; O'Dowd, B. F. : Discovery of three novel orphan G-protein- coupled r.

[26281] Further studies establishing the function and utilities of GPR44 are found in John Hopkins OMIM database record ID 604837, and in cited publications listed in Table 5, which are hereby incorporated by reference.Germ cell associated 1 (GSG1, Accession NP_722545.1) is another GAM175 target gene, herein designated TARGET GENE. GSG1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of GSG1 BINDING SITE, designated SEQ ID:8755, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26282] Another function of GAM175 is therefore inhibition of Germ cell associated 1 (GSG1, Accession NP_722545.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSG1.

[26283] HCNGP (Accession NP_037392.1) is another GAM175 target gene, herein designated TARGET GENE. HCNGP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HCNGP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HCNGP BINDING SITE, designated SEQ ID:12212, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26284] Another function of GAM175 is therefore inhibition of HCNGP (Accession NP_037392.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCNGP.

[26285] Heparan sulfate 6-o-sulfotransferase 2 (HS6ST2, Acces-

sion NP_671704.2) is another GAM175 target gene, herein designated TARGET GENE. HS6ST2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by HS6ST2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HS6ST2 BINDING SITE, designated SEQ ID:12074, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26286] Another function of GAM175 is therefore inhibition of Heparan sulfate 6-o-sulfotransferase 2 (HS6ST2, Accession NP_671704.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HS6ST2.

[26287] Interleukin 18 binding protein (IL18BP, Accession NP_766630.1) is another GAM175 target gene, herein designated TARGET GENE. IL18BP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL18BP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

IL18BP BINDING SITE, designated SEQ ID:17825, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26288] Another function of GAM175 is therefore inhibition of Interleukin 18 binding protein (IL18BP, Accession NP_766630.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL18BP.

[26289] Interleukin 18 binding protein (IL18BP, Accession NP_005690.1) is another GAM175 target gene, herein designated TARGET GENE. IL18BP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL18BP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL18BP BINDING SITE, designated SEQ ID:17825, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26290] Another function of GAM175 is therefore inhibition of Interleukin 18 binding protein (IL18BP, Accession NP_005690.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with IL18BP.

[26291] KIAA0193 (Accession NP_055581.2) is another GAM175 target gene, herein designated TARGET GENE. KIAA0193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0193, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0193 BINDING SITE, designated SEQ ID:7054, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26292] Another function of GAM175 is therefore inhibition of KIAA0193 (Accession NP_055581.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0193.

[26293] KIAA0354 (Accession NP_055687.1) is another GAM175 target gene, herein designated TARGET GENE. KIAA0354 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0354, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA0354 BINDING SITE, designated SEQ ID:6463, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26294] Another function of GAM175 is therefore inhibition of KIAA0354 (Accession NP_055687.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0354.

[26295] KIAA0478 (Accession NP_055685.1) is another GAM175 target gene, herein designated TARGET GENE. KIAA0478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0478, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0478 BINDING SITE, designated SEQ ID:4764, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26296] Another function of GAM175 is therefore inhibition of KIAA0478 (Accession NP_055685.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0478.

[26297] KIAA0493 (Accession XP_034717.1) is another GAM175 target gene, herein designated TARGET GENE. KIAA0493 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0493 BINDING SITE, designated SEQ ID:11550, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26298] Another function of GAM175 is therefore inhibition of KIAA0493 (Accession XP_034717.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0493.

[26299] KIAA0605 (Accession NP_055509.1) is another GAM175 target gene, herein designated TARGET GENE. KIAA0605 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0605, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0605 BINDING SITE, designated SEQ ID:9931, to the

nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26300] Another function of GAM175 is therefore inhibition of KIAA0605 (Accession NP_055509.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0605.

[26301] KIAA1671 (Accession XP_037809.1) is another GAM175 target gene, herein designated TARGET GENE. KIAA1671 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1671, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1671 BINDING SITE, designated SEQ ID:6252, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26302] Another function of GAM175 is therefore inhibition of KIAA1671 (Accession XP_037809.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1671.

[26303] KIAA1727 (Accession XP_034262.4) is another GAM175

target gene, herein designated TARGET GENE. KIAA1727 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1727, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1727 BINDING SITE, designated SEQ ID:15320, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26304] Another function of GAM175 is therefore inhibition of KIAA1727 (Accession XP_034262.4) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1727.

[26305] KIAA1804 (Accession NP_115811.1) is another GAM175 target gene, herein designated TARGET GENE. KIAA1804 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1804, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1804 BINDING SITE, designated SEQ ID:13721, to the nucleotide sequence of GAM175 RNA, herein designated

GAM RNA, also designated SEQ ID:265.

[26306] Another function of GAM175 is therefore inhibition of KIAA1804 (Accession NP_115811.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1804.

[26307] KIAA1858 (Accession XP_040592.3) is another GAM175 target gene, herein designated TARGET GENE. KIAA1858 BINDING SITE1 and KIAA1858 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1858, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1858 BINDING SITE1 and KIAA1858 BINDING SITE2, designated SEQ ID:7750 and SEQ ID:4361 respectively, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26308] Another function of GAM175 is therefore inhibition of KIAA1858 (Accession XP_040592.3) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1858.

[26309] Klotho (KL, Accession NP_710150.1) is another GAM175 target gene, herein designated TARGET GENE. KL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KL BINDING SITE, designated SEQ ID:5056, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26310] Another function of GAM175 is therefore inhibition of Klotho (KL, Accession NP_710150.1), a gene which has similarity to beta- glucosidases. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KL.

[26311] The function of KL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM48.2.Klotho (KL, Accession NP_004786.2) is another GAM175 target gene, herein designated TARGET GENE. KL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KL, corresponding to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KL BINDING SITE, designated SEQ ID:5056, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26312] Another function of GAM175 is therefore inhibition of Klotho (KL, Accession NP_004786.2), a gene which has similarity to beta- glucosidases. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KL.

[26313] The function of KL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM48.2.Kelch-like 3 (drosophila) (KLHL3, Accession NP_059111.1) is another GAM175 target gene, herein designated TARGET GENE. KLHL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KLHL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLHL3 BINDING SITE, designated SEQ ID:2953, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26314] Another function of GAM175 is therefore inhibition of Kelch-like 3 (drosophila) (KLHL3, Accession NP_059111.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLHL3.

[26315] Keratin associated protein 4-12 (KRTAP4-12, Accession NP_114060.1) is another GAM175 target gene, herein designated TARGET GENE. KRTAP4-12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KRTAP4-12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KRTAP4-12 BINDING SITE, designated SEQ ID:7123, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26316] Another function of GAM175 is therefore inhibition of Keratin associated protein 4-12 (KRTAP4-12, Accession NP_114060.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KRTAP4-12.

[26317] Laminin, alpha 4 (LAMA4, Accession NP_002281.1) is another GAM175 target gene, herein designated TARGET

GENE. LAMA4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAMA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMA4 BINDING SITE, designated SEQ ID:11842, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26318] Another function of GAM175 is therefore inhibition of Laminin, alpha 4 (LAMA4, Accession NP_002281.1), a gene which mediates the attachment, migration and organization of cells into tissues. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMA4.

[26319] The function of LAMA4 has been established by previous studies. Laminin, a multidomain glycoprotein, is the major noncollagenous constituent of basement membranes. It is composed of 3 nonidentical chains: A (OMIM Ref. No. 150320), B1 (OMIM Ref. No. 150240), and B2 (OMIM Ref. No. 150290). The laminins form a cruciform structure consisting of 3 short arms, each of which is formed from different chains, and a long arm composed of all 3 chains.

By screening a human keratinocyte cDNA library for type VII collagen sequences, Richards et al. (1994) isolated a new laminin alpha chain variant gene, LAMA4 (formerly called LAMA3). Northern blot analysis indicated that a cDNA encoding LAMA4 hybridized to a 6.45- kb mRNA, significantly smaller than the 9.5- to 10- kb mRNA of laminin A (Haaparanta et al., 1991). Using PCR on genomic DNA, flow- sorted chromosomes, and fluorescence in situ hybridization, Richards et al. (1994) localized the LAMA4 gene to human chromosome 6q21. In this abstract, the authors referred to the gene as LAMA3; in the related article, Richards et al. (1994) used the corrected symbol, LAMA4. Iivanainen et al. (1995) cloned the laminin alpha- 4 cDNA by screening a fetal lung library with a PCR product generated from primers based on a partial laminin- like sequence reported by GenBank. The complete cDNA is approximately 6.2 kb long and encodes a predicted protein of 1,816 amino acids. The domain structure of the protein is similar to the alpha- 3 chain (LAMA3, also called BM600), both of which resemble truncated versions of alpha- 1 and alpha- 2 in which approximately 1,200 residues at the amino end have been lost. Northern blots showed strong expression of the mRNA in

adult heart, lung, ovary, small and large intestines, liver, and placenta.

[26320]

[26321] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26322] Iivanainen, A.; Sainio, K.; Sariola, H.; Tryggvason, K. : Primary structure and expression of a novel human laminin alpha- 4 chain. FEBS Lett. 365: 183- 188, 1995. ; and

[26323] Richards, A. J.; Al- Imara, L.; Carter, N. P.; Lloyd, J. C.; Leversha, M. A.; Pope, F. M. : Localization of the gene (LAMA4) to chromosome 6q21 and isolation of a partial cDNA encoding a.

[26324] Further studies establishing the function and utilities of LAMA4 are found in John Hopkins OMIM database record ID 600133, and in cited publications listed in Table 5, which are hereby incorporated by reference.Laminin, gamma 1 (formerly lamb2) (LAMC1, Accession NP_002284.2) is another GAM175 target gene, herein designated TARGET GENE. LAMC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAMC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMC1 BINDING SITE, designated SEQ ID:18303, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26325] Another function of GAM175 is therefore inhibition of Laminin, gamma 1 (formerly lamb2) (LAMC1, Accession NP_002284.2), a gene which may mediate the attachment, migration, and organization of cells into tissues. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMC1.

[26326] The function of LAMC1 has been established by previous studies. Laminin is a heterotrimeric extracellular matrix protein consisting of 3 chains: alpha (LAMA1; 150320), beta (LAMB1; 150240), and gamma (formerly A, B1, and B2, respectively). Several isoforms of each chain have been identified. Laminin gamma- 1 is the most ubiquitously expressed laminin subunit (Burgeson et al., 1994; Miner et al., 1997). In mouse, the laminin subunits alpha- 1, beta- 1, and gamma- 1 are expressed in the preimplantation embryo before the appearance of the first basement membrane of the trophectodermal epithelium. Smyth et

al. (1999) targeted the LAMC1 gene by homologous recombination in mouse embryonic stem (ES) cells. Mice heterozygous for the mutation had a normal phenotype and were fertile, whereas homozygous mutant embryos did not survive beyond day 5.5 postcoitum. These embryos lacked basement membranes, and although the blastocysts had expanded, primitive endoderm cells remained in the inner mass, and the parietal yolk sac did not develop. Cultured ES cells appeared normal after targeting both LAMC1 genes, but the embryoid bodies derived from them also lacked basement membranes, having disorganized extracellular deposits of the basement membrane proteins collagen IV and perlecan, and the cells failed to differentiate into stable myotubes. Nomenclature: Burgeson et al. (1994), a group of 14 leading researchers in the field of connective tissue proteins, adopted a new nomenclature for the laminins. They were numbered with arabic numerals in the order discovered. The previous A, B1, and B2 chains, and their isoforms, are alpha, beta, and gamma, respectively, followed by an arabic numeral to identify the isoform. For example, the first laminin identified from the Engelbreth- Holm- Swarm tumor (EHS) was designated laminin- 1 with the chain composition alpha-

1/beta- 1/gamma- 1. The genes for these 3 chains are LAMA1, LAMB1 (OMIM Ref. No. 150240), and LAMC1.

[26327]

[26328] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26329] Smyth, N.; Vatansever, H. S.; Murray, P.; Meyer, M.; Frie, C.; Paulsson, M.; Edgar, D. : Absence of basement membranes after targeting the LAMC1 gene results in embryonic lethality due to failure of endoderm differentiation. J. Cell Biol. 144: 151- 160, 1999. ; and

[26330] Burgeson, R. E.; Chiquet, M.; Deutzmann, R.; Ekblom, P.; Engel, J.; Kleinman, H.; Martin, G. R.; Meneguzzi, G.; Paulsson, M.; Sanes, J.; Timpl, R.; Tryggvason, K.; Yamada, Y.; Yurchenco.

[26331] Further studies establishing the function and utilities of LAMC1 are found in John Hopkins OMIM database record ID 150290, and in cited publications listed in Table 5, which are hereby incorporated by reference.Lymphocyte cytosolic protein 2 (sh2 domain containing leukocyte protein of 76kda) (LCP2, Accession NP_005556.1) is another GAM175 target gene, herein designated TARGET GENE. LCP2 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by LCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCP2 BINDING SITE, designated SEQ ID:2817, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26332] Another function of GAM175 is therefore inhibition of Lymphocyte cytosolic protein 2 (sh2 domain containing leukocyte protein of 76kda) (LCP2, Accession NP_005556.1), a gene which involved in t cell antigen receptor mediated signaling. and therefore may be associated with Fetal hemorrhage and platelet dysfunction. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Fetal hemorrhage and platelet dysfunction, and of other diseases and clinical conditions associated with LCP2.

[26333] The function of LCP2 has been established by previous studies. Activation of tyrosine kinases of the src and syk family is required for T- cell receptor- mediated signaling. Jackman et al. (1995) identified a 76- kD protein that associates with the Grb2 adaptor protein (OMIM Ref. No. 108355) and is a substrate for tyrosine kinase in the acti-

vation pathway. The SLP76 (SH2 domain- containing leukocyte protein of 76 kD) cDNA encodes a predicted 533- amino acid protein with a single C- terminal Src homology 2 (SH2) domain, a proline- rich region with a binding site for Grb2, and an acidic N- terminal region with tyrosines that are phosphorylated after T- cell receptor engagement (Sunden et al., 1996). The human and mouse amino acid sequences are 84% identical. Northern blots demonstrated expression in peripheral blood leukocytes, thymus, and spleen and in human T- cell, B- cell, and monocytic cell lines. Recombinantly expressed SLP76 was shown to associate with a GST/Grb2 fusion protein. Overexpression of SLP76 has also been shown to enhance the activity of the promoter for the IL2 gene (Motto et al., 1996). Sunden et al. (1996) used a monochromosomal somatic cell hybrid panel to map the gene, designated LCP2, to chromosome 5. A 2- allele polymorphism within the gene was then used to map the locus genetically near the marker D5S429, which has been assigned to 5q33.1- qter

[26334] Animal model experiments lend further support to the function of LCP2. Clements et al. (1999) described fetal hemorrhage and perinatal mortality in mice deficient in SLP76. Although megakaryocyte and platelet development

proceeded normally in the absence of SLP76, collagen-induced platelet aggregation and granule release were markedly impaired. Furthermore, treatment of SLP76- deficient platelets with collagen failed to elicit tyrosine phosphorylation of phospholipase C- gamma- 2, suggesting that SLP76 functions upstream of PLC- gamma- 2 activation. The data provided a potential mechanism for the fetal hemorrhage observed in the SLP76- deficient mice and showed that SLP76 expression is required for optimal receptor- mediated signal transduction in platelets as well as in T lymphocytes.

[26335] It is appreciated that the abovementioned animal model for LCP2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[26336] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26337] Clements, J. L.; Lee, J. R.; Gross, B.; Yang, B.; Olson, J. D.; Sandra, A.; Watson, S. P.; Lentz, S. R.; Koretzky, G. A. : Fetal hemorrhage and platelet dysfunction in SLP- 76- deficient mice. J. Clin. Invest. 103: 19- 25, 1999. ; and

[26338] Sunden, S. L. F.; Carr, L. L.; Clements, J. L.; Motto, D. G.;

Koretzky, G. A. : Polymorphism in and localization of the gene LCP2 (SLP- 76) to chromosome 5q33.1- qter. Genomics 35: 269- 270.

[26339] Further studies establishing the function and utilities of LCP2 are found in John Hopkins OMIM database record ID 601603, and in cited publications listed in Table 5, which are hereby incorporated by reference.LOC118461 (Accession XP_060969.2) is another GAM175 target gene, herein designated TARGET GENE. LOC118461 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC118461, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118461 BINDING SITE, designated SEQ ID:9284, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26340] Another function of GAM175 is therefore inhibition of LOC118461 (Accession XP_060969.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118461.

[26341] LOC122282 (Accession XP_063046.4) is another GAM175

target gene, herein designated TARGET GENE. LOC122282 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC122282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC122282 BINDING SITE, designated SEQ ID:13483, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26342] Another function of GAM175 is therefore inhibition of LOC122282 (Accession XP_063046.4) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122282.

[26343] LOC125115 (Accession XP_064442.3) is another GAM175 target gene, herein designated TARGET GENE. LOC125115 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC125115, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC125115 BINDING SITE, designated SEQ ID:16189, to the nucleotide sequence of GAM175 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:265.

[26344] Another function of GAM175 is therefore inhibition of LOC125115 (Accession XP_064442.3) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125115.

[26345] LOC145609 (Accession XP_096817.1) is another GAM175 target gene, herein designated TARGET GENE. LOC145609 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145609, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145609 BINDING SITE, designated SEQ ID:4216, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26346] Another function of GAM175 is therefore inhibition of LOC145609 (Accession XP_096817.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145609.

[26347] LOC147381 (Accession XP_097230.2) is another GAM175 target gene, herein designated TARGET GENE. LOC147381

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147381, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147381 BINDING SITE, designated SEQ ID:3191, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26348] Another function of GAM175 is therefore inhibition of LOC147381 (Accession XP_097230.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147381.

[26349] LOC150933 (Accession XP_097971.1) is another GAM175 target gene, herein designated TARGET GENE. LOC150933 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150933, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150933 BINDING SITE, designated SEQ ID:17201, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26350] Another function of GAM175 is therefore inhibition of LOC150933 (Accession XP_097971.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150933.

[26351] LOC151201 (Accession XP_098021.1) is another GAM175 target gene, herein designated TARGET GENE. LOC151201 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE, designated SEQ ID:4667, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26352] Another function of GAM175 is therefore inhibition of LOC151201 (Accession XP_098021.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151201.

[26353] LOC153077 (Accession XP_098307.1) is another GAM175 target gene, herein designated TARGET GENE. LOC153077 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC153077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153077 BINDING SITE, designated SEQ ID:2394, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26354] Another function of GAM175 is therefore inhibition of LOC153077 (Accession XP_098307.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153077.

[26355] LOC153346 (Accession XP_098364.1) is another GAM175 target gene, herein designated TARGET GENE. LOC153346 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153346 BINDING SITE, designated SEQ ID:19725, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26356] Another function of GAM175 is therefore inhibition of

LOC153346 (Accession XP_098364.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153346.

[26357] LOC157858 (Accession XP_098833.2) is another GAM175 target gene, herein designated TARGET GENE. LOC157858 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC157858, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157858 BINDING SITE, designated SEQ ID:11755, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26358] Another function of GAM175 is therefore inhibition of LOC157858 (Accession XP_098833.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157858.

[26359] LOC158563 (Accession XP_088606.1) is another GAM175 target gene, herein designated TARGET GENE. LOC158563 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158563, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158563 BINDING SITE, designated SEQ ID:3708, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26360] Another function of GAM175 is therefore inhibition of LOC158563 (Accession XP_088606.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158563.

[26361] LOC158833 (Accession XP_088691.1) is another GAM175 target gene, herein designated TARGET GENE. LOC158833 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158833, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158833 BINDING SITE, designated SEQ ID:4444, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26362] Another function of GAM175 is therefore inhibition of LOC158833 (Accession XP_088691.1) . Accordingly, utili-

ties of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158833.

[26363] LOC162083 (Accession XP_091339.2) is another GAM175 target gene, herein designated TARGET GENE. LOC162083 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC162083, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162083 BINDING SITE, designated SEQ ID:9512, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26364] Another function of GAM175 is therefore inhibition of LOC162083 (Accession XP_091339.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162083.

[26365] LOC197342 (Accession XP_113869.1) is another GAM175 target gene, herein designated TARGET GENE. LOC197342 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC197342, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC197342 BINDING SITE, designated SEQ ID:14413, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26366] Another function of GAM175 is therefore inhibition of LOC197342 (Accession XP_113869.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197342.

[26367] LOC200197 (Accession XP_114148.1) is another GAM175 target gene, herein designated TARGET GENE. LOC200197 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200197, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200197 BINDING SITE, designated SEQ ID:4520, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26368] Another function of GAM175 is therefore inhibition of LOC200197 (Accession XP_114148.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC200197.

[26369] LOC201725 (Accession XP_114370.1) is another GAM175 target gene, herein designated TARGET GENE. LOC201725 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201725 BINDING SITE, designated SEQ ID:3083, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26370] Another function of GAM175 is therefore inhibition of LOC201725 (Accession XP_114370.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201725.

[26371] LOC219700 (Accession XP_167570.1) is another GAM175 target gene, herein designated TARGET GENE. LOC219700 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219700, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC219700 BINDING SITE, designated SEQ ID:7954, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26372] Another function of GAM175 is therefore inhibition of LOC219700 (Accession XP_167570.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219700.

[26373] LOC253142 (Accession XP_173229.1) is another GAM175 target gene, herein designated TARGET GENE. LOC253142 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253142 BINDING SITE, designated SEQ ID:6541, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26374] Another function of GAM175 is therefore inhibition of LOC253142 (Accession XP_173229.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC253142.

[26375] LOC282915 (Accession XP_212579.1) is another GAM175 target gene, herein designated TARGET GENE. LOC282915 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282915, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282915 BINDING SITE, designated SEQ ID:11235, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26376] Another function of GAM175 is therefore inhibition of LOC282915 (Accession XP_212579.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282915.

[26377] LOC282951 (Accession XP_212627.1) is another GAM175 target gene, herein designated TARGET GENE. LOC282951 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282951, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC282951 BINDING SITE, designated SEQ ID:11235, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26378] Another function of GAM175 is therefore inhibition of LOC282951 (Accession XP_212627.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282951.

[26379] LOC282976 (Accession XP_210838.1) is another GAM175 target gene, herein designated TARGET GENE. LOC282976 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282976, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282976 BINDING SITE, designated SEQ ID:4866, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26380] Another function of GAM175 is therefore inhibition of LOC282976 (Accession XP_210838.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282976.

[26381] LOC283126 (Accession XP_210900.1) is another GAM175 target gene, herein designated TARGET GENE. LOC283126 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283126, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283126 BINDING SITE, designated SEQ ID:17440, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26382] Another function of GAM175 is therefore inhibition of LOC283126 (Accession XP_210900.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283126.

[26383] LOC283142 (Accession XP_210925.1) is another GAM175 target gene, herein designated TARGET GENE. LOC283142 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283142 BINDING SITE, designated SEQ ID:2594, to

the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26384] Another function of GAM175 is therefore inhibition of LOC283142 (Accession XP_210925.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283142.

[26385] LOC283482 (Accession XP_211061.1) is another GAM175 target gene, herein designated TARGET GENE. LOC283482 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283482, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283482 BINDING SITE, designated SEQ ID:15588, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26386] Another function of GAM175 is therefore inhibition of LOC283482 (Accession XP_211061.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283482.

[26387] LOC283672 (Accession XP_211152.1) is another GAM175

target gene, herein designated TARGET GENE. LOC283672 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283672, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283672 BINDING SITE, designated SEQ ID:11064, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26388] Another function of GAM175 is therefore inhibition of LOC283672 (Accession XP_211152.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283672.

[26389] LOC283859 (Accession XP_211235.1) is another GAM175 target gene, herein designated TARGET GENE. LOC283859 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283859, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283859 BINDING SITE, designated SEQ ID:15537, to the nucleotide sequence of GAM175 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:265.

[26390] Another function of GAM175 is therefore inhibition of LOC283859 (Accession XP_211235.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283859.

[26391] LOC284080 (Accession XP_211322.1) is another GAM175 target gene, herein designated TARGET GENE. LOC284080 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284080, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284080 BINDING SITE, designated SEQ ID:17268, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26392] Another function of GAM175 is therefore inhibition of LOC284080 (Accession XP_211322.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284080.

[26393] LOC284116 (Accession XP_211338.2) is another GAM175 target gene, herein designated TARGET GENE. LOC284116

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284116, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284116 BINDING SITE, designated SEQ ID:9262, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26394] Another function of GAM175 is therefore inhibition of LOC284116 (Accession XP_211338.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284116.

[26395] LOC284296 (Accession NP_787104.1) is another GAM175 target gene, herein designated TARGET GENE. LOC284296 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284296, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284296 BINDING SITE, designated SEQ ID:17027, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26396] Another function of GAM175 is therefore inhibition of LOC284296 (Accession NP_787104.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284296.

[26397] LOC284462 (Accession XP_211475.1) is another GAM175 target gene, herein designated TARGET GENE. LOC284462 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284462, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284462 BINDING SITE, designated SEQ ID:5767, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26398] Another function of GAM175 is therefore inhibition of LOC284462 (Accession XP_211475.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284462.

[26399] LOC284568 (Accession XP_209263.1) is another GAM175 target gene, herein designated TARGET GENE. LOC284568 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC284568, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284568 BINDING SITE, designated SEQ ID:11550, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26400] Another function of GAM175 is therefore inhibition of LOC284568 (Accession XP_209263.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284568.

[26401] LOC284865 (Accession XP_211672.1) is another GAM175 target gene, herein designated TARGET GENE. LOC284865 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284865 BINDING SITE, designated SEQ ID:8040, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26402] Another function of GAM175 is therefore inhibition of

LOC284865 (Accession XP_211672.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284865.

[26403] LOC284982 (Accession XP_211721.1) is another GAM175 target gene, herein designated TARGET GENE. LOC284982 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284982, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284982 BINDING SITE, designated SEQ ID:17065, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26404] Another function of GAM175 is therefore inhibition of LOC284982 (Accession XP_211721.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284982.

[26405] LOC284993 (Accession XP_211722.1) is another GAM175 target gene, herein designated TARGET GENE. LOC284993 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284993, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284993 BINDING SITE, designated SEQ ID:10924, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26406] Another function of GAM175 is therefore inhibition of LOC284993 (Accession XP_211722.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284993.

[26407] LOC285026 (Accession XP_209440.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285026 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285026, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285026 BINDING SITE, designated SEQ ID:19445, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26408] Another function of GAM175 is therefore inhibition of LOC285026 (Accession XP_209440.1) . Accordingly, utili-

ties of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285026.

[26409] LOC285222 (Accession XP_211809.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285222 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285222, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285222 BINDING SITE, designated SEQ ID:17158, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26410] Another function of GAM175 is therefore inhibition of LOC285222 (Accession XP_211809.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285222.

[26411] LOC285229 (Accession XP_211812.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285229 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285229, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285229 BINDING SITE, designated SEQ ID:6284, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26412] Another function of GAM175 is therefore inhibition of LOC285229 (Accession XP_211812.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285229.

[26413] LOC285231 (Accession XP_211813.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285231 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285231, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285231 BINDING SITE, designated SEQ ID:2395, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26414] Another function of GAM175 is therefore inhibition of LOC285231 (Accession XP_211813.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285231.

[26415] LOC285246 (Accession XP_208303.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285246 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285246, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285246 BINDING SITE, designated SEQ ID:1260, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26416] Another function of GAM175 is therefore inhibition of LOC285246 (Accession XP_208303.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285246.

[26417] LOC285388 (Accession XP_208316.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285388 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285388, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC285388 BINDING SITE, designated SEQ ID:8111, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26418] Another function of GAM175 is therefore inhibition of LOC285388 (Accession XP_208316.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285388.

[26419] LOC285438 (Accession XP_209613.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285438 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285438, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285438 BINDING SITE, designated SEQ ID:10871, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26420] Another function of GAM175 is therefore inhibition of LOC285438 (Accession XP_209613.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285438.

[26421] LOC285486 (Accession XP_209633.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285486 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285486, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285486 BINDING SITE, designated SEQ ID:8485, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26422] Another function of GAM175 is therefore inhibition of LOC285486 (Accession XP_209633.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285486.

[26423] LOC285602 (Accession XP_209676.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285602 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285602, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC285602 BINDING SITE, designated SEQ ID:12446, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26424] Another function of GAM175 is therefore inhibition of LOC285602 (Accession XP_209676.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285602.

[26425] LOC285745 (Accession XP_212007.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285745 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285745, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285745 BINDING SITE, designated SEQ ID:19064, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26426] Another function of GAM175 is therefore inhibition of LOC285745 (Accession XP_212007.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285745.

[26427] LOC285747 (Accession XP_209742.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285747 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285747, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285747 BINDING SITE, designated SEQ ID:1009, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26428] Another function of GAM175 is therefore inhibition of LOC285747 (Accession XP_209742.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285747.

[26429] LOC285786 (Accession XP_208349.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285786 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285786, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285786 BINDING SITE, designated SEQ ID:19355, to

the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26430] Another function of GAM175 is therefore inhibition of LOC285786 (Accession XP_208349.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285786.

[26431] LOC285805 (Accession XP_212027.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285805 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285805, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285805 BINDING SITE, designated SEQ ID:6025, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26432] Another function of GAM175 is therefore inhibition of LOC285805 (Accession XP_212027.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285805.

[26433] LOC285833 (Accession XP_209790.1) is another GAM175

target gene, herein designated TARGET GENE. LOC285833 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285833, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285833 BINDING SITE, designated SEQ ID:11235, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26434] Another function of GAM175 is therefore inhibition of LOC285833 (Accession XP_209790.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285833.

[26435] LOC285945 (Accession XP_212092.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285945 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285945, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285945 BINDING SITE, designated SEQ ID:20077, to the nucleotide sequence of GAM175 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:265.

[26436] Another function of GAM175 is therefore inhibition of LOC285945 (Accession XP_212092.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285945.

[26437] LOC285992 (Accession XP_212126.1) is another GAM175 target gene, herein designated TARGET GENE. LOC285992 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285992, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285992 BINDING SITE, designated SEQ ID:9866, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26438] Another function of GAM175 is therefore inhibition of LOC285992 (Accession XP_212126.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285992.

[26439] LOC286002 (Accession XP_212132.1) is another GAM175 target gene, herein designated TARGET GENE. LOC286002

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286002, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286002 BINDING SITE, designated SEQ ID:12015, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26440] Another function of GAM175 is therefore inhibition of LOC286002 (Accession XP_212132.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286002.

[26441] LOC286132 (Accession XP_212194.1) is another GAM175 target gene, herein designated TARGET GENE. LOC286132 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286132 BINDING SITE, designated SEQ ID:4900, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26442] Another function of GAM175 is therefore inhibition of LOC286132 (Accession XP_212194.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286132.

[26443] LOC286214 (Accession XP_212231.1) is another GAM175 target gene, herein designated TARGET GENE. LOC286214 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286214, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286214 BINDING SITE, designated SEQ ID:2319, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26444] Another function of GAM175 is therefore inhibition of LOC286214 (Accession XP_212231.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286214.

[26445] LOC286471 (Accession XP_210061.1) is another GAM175 target gene, herein designated TARGET GENE. LOC286471 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC286471, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286471 BINDING SITE, designated SEQ ID:5576, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26446] Another function of GAM175 is therefore inhibition of LOC286471 (Accession XP_210061.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286471.

[26447] LOC338565 (Accession XP_294653.1) is another GAM175 target gene, herein designated TARGET GENE. LOC338565 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338565, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338565 BINDING SITE, designated SEQ ID:10504, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26448] Another function of GAM175 is therefore inhibition of

LOC338565 (Accession XP_294653.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338565.

[26449] LOC338585 (Accession XP_294658.1) is another GAM175 target gene, herein designated TARGET GENE. LOC338585 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338585, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338585 BINDING SITE, designated SEQ ID:9293, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26450] Another function of GAM175 is therefore inhibition of LOC338585 (Accession XP_294658.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338585.

[26451] LOC339071 (Accession XP_294800.1) is another GAM175 target gene, herein designated TARGET GENE. LOC339071 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339071, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339071 BINDING SITE, designated SEQ ID:11684, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26452] Another function of GAM175 is therefore inhibition of LOC339071 (Accession XP_294800.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339071.

[26453] LOC339152 (Accession XP_294829.1) is another GAM175 target gene, herein designated TARGET GENE. LOC339152 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339152, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339152 BINDING SITE, designated SEQ ID:18348, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26454] Another function of GAM175 is therefore inhibition of LOC339152 (Accession XP_294829.1) . Accordingly, utili-

ties of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339152.

[26455] LOC339666 (Accession XP_295024.1) is another GAM175 target gene, herein designated TARGET GENE. LOC339666 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339666, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339666 BINDING SITE, designated SEQ ID:4270, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26456] Another function of GAM175 is therefore inhibition of LOC339666 (Accession XP_295024.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339666.

[26457] LOC339831 (Accession XP_295080.1) is another GAM175 target gene, herein designated TARGET GENE. LOC339831 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339831, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339831 BINDING SITE, designated SEQ ID:7585, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26458] Another function of GAM175 is therefore inhibition of LOC339831 (Accession XP_295080.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339831.

[26459] LOC339834 (Accession NP_835467.1) is another GAM175 target gene, herein designated TARGET GENE. LOC339834 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC339834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339834 BINDING SITE, designated SEQ ID:14967, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26460] Another function of GAM175 is therefore inhibition of LOC339834 (Accession NP_835467.1) . Accordingly, utili-

ties of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339834.

[26461] LOC339834 (Accession XP_291033.1) is another GAM175 target gene, herein designated TARGET GENE. LOC339834 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC339834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339834 BINDING SITE, designated SEQ ID:14967, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26462] Another function of GAM175 is therefore inhibition of LOC339834 (Accession XP_291033.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339834.

[26463] LOC339872 (Accession XP_291050.1) is another GAM175 target gene, herein designated TARGET GENE. LOC339872 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339872, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339872 BINDING SITE, designated SEQ ID:5152, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26464] Another function of GAM175 is therefore inhibition of LOC339872 (Accession XP_291050.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339872.

[26465] LOC340090 (Accession XP_295154.1) is another GAM175 target gene, herein designated TARGET GENE. LOC340090 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340090, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340090 BINDING SITE, designated SEQ ID:10984, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26466] Another function of GAM175 is therefore inhibition of LOC340090 (Accession XP_295154.1) . Accordingly, utili-

ties of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340090.

[26467] LOC340397 (Accession XP_295237.1) is another GAM175 target gene, herein designated TARGET GENE. LOC340397 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340397, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340397 BINDING SITE, designated SEQ ID:11433, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26468] Another function of GAM175 is therefore inhibition of LOC340397 (Accession XP_295237.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340397.

[26469] LOC340408 (Accession XP_291274.1) is another GAM175 target gene, herein designated TARGET GENE. LOC340408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340408, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340408 BINDING SITE, designated SEQ ID:14607, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26470] Another function of GAM175 is therefore inhibition of LOC340408 (Accession XP_291274.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340408.

[26471] LOC340895 (Accession XP_295865.1) is another GAM175 target gene, herein designated TARGET GENE. LOC340895 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340895, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340895 BINDING SITE, designated SEQ ID:10036, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26472] Another function of GAM175 is therefore inhibition of LOC340895 (Accession XP_295865.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC340895.

[26473] LOC342125 (Accession XP_292375.1) is another GAM175 target gene, herein designated TARGET GENE. LOC342125 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC342125, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC342125 BINDING SITE, designated SEQ ID:12487, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26474] Another function of GAM175 is therefore inhibition of LOC342125 (Accession XP_292375.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC342125.

[26475] LOC347240 (Accession XP_294563.2) is another GAM175 target gene, herein designated TARGET GENE. LOC347240 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347240, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC347240 BINDING SITE, designated SEQ ID:8399, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26476] Another function of GAM175 is therefore inhibition of LOC347240 (Accession XP_294563.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347240.

[26477] LOC347759 (Accession XP_084325.1) is another GAM175 target gene, herein designated TARGET GENE. LOC347759 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC347759, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347759 BINDING SITE, designated SEQ ID:5676, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26478] Another function of GAM175 is therefore inhibition of LOC347759 (Accession XP_084325.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC347759.

[26479] LOC348158 (Accession XP_300646.1) is another GAM175 target gene, herein designated TARGET GENE. LOC348158 BINDING SITE1 and LOC348158 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348158, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348158 BINDING SITE1 and LOC348158 BINDING SITE2, designated SEQ ID:17028 and SEQ ID:9642 respectively, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26480] Another function of GAM175 is therefore inhibition of LOC348158 (Accession XP_300646.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348158.

[26481] LOC348370 (Accession XP_300721.1) is another GAM175 target gene, herein designated TARGET GENE. LOC348370 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348370, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348370 BINDING SITE, designated SEQ ID:11550, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26482] Another function of GAM175 is therefore inhibition of LOC348370 (Accession XP_300721.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348370.

[26483] LOC348378 (Accession XP_300723.1) is another GAM175 target gene, herein designated TARGET GENE. LOC348378 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348378, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348378 BINDING SITE, designated SEQ ID:15891, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26484] Another function of GAM175 is therefore inhibition of LOC348378 (Accession XP_300723.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348378.

[26485] LOC348383 (Accession XP_300726.1) is another GAM175 target gene, herein designated TARGET GENE. LOC348383 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348383, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348383 BINDING SITE, designated SEQ ID:11550, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26486] Another function of GAM175 is therefore inhibition of LOC348383 (Accession XP_300726.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348383.

[26487] LOC351256 (Accession XP_301805.1) is another GAM175 target gene, herein designated TARGET GENE. LOC351256 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC351256, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC351256 BINDING SITE, designated SEQ ID:6773, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26488] Another function of GAM175 is therefore inhibition of LOC351256 (Accession XP_301805.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC351256.

[26489] LOC92078 (Accession XP_042684.1) is another GAM175 target gene, herein designated TARGET GENE. LOC92078 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC92078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92078 BINDING SITE, designated SEQ ID:4921, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26490] Another function of GAM175 is therefore inhibition of LOC92078 (Accession XP_042684.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC92078.

[26491] LOC96597 (Accession XP_039922.1) is another GAM175 target gene, herein designated TARGET GENE. LOC96597 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC96597, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC96597 BINDING SITE, designated SEQ ID:1106, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26492] Another function of GAM175 is therefore inhibition of LOC96597 (Accession XP_039922.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC96597.

[26493] LPHN2 (Accession NP_036434.1) is another GAM175 target gene, herein designated TARGET GENE. LPHN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LPHN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LPHN2

BINDING SITE, designated SEQ ID:9096, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26494] Another function of GAM175 is therefore inhibition of LPHN2 (Accession NP_036434.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPHN2.

[26495] MGC11242 (Accession NP_077296.1) is another GAM175 target gene, herein designated TARGET GENE. MGC11242 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC11242, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC11242 BINDING SITE, designated SEQ ID:8334, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26496] Another function of GAM175 is therefore inhibition of MGC11242 (Accession NP_077296.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11242.

[26497] MGC20785 (Accession NP_689934.1) is another GAM175

target gene, herein designated TARGET GENE. MGC20785 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC20785, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC20785 BINDING SITE, designated SEQ ID:14606, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26498] Another function of GAM175 is therefore inhibition of MGC20785 (Accession NP_689934.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC20785.

[26499] MGC22014 (Accession XP_035307.1) is another GAM175 target gene, herein designated TARGET GENE. MGC22014 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC22014, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC22014 BINDING SITE, designated SEQ ID:6173, to the nucleotide sequence of GAM175 RNA, herein designated

GAM RNA, also designated SEQ ID:265.

[26500] Another function of GAM175 is therefore inhibition of MGC22014 (Accession XP_035307.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC22014.

[26501] MGC23908 (Accession XP_038290.2) is another GAM175 target gene, herein designated TARGET GENE. MGC23908 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC23908, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC23908 BINDING SITE, designated SEQ ID:2079, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26502] Another function of GAM175 is therefore inhibition of MGC23908 (Accession XP_038290.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC23908.

[26503] MGC2848 (Accession NP_116306.1) is another GAM175 target gene, herein designated TARGET GENE. MGC2848

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2848, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2848 BINDING SITE, designated SEQ ID:12200, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26504] Another function of GAM175 is therefore inhibition of MGC2848 (Accession NP_116306.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2848.

[26505] MGC33971 (Accession NP_699174.1) is another GAM175 target gene, herein designated TARGET GENE. MGC33971 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC33971, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC33971 BINDING SITE, designated SEQ ID:10456, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26506] Another function of GAM175 is therefore inhibition of MGC33971 (Accession NP_699174.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33971.

[26507] MGC34728 (Accession NP_689746.1) is another GAM175 target gene, herein designated TARGET GENE. MGC34728 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC34728, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34728 BINDING SITE, designated SEQ ID:14010, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26508] Another function of GAM175 is therefore inhibition of MGC34728 (Accession NP_689746.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34728.

[26509] MGC39320 (Accession NP_689642.2) is another GAM175 target gene, herein designated TARGET GENE. MGC39320 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC39320, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC39320 BINDING SITE, designated SEQ ID:18878, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26510] Another function of GAM175 is therefore inhibition of MGC39320 (Accession NP_689642.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC39320.

[26511] MGC40053 (Accession NP_689796.1) is another GAM175 target gene, herein designated TARGET GENE. MGC40053 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC40053, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40053 BINDING SITE, designated SEQ ID:1339, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26512] Another function of GAM175 is therefore inhibition of

MGC40053 (Accession NP_689796.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40053.

[26513] MGC4368 (Accession NP_078786.2) is another GAM175 target gene, herein designated TARGET GENE. MGC4368 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC4368, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4368 BINDING SITE, designated SEQ ID:5575, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26514] Another function of GAM175 is therefore inhibition of MGC4368 (Accession NP_078786.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4368.

[26515] MIG-6 (Accession NP_061821.1) is another GAM175 target gene, herein designated TARGET GENE. MIG-6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MIG-6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIG-6 BINDING SITE, designated SEQ ID:11440, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26516] Another function of GAM175 is therefore inhibition of MIG-6 (Accession NP_061821.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIG-6.

[26517] Mitochondrial ribosomal protein s12 (MRPS12, Accession NP_066930.1) is another GAM175 target gene, herein designated TARGET GENE. MRPS12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPS12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPS12 BINDING SITE, designated SEQ ID:18531, to the

nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26518] Another function of GAM175 is therefore inhibition of Mitochondrial ribosomal protein s12 (MRPS12, Accession NP_066930.1), a gene which is a component of the mitochondrial ribosome. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS12.

[26519] The function of MRPS12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Mitochondrial ribosomal protein s12 (MRPS12, Accession NP_203527.1) is another GAM175 target gene, herein designated TARGET GENE. MRPS12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPS12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPS12 BINDING SITE, designated SEQ ID:18531, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26520] Another function of GAM175 is therefore inhibition of Mitochondrial ribosomal protein s12 (MRPS12, Accession NP_203527.1), a gene which is a component of the mitochondrial ribosome. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS12.

[26521] The function of MRPS12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Mitochondrial ribosomal protein s12 (MRPS12, Accession NP_203526.1) is another GAM175 target gene, herein designated TARGET GENE. MRPS12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPS12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPS12 BINDING SITE, designated SEQ ID:18531, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26522] Another function of GAM175 is therefore inhibition of Mitochondrial ribosomal protein s12 (MRPS12, Accession

NP_203526.1), a gene which is a component of the mitochondrial ribosome. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS12.

[26523] The function of MRPS12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.MTA3 (Accession XP_038567.5) is another GAM175 target gene, herein designated TARGET GENE. MTA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTA3 BINDING SITE, designated SEQ ID:5772, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26524] Another function of GAM175 is therefore inhibition of MTA3 (Accession XP_038567.5) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTA3.

[26525] MUM-1 (Accession XP_300238.1) is another GAM175 target gene, herein designated TARGET GENE. MUM-1 BIND-

ING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MUM-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MUM-1 BINDING SITE, designated SEQ ID:17769, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26526] Another function of GAM175 is therefore inhibition of MUM-1 (Accession XP_300238.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MUM-1.

[26527] Max interacting protein 1 (MXI1, Accession NP_569157.1) is another GAM175 target gene, herein designated TARGET GENE. MXI1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MXI1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MXI1 BINDING SITE, designated SEQ ID:14939, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA,

also designated SEQ ID:265.

[26528] Another function of GAM175 is therefore inhibition of Max interacting protein 1 (MXI1, Accession NP_569157.1), a gene which acts as a tumor suppressor in vivo, engages the MYC network in a functionally relevant manner and therefore may be associated with Prostate cancer, neurofibrosarcoma. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Prostate cancer, neurofibrosarcoma, and of other diseases and clinical conditions associated with MXI1.

[26529] The function of MXI1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Max interacting protein 1 (MXI1, Accession NP_005953.2) is another GAM175 target gene, herein designated TARGET GENE. MXI1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MXI1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MXI1 BINDING SITE, designated SEQ ID:14939, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA,

also designated SEQ ID:265.

[26530] Another function of GAM175 is therefore inhibition of Max interacting protein 1 (MXI1, Accession NP_005953.2), a gene which acts as a tumor suppressor in vivo, engages the MYC network in a functionally relevant manner and therefore may be associated with Prostate cancer, neurofibrosarcoma. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Prostate cancer, neurofibrosarcoma, and of other diseases and clinical conditions associated with MXI1.

[26531] The function of MXI1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.N4BP3 (Accession XP_038920.2) is another GAM175 target gene, herein designated TARGET GENE. N4BP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by N4BP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of N4BP3 BINDING SITE, designated SEQ ID:18724, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26532] Another function of GAM175 is therefore inhibition of N4BP3 (Accession XP_038920.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with N4BP3.

[26533] Nucleosome assembly protein 1-like 1 (NAP1L1, Accession NP_631946.1) is another GAM175 target gene, herein designated TARGET GENE. NAP1L1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NAP1L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NAP1L1 BINDING SITE, designated SEQ ID:12445, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26534] Another function of GAM175 is therefore inhibition of Nucleosome assembly protein 1-like 1 (NAP1L1, Accession NP_631946.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAP1L1.

[26535] Nucleosome assembly protein 1-like 1 (NAP1L1, Accession NP_004528.1) is another GAM175 target gene, herein designated TARGET GENE. NAP1L1 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NAP1L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NAP1L1 BINDING SITE, designated SEQ ID:12445, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26536] Another function of GAM175 is therefore inhibition of Nucleosome assembly protein 1-like 1 (NAP1L1, Accession NP_004528.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAP1L1.

[26537] NCE2 (Accession NP_057594.2) is another GAM175 target gene, herein designated TARGET GENE. NCE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NCE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCE2 BINDING SITE, designated SEQ ID:5057, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26538] Another function of GAM175 is therefore inhibition of NCE2 (Accession NP_057594.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCE2.

[26539] N-myc downstream regulated gene 1 (NDRG1, Accession NP_006087.1) is another GAM175 target gene, herein designated TARGET GENE. NDRG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDRG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDRG1 BINDING SITE, designated SEQ ID:5659, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26540] Another function of GAM175 is therefore inhibition of N-myc downstream regulated gene 1 (NDRG1, Accession NP_006087.1), a gene which may have a growth inhibitory role. and therefore may be associated with Hereditary motor and sensory neuropathy, lom type. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Hereditary motor and sensory neuropathy, lom type, and of other diseases and clinical conditions associated with NDRG1.

[26541] The function of NDRG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.NUPL1 (Accession NP_055593.1) is another GAM175 target gene, herein designated TARGET GENE. NUPL1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NUPL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUPL1 BINDING SITE, designated SEQ ID:14772, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26542] Another function of GAM175 is therefore inhibition of NUPL1 (Accession NP_055593.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUPL1.

[26543] NUPL1 (Accession NP_054808.1) is another GAM175 target gene, herein designated TARGET GENE. NUPL1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NUPL1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUPL1 BINDING SITE, designated SEQ ID:14772, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26544] Another function of GAM175 is therefore inhibition of NUPL1 (Accession NP_054808.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUPL1.

[26545] Nuclear transport factor 2-like export factor 2 (NXT2, Accession NP_061168.2) is another GAM175 target gene, herein designated TARGET GENE. NXT2 BINDING SITE1 and NXT2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NXT2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NXT2 BINDING SITE1 and NXT2 BINDING SITE2, designated SEQ ID:9223 and SEQ ID:5917 respectively, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26546] Another function of GAM175 is therefore inhibition of Nu-

clear transport factor 2-like export factor 2 (NXT2, Accession NP_061168.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXT2.

[26547] Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) is another GAM175 target gene, herein designated TARGET GENE. PASK BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PASK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PASK BINDING SITE, designated SEQ ID:7891, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26548] Another function of GAM175 is therefore inhibition of Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PASK.

[26549] Phosphodiesterase 11a (PDE11A, Accession NP_058649.2) is another GAM175 target gene, herein designated TARGET GENE. PDE11A BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by PDE11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDE11A BINDING SITE, designated SEQ ID:16840, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26550] Another function of GAM175 is therefore inhibition of Phosphodiesterase 11a (PDE11A, Accession NP_058649.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE11A.

[26551] Period homolog 3 (drosophila) (PER3, Accession NP_058515.1) is another GAM175 target gene, herein designated TARGET GENE. PER3 BINDING SITE1 and PER3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PER3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PER3 BINDING SITE1 and PER3 BINDING SITE2, designated SEQ ID:2006 and SEQ ID:3046 respectively, to the nucleotide sequence

of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26552] Another function of GAM175 is therefore inhibition of Period homolog 3 (drosophila) (PER3, Accession NP_058515.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PER3.

[26553] Phospholipase a2, group iii (PLA2G3, Accession NP_056530.1) is another GAM175 target gene, herein designated TARGET GENE. PLA2G3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLA2G3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PLA2G3 BINDING SITE, designated SEQ ID:14052, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26554] Another function of GAM175 is therefore inhibition of Phospholipase a2, group iii (PLA2G3, Accession NP_056530.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLA2G3.

[26555] Paired mesoderm homeo box 1 (PMX1, Accession NP_073207.1) is another GAM175 target gene, herein designated TARGET GENE. PMX1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PMX1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMX1 BINDING SITE, designated SEQ ID:10080, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26556] Another function of GAM175 is therefore inhibition of Paired mesoderm homeo box 1 (PMX1, Accession NP_073207.1), a gene which acts as a transcriptional regulator of muscle creatine kinase. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMX1.

[26557] The function of PMX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Paired mesoderm homeo box 1 (PMX1, Accession NP_008833.1) is another GAM175 target gene, herein designated TARGET GENE. PMX1 BINDING SITE is a

target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PMX1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMX1 BINDING SITE, designated SEQ ID:10080, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26558] Another function of GAM175 is therefore inhibition of Paired mesoderm homeo box 1 (PMX1, Accession NP_008833.1), a gene which acts as a transcriptional regulator of muscle creatine kinase. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMX1.

[26559] The function of PMX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Polymerase (dna directed), eta (POLH, Accession NP_006493.1) is another GAM175 target gene, herein designated TARGET GENE. POLH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLH BINDING SITE, designated SEQ ID:9909, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26560] Another function of GAM175 is therefore inhibition of Polymerase (dna directed), eta (POLH, Accession NP_006493.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLH.

[26561] Ppar binding protein (PPARBP, Accession NP_004765.2) is another GAM175 target gene, herein designated TARGET GENE. PPARBP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPARBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPARBP BINDING SITE, designated SEQ ID:18113, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26562] Another function of GAM175 is therefore inhibition of Ppar binding protein (PPARBP, Accession NP_004765.2), a gene which interacts with thyroid hormone receptors to

regulate nuclear receptor- mediated transcription; binds dna and p53 protein. and therefore may be associated with Breast cancer. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of Breast cancer, and of other diseases and clinical conditions associated with PPARBP.

[26563] The function of PPARBP has been established by previous studies. By immunoscreening a human B- lymphoma cell cDNA expression library with the anti- p53 (see OMIM Ref. No. TP53; 191170) monoclonal antibody PAb1801, Drane et al. (1997) identified PPARBP, which they called RB18A for 'recognized by PAb1801 monoclonal antibody.' The predicted 1,566- amino acid RB18A protein contains several potential nuclear localization signals, 13 potential N-glycosylation sites, and a high number of potential phosphorylation sites. Despite sharing common antigenic determinants with p53, RB18A does not show significant nucleotide or amino acid sequence similarity with p53. Whereas the calculated molecular mass of RB18A is 166 kD, the apparent mass of recombinant RB18A was 205 kD by SDS- PAGE analysis. Drane et al. (1997) demonstrated that RB18A shares functional properties with p53, including DNA binding, p53 binding, and self- oligomerization.

Furthermore, RB18A was able to activate the sequence-specific binding of p53 to DNA, which was induced through an unstable interaction between both proteins. Northern blot analysis of human tissues detected an 8.5-kb RB18A transcript in all tissues examined except kidney, with highest expression in heart.

[26564] Animal model experiments lend further support to the function of PPARBP. Ito et al. (2000) generated mouse mutants with targeted disruption of the Trap220 gene. The null mutants died during an early gestational stage with heart failure and exhibited impaired neuronal development with extensive apoptosis. Primary embryonic fibroblasts derived from null mutants showed impaired cell cycle regulation and a prominent decrease of thyroid hormone receptor (see OMIM Ref. No. 190160) function that was restored by ectopic Trap220; no defect in activation by Gal4- RARA, Gal4- RXRA, p53, or Gal4- VP16 (see OMIM Ref. No. 300019) was detected. Haploinsufficient mice showed growth retardation, pituitary hypothyroidism, and widely impaired transcription in certain organs. The results indicated that TRAP220 is essential for a wide range of physiologic processes and that it also has gene- and activator- selective functions.

[26565] It is appreciated that the abovementioned animal model for PPARBP is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[26566] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26567] Drane, P.; Barel, M.; Balbo, M.; Frade, R. : Identification of RB18A, a 205 kDa new p53 regulatory protein which shares antigenic and functional properties with p53. Oncogene 15: 3013- 3024, 1997. ; and

[26568] Ito, M.; Yuan, C.- X.; Okano, H. J.; Darnell, R. B.; Roeder, R. G. : Involvement of the TRAP220 component of the TRAP/SMCC coactivator complex in embryonic development and thyroid hormone.

[26569] Further studies establishing the function and utilities of PPARBP are found in John Hopkins OMIM database record ID 604311, and in cited publications listed in Table 5, which are hereby incorporated by reference.Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) is another GAM175 target gene, herein designated TARGET GENE. PPIL2 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by PPIL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPIL2 BINDING SITE, designated SEQ ID:19201, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26570] Another function of GAM175 is therefore inhibition of Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPIL2.

[26571] Phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN, Accession NP_000305.1) is another GAM175 target gene, herein designated TARGET GENE. PTEN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTEN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTEN BINDING SITE, designated SEQ ID:17273, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26572] Another function of GAM175 is therefore inhibition of Phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN, Accession NP_000305.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTEN.

[26573] Prostaglandin e synthase 2 (PTGES2, Accession NP_079348.1) is another GAM175 target gene, herein designated TARGET GENE. PTGES2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGES2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGES2 BINDING SITE, designated SEQ ID:10220, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26574] Another function of GAM175 is therefore inhibition of Prostaglandin e synthase 2 (PTGES2, Accession NP_079348.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGES2.

[26575] RAB11-FIP4 (Accession NP_116321.2) is another GAM175

target gene, herein designated TARGET GENE. RAB11-FIP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB11-FIP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB11-FIP4 BINDING SITE, designated SEQ ID:12040, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26576] Another function of GAM175 is therefore inhibition of RAB11-FIP4 (Accession NP_116321.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB11-FIP4.

[26577] Retinoic acid induced 17 (RAI17, Accession NP_065071.1) is another GAM175 target gene, herein designated TARGET GENE. RAI17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAI17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI17 BINDING SITE, designated SEQ ID:9293, to the nucleotide sequence

of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26578] Another function of GAM175 is therefore inhibition of Retinoic acid induced 17 (RAI17, Accession NP_065071.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI17.

[26579] Ribonuclease, rnase a family, k6 (RNASE6, Accession NP_005606.1) is another GAM175 target gene, herein designated TARGET GENE. RNASE6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RNASE6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNASE6 BINDING SITE, designated SEQ ID:15669, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26580] Another function of GAM175 is therefore inhibition of Ribonuclease, rnase a family, k6 (RNASE6, Accession NP_005606.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNASE6.

[26581] Ribosomal protein s6 kinase, 90kda, polypeptide 2 (RPS6KA2, Accession NP_066958.2) is another GAM175 target gene, herein designated TARGET GENE. RPS6KA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RPS6KA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RPS6KA2 BINDING SITE, designated SEQ ID:4835, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26582] Another function of GAM175 is therefore inhibition of Ribosomal protein s6 kinase, 90kda, polypeptide 2 (RPS6KA2, Accession NP_066958.2), a gene which phosphorylates a wide range of substrates including ribosomal protein s6. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPS6KA2.

[26583] The function of RPS6KA2 has been established by previous studies. Serine/threonine protein kinases in the ribosomal S6 kinase (RSK) family have been implicated as signaling intermediates in the cellular response to several growth factors. Moller et al. (1994) described the cloning and

characterization of 3 genes encoding 3 isoforms of ribosomal protein S6 kinase, which they called HU1 (RPS6KA1; 601684), HU2 (RPS6KA2), and HU3 (RPS6KA3; 300075). The partial HU2 cDNA (GenBank L07598) encodes a predicted protein containing 2 distinct consensus ATP- binding site sequences. Northern blot and RNase protection analyses detected major 7.5- kb and minor 3.5- kb HU2 transcripts in fibroblasts, skeletal muscle, lymphocytes, and placenta. Zhao et al. (1995) cloned a full- length cDNA encoding the RPS6KA2 isoform of ribosomal protein S6 kinase, which they designated RSK3. The deduced 733- amino acid RSK3 protein has 84% and 75% sequence identity with RSK2 (RPS6KA3) and RSK1 (RPS6KA1), respectively. RSK3 has a unique N- terminal sequence which contains a putative bipartite nuclear localization signal. Immunoblot analysis of human cell lysates detected an 83- kD RSK protein. The authors demonstrated serum-stimulated nuclear translocation of endogenous RSK3 in HeLa cells. RSK3 exhibited growth- stimulated autophosphorylation and kinase activity; however, its relative activity toward several known RSK substrates differed from the activities of other RSKs. Unlike RSK1, RSK3 was not activated by ERK2 (PRKM1; 176948) in vitro. Northern blot

analysis detected a single 6.5- kb RSK3 transcript in all tissues examined, with the highest expression in lung and skeletal muscle.

[26584]

[26585] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26586] Moller, D. E.; Xia, C. H.; Tang, W.; Zhu, A. X.; Jakubowski, M. : Human rsk isoforms: cloning and characterization of tissue- specific expression. Am. J. Physiol. 266: C351-C359, 1994. ; and

[26587] Zhao, Y.; Bjorbaek, C.; Weremowicz, S.; Morton, C. C.; Moller, D. E. : RSK3 encodes a novel pp90rsk isoform with a unique N- terminal sequence: growth factor- stimulated kinase function and n.

[26588] Further studies establishing the function and utilities of RPS6KA2 are found in John Hopkins OMIM database record ID 601685, and in cited publications listed in Table 5, which are hereby incorporated by refer-ence.Stearoyl-coa desaturase (delta-9-desaturase) (SCD, Accession NP_005054.2) is another GAM175 target gene, herein designated TARGET GENE. SCD BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by SCD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCD BINDING SITE, designated SEQ ID:15911, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26589] Another function of GAM175 is therefore inhibition of Stearoyl-coa desaturase (delta-9-desaturase) (SCD, Accession NP_005054.2), a gene which functions in the synthesis of unsaturated fatty acids. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCD.

[26590] The function of SCD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.Sidekick homolog 1 (chicken) (SDK1, Accession NP_689957.1) is another GAM175 target gene, herein designated TARGET GENE. SDK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SDK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of SDK1 BINDING SITE, designated SEQ ID:6489, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26591] Another function of GAM175 is therefore inhibition of Sidekick homolog 1 (chicken) (SDK1, Accession NP_689957.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDK1.

[26592] SEI1 (Accession NP_037508.1) is another GAM175 target gene, herein designated TARGET GENE. SEI1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEI1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEI1 BINDING SITE, designated SEQ ID:3289, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26593] Another function of GAM175 is therefore inhibition of SEI1 (Accession NP_037508.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEI1.

[26594] Selenoprotein n, 1 (SEPN1, Accession NP_065184.1) is an-

other GAM175 target gene, herein designated TARGET GENE. SEPN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEPN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEPN1 BINDING SITE, designated SEQ ID:12396, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26595] Another function of GAM175 is therefore inhibition of Selenoprotein n, 1 (SEPN1, Accession NP_065184.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEPN1.

[26596] SERP1 (Accession NP_055260.1) is another GAM175 target gene, herein designated TARGET GENE. SERP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERP1 BINDING SITE, designated SEQ ID:14919, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA,

also designated SEQ ID:265.

[26597] Another function of GAM175 is therefore inhibition of SERP1 (Accession NP_055260.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERP1.

[26598] Sh3 domain binding glutamic acid-rich protein like 3 (SH3BGRL3, Accession NP_112576.1) is another GAM175 target gene, herein designated TARGET GENE. SH3BGRL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SH3BGRL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SH3BGRL3 BINDING SITE, designated SEQ ID:9406, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26599] Another function of GAM175 is therefore inhibition of Sh3 domain binding glutamic acid-rich protein like 3 (SH3BGRL3, Accession NP_112576.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BGRL3.

[26600] Sh3 and multiple ankyrin repeat domains 3 (SHANK3, Ac-

cession XP_037493.1) is another GAM175 target gene, herein designated TARGET GENE. SHANK3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SHANK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SHANK3 BINDING SITE, designated SEQ ID:2299, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26601] Another function of GAM175 is therefore inhibition of Sh3 and multiple ankyrin repeat domains 3 (SHANK3, Accession XP_037493.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHANK3.

[26602] Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (SLC11A2, Accession NP_000608.1) is another GAM175 target gene, herein designated TARGET GENE. SLC11A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC11A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of SLC11A2 BINDING SITE, designated SEQ ID:17770, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26603] Another function of GAM175 is therefore inhibition of Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (SLC11A2, Accession NP_000608.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC11A2.

[26604] Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) is another GAM175 target gene, herein designated TARGET GENE. SLC16A6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC16A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A6 BINDING SITE, designated SEQ ID:12166, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26605] Another function of GAM175 is therefore inhibition of So-

lute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A6.

[26606] Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (SLC1A4, Accession NP_003029.2) is another GAM175 target gene, herein designated TARGET GENE. SLC1A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC1A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC1A4 BINDING SITE, designated SEQ ID:15625, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26607] Another function of GAM175 is therefore inhibition of Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (SLC1A4, Accession NP_003029.2), a gene which transports alanine, serine, cysteine, and threonine. exhibits sodium dependence. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with SLC1A4.

[26608] The function of SLC1A4 has been established by previous studies. In a screening for cDNAs encoding proteins similar to the sodium- coupled glutamate transporter GLAST1, Hofmann et al. (1994) isolated a cDNA clone encoding a protein that turned out to be identical to the neutral amino acid transporter ASCT1 (Arriza et al., 1993; Shafqat et al., 1993). The new member of the GLAST- related transporter family did not transport glutamate or aspartate but alanine, serine, cysteine, and threonine instead. The open reading frame of 1,572 basepairs encodes 524 amino acid residues distributed over 8 exons spanning at least 40 kb of genomic DNA. The gene for ASCT1, designated SLC1A4, was assigned to 2p15- p13 by fluorescence in situ hybridization. The gene structure was not related to any previously characterized transporter gene. Zerangue and Kavanaugh (1996) found that the ASCT1 transporter functions primarily as an amino acid exchanger. Transport is associated with a chloride channel activity that is thermodynamically uncoupled from amino acid transport.

[26609]

[26610] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26611] Arriza, J. L.; Kavanaugh, M. P.; Fairman, W. A.; Wu, Y.- N.; Murdoch, G. H.; North, R. A.; Amara, S. G. : Cloning and expression of a human neutral amino acid transporter with structural similarity to the glutamate transporter gene family. J. Biol. Chem. 268: 15329- 15332, 1993. ; and

[26612] Zerangue, N.; Kavanaugh, M. P. : ASCT- 1 is a neutral amino acid exchanger with chloride channel activity. J. Biol. Chem. 271: 27991- 27994, 1996.

[26613] Further studies establishing the function and utilities of SLC1A4 are found in John Hopkins OMIM database record ID 600229, and in cited publications listed in Table 5, which are hereby incorporated by reference.Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2) is another GAM175 target gene, herein designated TARGET GENE. SLC39A1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC39A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of SLC39A1 BINDING SITE, designated SEQ ID:12020, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26614] Another function of GAM175 is therefore inhibition of Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2), a gene which is a divalent (zinc/iron) metal ion transporter. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC39A1.

[26615] The function of SLC39A1 has been established by previous studies. The ZRT- and IRT- related protein (ZIP) family is composed of divalent metal ion transporters, including A. thaliana IRT1 (iron- regulated transporter- 1), which appears to play a role in iron uptake, and S. cerevisiae ZRT1 (zinc- regulated transporter- 1) and ZRT2, and A. thaliana ZIP1 to ZIP4, all of which are probably zinc transporters (reviewed by Eng et al., 1998). The human growth arrest- inducible gene product (GAIP) is also a ZIP family member based on sequence similarity. Lioumi et al. (1998) generated a transcript map of the region within and in the proximity of the epidermal differentiation com-

plex (EDC; 601588), which is located in 1q21. They identified a partial ZIRTL cDNA as mapping to the distal end of the EDC, 200 kb from the S100A1 gene (OMIM Ref. No. 176940). Lioumi et al. (1998) found that a portion of the ZIRTL cDNA encodes a polypeptide with significant sequence similarity to the ZIP family of iron and zinc transporters from plants and yeast. By screening a human keratinocyte cDNA library with the partial ZIRTL cDNA, Lioumi et al. (1999) isolated a full- length ZIRTL cDNA. The predicted 324- amino acid ZIRTL protein contains 8 transmembrane domains, 9 possible N- myristylation sites, a potential protein kinase C phosphorylation site, and 4 potential protein kinase II phosphorylation sites. Human ZIRTL shares 21 to 22% amino acid sequence identity with A. thaliana IRT1 and ZIP1 to ZIP4, Pisum sativum Rit1, and S. cerevisiae ZRT1 and ZRT2. ZIRTL also shares 34% amino acid sequence identity with GAIP. The human and mouse Zirtl proteins are 90% similar. The ZIRTL gene contains 4 exons. Northern blot analysis detected a 2.1- kb ZIRTL transcript in all human tissues tested, namely adult heart, lung, brain, liver, pancreas, small intestine, colon, kidney, spleen, thymus, peripheral blood leukocytes, skeletal muscle, testis, ovary, placenta, prostate, and ker-

atinocytes, and fetal heart, kidney, small intestine, and skin. In situ hybridization showed that mouse Zirtl is developmentally regulated in the skin, where it was expressed in the epidermal layer, excluding the dermis, at E17.5, but not in embryonic days 10.5 and 15.5 or P21. In the small intestine, Zirtl was found toward the base of the intestinal villi from E17.5. In the pancreas, Zirtl expression was found from E17.5. Zirtl expression was not detected in the liver. Zirtl was expressed in osteoblasts of developing bone from E15.5 and in ameloblasts and odontoblasts at late stages of tooth development at P21. Moderate expression of Zirtl was observed in brain in the hippocampus

[26616]

[26617] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26618] Lioumi, M.; Ferguson, C. A.; Sharpe, P. T.; Freeman, T.; Marenholz, I.; Mischke, D.; Heizmann, C.; Ragoussis, J. : Isolation and characterization of human and mouse ZIRTL, a member of the IRT1 family of transporters, mapping within the epidermal differentiation complex. Genomics 62: 272- 280, 1999. ; and

[26619] Lioumi, M.; Olavesen, M. G.; Nizetic, D.; Ragoussis, J. : High- resolution YAC fragmentation map of 1q21. Genomics 49: 200- 208, 1998.

[26620] Further studies establishing the function and utilities of SLC39A1 are found in John Hopkins OMIM database record ID 604740, and in cited publications listed in Table 5, which are hereby incorporated by reference.SMURF1 (Accession XP_166483.1) is another GAM175 target gene, herein designated TARGET GENE. SMURF1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMURF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMURF1 BINDING SITE, designated SEQ ID:17695, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26621] Another function of GAM175 is therefore inhibition of SMURF1 (Accession XP_166483.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMURF1.

[26622] SMURF1 (Accession NP_065162.1) is another GAM175 tar-

get gene, herein designated TARGET GENE. SMURF1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMURF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMURF1 BINDING SITE, designated SEQ ID:17695, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26623] Another function of GAM175 is therefore inhibition of SMURF1 (Accession NP_065162.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMURF1.

[26624] SMURF1 (Accession NP_851994.1) is another GAM175 target gene, herein designated TARGET GENE. SMURF1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMURF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMURF1 BINDING SITE, designated

SEQ ID:17695, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26625] Another function of GAM175 is therefore inhibition of SMURF1 (Accession NP_851994.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMURF1.

[26626] Sry (sex determining region y)-box 13 (SOX13, Accession NP_005677.1) is another GAM175 target gene, herein designated TARGET GENE. SOX13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SOX13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SOX13 BINDING SITE, designated SEQ ID:17045, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26627] Another function of GAM175 is therefore inhibition of Sry (sex determining region y)-box 13 (SOX13, Accession NP_005677.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with SOX13.

[26628] Serine racemase (SRR, Accession NP_068766.1) is another GAM175 target gene, herein designated TARGET GENE. SRR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SRR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRR BINDING SITE, designated SEQ ID:14627, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26629] Another function of GAM175 is therefore inhibition of Serine racemase (SRR, Accession NP_068766.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRR.

[26630] Suppression of tumorigenicity 7 like (ST7L, Accession NP_620056.1) is another GAM175 target gene, herein designated TARGET GENE. ST7L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ST7L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of ST7L BINDING SITE, designated SEQ ID:19906, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26631] Another function of GAM175 is therefore inhibition of Suppression of tumorigenicity 7 like (ST7L, Accession NP_620056.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ST7L.

[26632] Suppression of tumorigenicity 7 like (ST7L, Accession NP_620055.1) is another GAM175 target gene, herein designated TARGET GENE. ST7L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ST7L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ST7L BINDING SITE, designated SEQ ID:19906, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26633] Another function of GAM175 is therefore inhibition of Suppression of tumorigenicity 7 like (ST7L, Accession NP_620055.1) . Accordingly, utilities of GAM175 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with ST7L.

[26634] Suppression of tumorigenicity 7 like (ST7L, Accession NP_060214.2) is another GAM175 target gene, herein designated TARGET GENE. ST7L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ST7L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ST7L BINDING SITE, designated SEQ ID:19906, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26635] Another function of GAM175 is therefore inhibition of Suppression of tumorigenicity 7 like (ST7L, Accession NP_060214.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ST7L.

[26636] Thrombomodulin (THBD, Accession NP_000352.1) is another GAM175 target gene, herein designated TARGET GENE. THBD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by THBD, corresponding to a target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of THBD BINDING SITE, designated SEQ ID:6439, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26637] Another function of GAM175 is therefore inhibition of Thrombomodulin (THBD, Accession NP_000352.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THBD.

[26638] Thy-1 cell surface antigen (THY1, Accession NP_006279.2) is another GAM175 target gene, herein designated TARGET GENE. THY1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by THY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of THY1 BINDING SITE, designated SEQ ID:15926, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26639] Another function of GAM175 is therefore inhibition of Thy-1 cell surface antigen (THY1, Accession

NP_006279.2), a gene which plays a role in cell- cell or cell- ligand interactions during synaptogenesis. Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THY1.

[26640] The function of THY1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM74.1.Transmembrane protease, serine 2 (TMPRSS2, Accession NP_005647.2) is another GAM175 target gene, herein designated TARGET GENE. TMPRSS2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TMPRSS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS2 BINDING SITE, designated SEQ ID:3601, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26641] Another function of GAM175 is therefore inhibition of Transmembrane protease, serine 2 (TMPRSS2, Accession NP_005647.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with TMPRSS2.

[26642] TU12B1-TY (Accession NP_057659.1) is another GAM175 target gene, herein designated TARGET GENE. TU12B1-TY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TU12B1-TY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TU12B1-TY BINDING SITE, designated SEQ ID:9561, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26643] Another function of GAM175 is therefore inhibition of TU12B1-TY (Accession NP_057659.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TU12B1-TY.

[26644] TULP4 (Accession NP_064630.1) is another GAM175 target gene, herein designated TARGET GENE. TULP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TULP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TULP4

BINDING SITE, designated SEQ ID:10089, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26645] Another function of GAM175 is therefore inhibition of TULP4 (Accession NP_064630.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TULP4.

[26646] UMP-CMPK (Accession NP_057392.1) is another GAM175 target gene, herein designated TARGET GENE. UMP-CMPK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UMP-CMPK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UMP-CMPK BINDING SITE, designated SEQ ID:5399, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26647] Another function of GAM175 is therefore inhibition of UMP-CMPK (Accession NP_057392.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UMP-CMPK.

[26648] Unc-84 homolog a (c. elegans) (UNC84B, Accession

XP_039332.1) is another GAM175 target gene, herein designated TARGET GENE. UNC84B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UNC84B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UNC84B BINDING SITE, designated SEQ ID:8301, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26649] Another function of GAM175 is therefore inhibition of Unc-84 homolog a (c. elegans) (UNC84B, Accession XP_039332.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC84B.

[26650] Unc-84 homolog a (c. elegans) (UNC84B, Accession NP_056189.1) is another GAM175 target gene, herein designated TARGET GENE. UNC84B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UNC84B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

UNC84B BINDING SITE, designated SEQ ID:8301, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26651] Another function of GAM175 is therefore inhibition of Unc-84 homolog a (c. elegans) (UNC84B, Accession NP_056189.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC84B.

[26652] Ubiquitin specific protease 25 (USP25, Accession NP_037528.2) is another GAM175 target gene, herein designated TARGET GENE. USP25 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by USP25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of USP25 BINDING SITE, designated SEQ ID:3776, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26653] Another function of GAM175 is therefore inhibition of Ubiquitin specific protease 25 (USP25, Accession NP_037528.2) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP25.

[26654] Zinc finger protein 313 (ZNF313, Accession NP_061153.1) is another GAM175 target gene, herein designated TARGET GENE. ZNF313 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF313, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF313 BINDING SITE, designated SEQ ID:1924, to the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, also designated SEQ ID:265.

[26655] Another function of GAM175 is therefore inhibition of Zinc finger protein 313 (ZNF313, Accession NP_061153.1) . Accordingly, utilities of GAM175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF313.

[26656]

[26657] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 176 (GAM176), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26658] GAM176 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM176 was detected is described hereinabove with reference to Figs. 8-15.

[26659] GAM176 gene, herein designated GAM GENE, and GAM176 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[26660] GAM176 gene encodes a GAM176 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM176 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM176 precursor RNA is designated SEQ ID:73, and is provided hereinbelow with reference to the sequence listing part.

[26661] GAM176 precursor RNA folds onto itself, forming GAM176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26662] GAM176 precursor RNA folds onto itself, forming GAM176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[26663] Nucleotide sequence of GAM176 precursor RNA, designated SEQ-ID: 73, and a schematic representation of a predicted secondary folding of GAM176 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[26664] An enzyme complex designated DICER COMPLEX, `dices` the GAM176 folded precursor RNA into GAM176 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM176 RNA is desig-

nated SEQ ID:345, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[26665] GAM176 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM176 target RNA, herein designated GAM TARGET RNA. GAM176 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[26666] GAM176 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM176 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM176 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM176 RNA may have a different number of target

binding sites in untranslated regions of a GAM176 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[26667] The complementary binding of GAM176 RNA, herein designated GAM RNA, to target binding sites on GAM176 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM176 target RNA into GAM176 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26668] It is appreciated that GAM176 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM176 target genes. The mRNA of each one of this plurality of GAM176 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM176 RNA, herein designated GAM RNA, and which when bound by GAM176 RNA causes inhibition of translation of respective one or more GAM176 target proteins.

[26669] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM176 gene, herein designated GAM GENE, on one or more GAM176 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26670] It is appreciated that specific functions and accordingly utilities of GAM176 correlate with, and may be deduced from, the identity of the target genes which GAM176 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26671]

[26672]

[26673] V-myb myeloblastosis viral oncogene homolog (avian)-like 1 (MYBL1, Accession XM_034274.10) is a GAM176 target gene, herein designated TARGET GENE. MYBL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYBL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYBL1 BINDING SITE, designated SEQ ID:18625, to the nucleotide sequence of GAM176 RNA, herein designated GAM RNA, also designated SEQ ID:345.

[26674] A function of GAM176 is therefore inhibition of V-myb myeloblastosis viral oncogene homolog (avian)-like 1 (MYBL1, Accession XM_034274.10), a gene which could have a role in the proliferation and/or differentiation of neurogenic, spermatogenic and b- lymphoid cells. Accordingly, utilities of GAM176 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYBL1.

[26675] The function of MYBL1 has been established by previous studies. Nomura et al. (1988) isolated and characterized cDNA clones for 2 human MYB- related genes, AMYB and BMYB (OMIM Ref. No. 601415). Using probes in Southern

blot analysis of rodent- human hybrid DNAs, Barletta et al. (1991) localized the MYBL1 locus to 8cen- q22 and refined the localization to 8q22- q23 by in situ hybridization. Takahashi et al. (1995) found that MYBL1 mRNA is expressed mainly in testis and peripheral blood leukocytes. AMYB could activate transcription from the promoter- containing MYB- binding sites in all cells examined. In addition to the 2 domains (a DNA- binding domain and a transcriptional activation domain), 2 negative regulatory domains were identified in the MYBL1 gene. These results indicated that the gene functions as a transcriptional activator and that the regulatory mechanism of gene activity is similar to that of the MYB (OMIM Ref. No. 189990) gene.

[26676]

[26677] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26678] Nomura, N.; Takahashi, M.; Matsui, M.; Ishii, S.; Date, T.; Sasamoto, S.; Ishizaki, R. : Isolation of human cDNA clones of MYB- related genes, A- MYB and B- MYB. Nucleic Acids Res. 16: 11075- 11089, 1988. ; and

[26679] Takahashi, T.; Nakagoshi, H.; Sarai, A.; Nomura, N.; Ya-

mamoto, T.; Ishii, S. : Human A- myb gene encodes a transcriptional activator containing the negative regulatory domains. FEBS Lett.

[26680] Further studies establishing the function and utilities of MYBL1 are found in John Hopkins OMIM database record ID 159405, and in cited publications listed in Table 5, which are hereby incorporated by reference.

[26681] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 177 (GAM177), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26682] GAM177 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM177 was detected is described hereinabove with reference to Figs. 8-15.

[26683] GAM177 gene, herein designated GAM GENE, and GAM177 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[26684] GAM177 gene encodes a GAM177 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM177 precur-

sor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM177 precursor RNA is designated SEQ ID:133, and is provided hereinbelow with reference to the sequence listing part.

[26685] GAM177 precursor RNA folds onto itself, forming GAM177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26686] GAM177 precursor RNA folds onto itself, forming GAM177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[26687] Nucleotide sequence of GAM177 precursor RNA, designated SEQ-ID: 133, and a schematic representation of a predicted secondary folding of GAM177 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[26688] An enzyme complex designated DICER COMPLEX, `dices` the GAM177 folded precursor RNA into GAM177 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM177 RNA is designated SEQ ID:385, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[26689] GAM177 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM177 target RNA, herein designated GAM TARGET RNA. GAM177 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[26690] GAM177 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM177 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM177 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM177 RNA may have a different number of target binding sites in untranslated regions of a GAM177 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[26691] The complementary binding of GAM177 RNA, herein designated GAM RNA, to target binding sites on GAM177 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM177 target RNA into GAM177 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26692] It is appreciated that GAM177 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM177 target genes. The mRNA of each one of this plurality of GAM177 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM177 RNA, herein designated GAM RNA, and which when bound by GAM177 RNA causes inhibition of translation of respective one or more GAM177 target proteins.

[26693] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM177 gene, herein designated GAM GENE, on one or more GAM177 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26694] It is appreciated that specific functions and accordingly utilities of GAM177 correlate with, and may be deduced from, the identity of the target genes which GAM177 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26695]

[26696]

[26697] B-cell cll/lymphoma 7a (BCL7A, Accession NM_020993.2) is a GAM177 target gene, herein designated TARGET GENE. BCL7A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCL7A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCL7A BINDING SITE, designated SEQ ID:9800, to the nucleotide sequence of GAM177 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:385.

[26698] A function of GAM177 is therefore inhibition of B-cell cll/lymphoma 7a (BCL7A, Accession NM_020993.2) . Accordingly, utilities of GAM177 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL7A.

[26699] CLONE24945 (Accession NM_015683.1) is another GAM177 target gene, herein designated TARGET GENE. CLONE24945 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLONE24945, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLONE24945 BINDING SITE, designated SEQ ID:4969, to the nucleotide sequence of GAM177 RNA, herein designated GAM RNA, also designated SEQ ID:385.

[26700] Another function of GAM177 is therefore inhibition of CLONE24945 (Accession NM_015683.1) . Accordingly, utilities of GAM177 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLONE24945.

[26701] Protein tyrosine phosphatase, non-receptor type 3

(PTPN3, Accession NM_002829.2) is another GAM177 target gene, herein designated TARGET GENE. PTPN3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTPN3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPN3 BINDING SITE, designated SEQ ID:12354, to the nucleotide sequence of GAM177 RNA, herein designated GAM RNA, also designated SEQ ID:385.

[26702] Another function of GAM177 is therefore inhibition of Protein tyrosine phosphatase, non-receptor type 3 (PTPN3, Accession NM_002829.2) . Accordingly, utilities of GAM177 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN3.

[26703]

[26704] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 178 (GAM178), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26705] GAM178 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM178 was detected is described hereinabove with reference to Figs. 8-15.

[26706] GAM178 gene, herein designated GAM GENE, and GAM178 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[26707] GAM178 gene encodes a GAM178 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM178 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM178 precursor RNA is designated SEQ ID:32, and is provided hereinbelow with reference to the sequence listing part.

[26708] GAM178 precursor RNA folds onto itself, forming GAM178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26709] GAM178 precursor RNA folds onto itself, forming GAM178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[26710] Nucleotide sequence of GAM178 precursor RNA, designated SEQ-ID: 32, and a schematic representation of a predicted secondary folding of GAM178 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[26711] An enzyme complex designated DICER COMPLEX, `dices` the GAM178 folded precursor RNA into GAM178 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM178 RNA is desig-

nated SEQ ID:223, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[26712] GAM178 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM178 target RNA, herein designated GAM TARGET RNA. GAM178 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[26713] GAM178 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM178 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM178 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM178 RNA may have a different number of target

binding sites in untranslated regions of a GAM178 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[26714] The complementary binding of GAM178 RNA, herein designated GAM RNA, to target binding sites on GAM178 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM178 target RNA into GAM178 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26715] It is appreciated that GAM178 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM178 target genes. The mRNA of each one of this plurality of GAM178 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM178 RNA, herein designated GAM RNA, and which when bound by GAM178 RNA causes inhibition of translation of respective one or more GAM178 target proteins.

[26716] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM178 gene, herein designated GAM GENE, on one or more GAM178 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26717] It is appreciated that specific functions and accordingly utilities of GAM178 correlate with, and may be deduced from, the identity of the target genes which GAM178 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26718]

[26719]

[26720] Digeorge syndrome critical region gene 2 (DGCR2, Accession NM_005137.1) is a GAM178 target gene, herein designated TARGET GENE. DGCR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DGCR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DGCR2 BINDING SITE, designated SEQ ID:17601, to the nucleotide sequence of GAM178 RNA, herein designated GAM RNA, also designated SEQ ID:223.

[26721] A function of GAM178 is therefore inhibition of Digeorge syndrome critical region gene 2 (DGCR2, Accession NM_005137.1), a gene which is putative adhesion receptor and intervenes in cell- cell or cell- matrix interactions and therefore may be associated with Digeorge syndrome . Accordingly, utilities of GAM178 include diagnosis, prevention and treatment of Digeorge syndrome ., and of other diseases and clinical conditions associated with DGCR2.

[26722] The function of DGCR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM84.1.Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NM_130436.1) is another GAM178 target gene, herein designated TARGET GENE. DYRK1A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DYRK1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DYRK1A BINDING SITE, designated SEQ ID:7463, to the nucleotide sequence of GAM178 RNA, herein designated GAM RNA, also designated SEQ ID:223.

[26723] Another function of GAM178 is therefore inhibition of Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NM_130436.1), a gene which regulates cell proliferation and may be involved in brain development . and therefore may be associated with Down syndrome. Accordingly, utilities of GAM178 include diagnosis, prevention and treatment of Down syndrome, and of other diseases and clinical conditions associated with DYRK1A.

[26724] The function of DYRK1A and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM63.1.FLJ11795 (Accession NM_024669.1) is another GAM178 target gene, herein designated TARGET GENE. FLJ11795 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11795, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11795 BINDING SITE, designated SEQ ID:8358, to the nucleotide sequence of GAM178 RNA, herein designated GAM RNA, also designated SEQ ID:223.

[26725] Another function of GAM178 is therefore inhibition of FLJ11795 (Accession NM_024669.1) . Accordingly, utilities of GAM178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11795.

[26726] Junctional adhesion molecule 1 (JAM1, Accession) is another GAM178 target gene, herein designated TARGET GENE. JAM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JAM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of JAM1 BINDING SITE, designated SEQ ID:7807, to the nucleotide sequence of GAM178 RNA, herein designated GAM RNA, also designated SEQ ID:223.

[26727] Another function of GAM178 is therefore inhibition of Junctional adhesion molecule 1 (JAM1, Accession) . Accordingly, utilities of GAM178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAM1.

[26728] Kelch-like 3 (drosophila) (KLHL3, Accession NM_017415.1) is another GAM178 target gene, herein designated TARGET GENE. KLHL3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KLHL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLHL3 BINDING SITE, designated SEQ ID:5694, to the nucleotide sequence of GAM178 RNA, herein designated GAM RNA, also designated SEQ ID:223.

[26729] Another function of GAM178 is therefore inhibition of Kelch-like 3 (drosophila) (KLHL3, Accession NM_017415.1) . Accordingly, utilities of GAM178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLHL3.

[26730] LOC221596 (Accession) is another GAM178 target gene, herein designated TARGET GENE. LOC221596 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221596, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221596 BINDING SITE, designated SEQ ID:13446, to the nucleotide sequence of GAM178 RNA, herein designated GAM RNA, also designated SEQ ID:223.

[26731] Another function of GAM178 is therefore inhibition of LOC221596 (Accession) . Accordingly, utilities of GAM178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221596.

[26732] O-linked n-acetylglucosamine (glcnac) transferase (udp-n-acetylglucosamine:polypeptide-n-acetylglucosaminyl transferase) (OGT, Accession NM_003605.2) is another GAM178 target gene, herein designated TARGET GENE. OGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OGT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of OGT BINDING SITE, designated SEQ ID:16443, to the nucleotide sequence of GAM178 RNA, herein designated GAM RNA, also designated SEQ ID:223.

[26733] Another function of GAM178 is therefore inhibition of O-linked n-acetylglucosamine (glcnac) transferase (udp-n-acetylglucosamine:polypeptide-n-acetylglucosaminyl transferase) (OGT, Accession NM_003605.2), a gene which has a role in the glycosylation of nuclear and cytoplasmic proteins. Accordingly, utilities of GAM178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OGT.

[26734] The function of OGT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM100.1.Protein tyrosine phosphatase, receptor type, u (PTPRU, Accession NM_005704.2) is another GAM178 target gene, herein designated TARGET GENE. PTPRU BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTPRU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of PTPRU BINDING SITE, designated SEQ ID:17915, to the nucleotide sequence of GAM178 RNA, herein designated GAM RNA, also designated SEQ ID:223.

[26735] Another function of GAM178 is therefore inhibition of Protein tyrosine phosphatase, receptor type, u (PTPRU, Accession NM_005704.2) . Accordingly, utilities of GAM178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRU.

[26736]

[26737] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 179 (GAM179), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[26738] GAM179 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM179 was detected is described hereinabove with reference to Figs. 8-15.

[26739] GAM179 gene, herein designated GAM GENE, and GAM179 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[26740] GAM179 gene encodes a GAM179 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM179 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM179 precursor RNA is designated SEQ ID:19, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:19 is located at position 33981297 relative to chromosome 15.

[26741] GAM179 precursor RNA folds onto itself, forming GAM179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[26742] GAM179 precursor RNA folds onto itself, forming GAM179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is

due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[26743] Nucleotide sequence of GAM179 precursor RNA, designated SEQ-ID: 19, and a schematic representation of a predicted secondary folding of GAM179 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[26744] An enzyme complex designated DICER COMPLEX, `dices` the GAM179 folded precursor RNA into GAM179 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: B) nucleotide sequence of GAM179 RNA is designated SEQ ID:300, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[26745] GAM179 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM179 target

RNA, herein designated GAM TARGET RNA. GAM179 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[26746] GAM179 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM179 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM179 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM179 RNA may have a different number of target binding sites in untranslated regions of a GAM179 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[26747] The complementary binding of GAM179 RNA, herein designated GAM RNA, to target binding sites on GAM179 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM179 target RNA into GAM179 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[26748] It is appreciated that GAM179 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM179 target genes. The mRNA of each one of this plurality of GAM179 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM179 RNA, herein designated GAM RNA, and which when bound by GAM179 RNA causes inhibition of translation of respective one or more GAM179 target proteins.

[26749] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM179 gene, herein designated GAM GENE, on one or more GAM179 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes.

As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[26750] It is appreciated that specific functions and accordingly utilities of GAM179 correlate with, and may be deduced from, the identity of the target genes which GAM179 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[26751]

[26752]

[26753] 7h3 (Accession NP_149014.2) is a GAM179 target gene, herein designated TARGET GENE. 7h3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by 7h3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of 7h3 BINDING SITE, designated SEQ ID:1101, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26754] A function of GAM179 is therefore inhibition of 7h3 (Accession NP_149014.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 7h3.

[26755] Active bcr-related gene (ABR, Accession NP_068781.1) is another GAM179 target gene, herein designated TARGET GENE. ABR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABR BINDING SITE, designated SEQ ID:16042, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26756] Another function of GAM179 is therefore inhibition of Active bcr-related gene (ABR, Accession NP_068781.1), a gene which gtpase- activating protein for rac and cdc42. and therefore may be associated with Medulloblastoma.

Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of Medulloblastoma, and of other diseases and clinical conditions associated with ABR.

[26757] The function of ABR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Active bcr-related gene (ABR, Accession NP_001083.1) is another GAM179 target gene, herein designated TARGET GENE. ABR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABR BINDING SITE, designated SEQ ID:16042, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26758] Another function of GAM179 is therefore inhibition of Active bcr-related gene (ABR, Accession NP_001083.1), a gene which gtpase- activating protein for rac and cdc42. and therefore may be associated with Medulloblastoma. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of Medulloblastoma, and of other

diseases and clinical conditions associated with ABR.

[26759] The function of ABR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_542118.1) is another GAM179 target gene, herein designated TARGET GENE. AP1GBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1GBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1GBP1 BINDING SITE, designated SEQ ID:16827, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26760] Another function of GAM179 is therefore inhibition of Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_542118.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1GBP1.

[26761] Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_542117.1) is another GAM179 target gene, herein

designated TARGET GENE. AP1GBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1GBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1GBP1 BINDING SITE, designated SEQ ID:16827, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26762] Another function of GAM179 is therefore inhibition of Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_542117.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1GBP1.

[26763] Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_009178.2) is another GAM179 target gene, herein designated TARGET GENE. AP1GBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1GBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1GBP1 BINDING SITE, designated SEQ ID:16827, to the

nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26764] Another function of GAM179 is therefore inhibition of Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_009178.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1GBP1.

[26765] APRG1 (Accession NP_848031.1) is another GAM179 target gene, herein designated TARGET GENE. APRG1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by APRG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APRG1 BINDING SITE, designated SEQ ID:15841, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26766] Another function of GAM179 is therefore inhibition of APRG1 (Accession NP_848031.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APRG1.

[26767] Atpase, class vi, type 11b (ATP11B, Accession

XP_087254.2) is another GAM179 target gene, herein designated TARGET GENE. ATP11B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP11B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP11B BINDING SITE, designated SEQ ID:4094, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26768] Another function of GAM179 is therefore inhibition of Atpase, class vi, type 11b (ATP11B, Accession XP_087254.2), a gene which is phosphorylated in their intermediate state, drives uphill transport of ions across membranes. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP11B.

[26769] The function of ATP11B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Bactericidal/permeability-increasing protein (BPI, Accession NP_001716.1) is another GAM179 target gene, herein designated TARGET GENE. BPI BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by BPI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BPI BINDING SITE, designated SEQ ID:12380, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26770] Another function of GAM179 is therefore inhibition of Bactericidal/permeability-increasing protein (BPI, Accession NP_001716.1), a gene which is associated with human neutrophil granules and has bactericidal activity on gram- negative organisms. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BPI.

[26771] The function of BPI has been established by previous studies. Using oligonucleotides derived from the human BPI protein sequence to screen a human genomic library, Gray et al. (1989) isolated BPI genomic sequence. They screened a dimethyl sulfoxide- induced HL- 60 cell cDNA library with oligonucleotides based on the genomic sequence and isolated a full- length human BPI cDNA. The cDNA predicts a 31- amino acid signal peptide followed

by a 456- amino acid mature protein. The N- terminal half of the protein, which exhibits the antimicrobial activity, is basic and hydrophilic, whereas the C- terminal half is slightly acidic and contains several potential transmembrane regions. The difference between the calculated molecular mass of 50.6 kD and the experimental mass of approximately 58 kD may reflect the usage of 2 potential N- linked glycosylation sites. Northern blot analysis detected a 2- kb BPI transcript in mRNA prepared from the spleen of a patient with CML (OMIM Ref. No. 151410); a lower level of BPI expression was found in normal spleen, but no BPI expression was detected in normal liver, placenta, or brain. Hubacek et al. (1997) found that the BPI gene spans approximately 31.5 kb of DNA and contains 15 exons. Comparison of the genomic structures of BPI, LBP, PLTP (OMIM Ref. No. 172425), and CETP (OMIM Ref. No. 118470), which constitute a family of functionally related proteins, revealed a remarkable conservation of exon/intron junctions and exon size.

[26772]

[26773] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26774] Gray, P. W.; Flaggs, G.; Leong, S. R.; Gumina, R. J.; Weiss, J.; Ooi, C. E.; Elsbach, P. : Cloning of the cDNA of a human neutrophil bactericidal protein: structural and functional correlations. J. Biol. Chem. 264: 9505- 9509, 1989. ; and

[26775] Hubacek, J. A.; Buchler, C.; Aslanidis, C.; Schmitz, G. : The genomic organization of the genes for human lipopolysaccharide binding protein (LBP) and bactericidal permeability increasin.

[26776] Further studies establishing the function and utilities of BPI are found in John Hopkins OMIM database record ID 109195, and in cited publications listed in Table 5, which are hereby incorporated by reference.C14orf92 (Accession NP_055643.1) is another GAM179 target gene, herein designated TARGET GENE. C14orf92 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf92, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf92 BINDING SITE, designated SEQ ID:4439, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26777] Another function of GAM179 is therefore inhibition of

C14orf92 (Accession NP_055643.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf92.

[26778] Chromosome 20 open reading frame 175 (C20orf175, Accession NP_543019.1) is another GAM179 target gene, herein designated TARGET GENE. C20orf175 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf175, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf175 BINDING SITE, designated SEQ ID:6704, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26779] Another function of GAM179 is therefore inhibition of Chromosome 20 open reading frame 175 (C20orf175, Accession NP_543019.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf175.

[26780] C4ST3 (Accession NP_690849.1) is another GAM179 target gene, herein designated TARGET GENE. C4ST3 BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by C4ST3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C4ST3 BINDING SITE, designated SEQ ID:3672, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26781] Another function of GAM179 is therefore inhibition of C4ST3 (Accession NP_690849.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C4ST3.

[26782] Cyclin t2 (CCNT2, Accession NP_001232.1) is another GAM179 target gene, herein designated TARGET GENE. CCNT2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CCNT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCNT2 BINDING SITE, designated SEQ ID:12201, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26783] Another function of GAM179 is therefore inhibition of Cy-

clin t2 (CCNT2, Accession NP_001232.1), a gene which is a regulatory subunit of the cyclin- dependent kinase pair (cdk9/cyclin t) complex. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNT2.

[26784] The function of CCNT2 has been established by previous studies. Positive transcription elongation factor b (OMIM Ref. No. P- TEFb) is thought to facilitate the transition from abortive to productive elongation by phosphorylating the C- terminal domain (CTD) of the largest subunit of RNA polymerase II (POLR2A; 180660). Drosophila P- TEFb is composed of CDK9 (OMIM Ref. No. 603251) and cyclin T. By searching an EST database for homologs of Drosophila cyclin T, Peng et al. (1998) identified cDNAs encoding human cyclins T1 (OMIM Ref. No. 602506) and T2. Alternative splicing of the primary T2 transcript results in 2 isoforms termed T2a and T2b. The predicted 663- amino acid T2a and 730- amino acid T2b isoforms have different C- termini. Within the conserved N- terminal cyclin box region, cyclin T2 shares 64% and 81% identity with Drosophila cyclin T and human cyclin T1, respectively. Immunoprecipitation studies demonstrated that CDK9 is complexed with the cyclins T1 and T2 in HeLa cell

nuclear extracts. Approximately 80% of CDK9 is complexed with cyclin T1, 10% with cyclin T2a and 10% with T2b. Each complex is an active P- TEFb molecule that can phosphorylate the CTD of RNA polymerase II and cause the transition from abortive elongation into productive elongation. When expressed in mammalian cells, all 3 CDK9/cyclin T combinations strongly activated a CMV promoter. Northern blot analysis revealed that cyclin T2 was expressed as multiple mRNAs in all human tissues tested. Yang et al. (2001) identified 7SK snRNA (OMIM Ref. No. 606515) as a specific P- TEFb- associated factor. 7SK inhibits general and HIV- 1 Tat- specific transcriptional activities of P- TEFb in vivo and in vitro by inhibiting the kinase activity of CDK9 and preventing recruitment of P-TEFb to the HIV- 1 promoter. 7SK is efficiently dissociated from P- TEFb (the CDK9/cyclin T1 heterodimer) by treatment of cells with ultraviolet irradiation and actinomycin D. As these 2 agents have been shown to enhance significantly HIV- 1 transcription and phosphorylation of Pol- II, Yang et al. (2001) concluded that their data provide a mechanistic explanation for this stimulatory effect. Yang et al. (2001) further suggested that the 7SK/P- TEFb interaction may serve as a principal control point for the in-

duction of cellular and HIV- 1 viral gene expression during stress- related responses. The study demonstrated the involvement of an snRNA in controlling the activity of CDK/cyclin kinase.

[26785]

[26786] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26787] Peng, J.; Zhu, Y.; Milton, J. T.; Price, D. H. : Identification of multiple cyclin subunits of human P- TEFb. Genes Dev. 12: 755- 762, 1998. ; and

[26788] Yang, Z.; Zhu, Q.; Luo, K.; Zhou, Q. : The 7SK small nuclear RNA inhibits the CDK9/cyclin T1 kinase to control transcription. Nature 414: 317- 322, 2001.

[26789] Further studies establishing the function and utilities of CCNT2 are found in John Hopkins OMIM database record ID 603862, and in cited publications listed in Table 5, which are hereby incorporated by reference.Cyclin t2 (CCNT2, Accession NP_490595.1) is another GAM179 target gene, herein designated TARGET GENE. CCNT2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CCNT2, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCNT2 BINDING SITE, designated SEQ ID:12201, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26790] Another function of GAM179 is therefore inhibition of Cyclin t2 (CCNT2, Accession NP_490595.1), a gene which is a regulatory subunit of the cyclin- dependent kinase pair (cdk9/cyclin t) complex. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNT2.

[26791] The function of CCNT2 has been established by previous studies. Positive transcription elongation factor b (OMIM Ref. No. P- TEFb) is thought to facilitate the transition from abortive to productive elongation by phosphorylating the C- terminal domain (CTD) of the largest subunit of RNA polymerase II (POLR2A; 180660). Drosophila P- TEFb is composed of CDK9 (OMIM Ref. No. 603251) and cyclin T. By searching an EST database for homologs of Drosophila cyclin T, Peng et al. (1998) identified cDNAs encoding human cyclins T1 (OMIM Ref. No. 602506) and T2. Alternative splicing of the primary T2 transcript re-

sults in 2 isoforms termed T2a and T2b. The predicted 663- amino acid T2a and 730- amino acid T2b isoforms have different C- termini. Within the conserved N- terminal cyclin box region, cyclin T2 shares 64% and 81% identity with Drosophila cyclin T and human cyclin T1, respectively. Immunoprecipitation studies demonstrated that CDK9 is complexed with the cyclins T1 and T2 in HeLa cell nuclear extracts. Approximately 80% of CDK9 is complexed with cyclin T1, 10% with cyclin T2a and 10% with T2b. Each complex is an active P- TEFb molecule that can phosphorylate the CTD of RNA polymerase II and cause the transition from abortive elongation into productive elongation. When expressed in mammalian cells, all 3 CDK9/cyclin T combinations strongly activated a CMV promoter. Northern blot analysis revealed that cyclin T2 was expressed as multiple mRNAs in all human tissues tested. Yang et al. (2001) identified 7SK snRNA (OMIM Ref. No. 606515) as a specific P- TEFb- associated factor. 7SK inhibits general and HIV- 1 Tat- specific transcriptional activities of P- TEFb in vivo and in vitro by inhibiting the kinase activity of CDK9 and preventing recruitment of P- TEFb to the HIV- 1 promoter. 7SK is efficiently dissociated from P- TEFb (the CDK9/cyclin T1 heterodimer) by treat-

ment of cells with ultraviolet irradiation and actinomycin D. As these 2 agents have been shown to enhance significantly HIV- 1 transcription and phosphorylation of Pol- II, Yang et al. (2001) concluded that their data provide a mechanistic explanation for this stimulatory effect. Yang et al. (2001) further suggested that the 7SK/P- TEFb interaction may serve as a principal control point for the induction of cellular and HIV- 1 viral gene expression during stress- related responses. The study demonstrated the involvement of an snRNA in controlling the activity of CDK/cyclin kinase.

[26792]

[26793] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26794] Peng, J.; Zhu, Y.; Milton, J. T.; Price, D. H. : Identification of multiple cyclin subunits of human P- TEFb. Genes Dev. 12: 755- 762, 1998. ; and

[26795] Yang, Z.; Zhu, Q.; Luo, K.; Zhou, Q. : The 7SK small nuclear RNA inhibits the CDK9/cyclin T1 kinase to control transcription. Nature 414: 317- 322, 2001.

[26796] Further studies establishing the function and utilities of CCNT2 are found in John Hopkins OMIM database record

ID 603862, and in cited publications listed in Table 5, which are hereby incorporated by reference.Cytidine deaminase (CDA, Accession NP_001776.1) is another GAM179 target gene, herein designated TARGET GENE. CDA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDA BINDING SITE, designated SEQ ID:17937, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26797] Another function of GAM179 is therefore inhibition of Cytidine deaminase (CDA, Accession NP_001776.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDA.

[26798] Cysteine-rich protein 1 (intestinal) (CRIP1, Accession NP_001302.1) is another GAM179 target gene, herein designated TARGET GENE. CRIP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRIP1 BINDING SITE, designated SEQ ID:12094, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26799] Another function of GAM179 is therefore inhibition of Cysteine-rich protein 1 (intestinal) (CRIP1, Accession NP_001302.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRIP1.

[26800] DKFZP434P211 (Accession NP_055364.1) is another GAM179 target gene, herein designated TARGET GENE. DKFZP434P211 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434P211, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434P211 BINDING SITE, designated SEQ ID:12743, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26801] Another function of GAM179 is therefore inhibition of DKFZP434P211 (Accession NP_055364.1) . Accordingly, utili-

ties of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434P211.

[26802] DKFZp762E1312 (Accession NP_060880.2) is another GAM179 target gene, herein designated TARGET GENE. DKFZp762E1312 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp762E1312, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762E1312 BINDING SITE, designated SEQ ID:9021, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26803] Another function of GAM179 is therefore inhibition of DKFZp762E1312 (Accession NP_060880.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762E1312.

[26804] DKFZP762N2316 (Accession XP_040560.4) is another GAM179 target gene, herein designated TARGET GENE. DKFZP762N2316 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts

of mRNA encoded by DKFZP762N2316, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP762N2316 BINDING SITE, designated SEQ ID:10781, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26805] Another function of GAM179 is therefore inhibition of DKFZP762N2316 (Accession XP_040560.4) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP762N2316.

[26806] Dynein, axonemal, light polypeptide 4 (DNAL4, Accession NP_005731.1) is another GAM179 target gene, herein designated TARGET GENE. DNAL4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DNAL4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DNAL4 BINDING SITE, designated SEQ ID:2920, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26807] Another function of GAM179 is therefore inhibition of

Dynein, axonemal, light polypeptide 4 (DNAL4, Accession NP_005731.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAL4.

[26808] Deoxynucleotidyltransferase, terminal (DNTT, Accession NP_004079.2) is another GAM179 target gene, herein designated TARGET GENE. DNTT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DNTT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DNTT BINDING SITE, designated SEQ ID:13119, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26809] Another function of GAM179 is therefore inhibition of Deoxynucleotidyltransferase, terminal (DNTT, Accession NP_004079.2), a gene which is terminal deoxynucleotidyl transferase. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNTT.

[26810] The function of DNTT and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM129.1.Docking protein 4 (DOK4, Accession NP_060580.2) is another GAM179 target gene, herein designated TARGET GENE. DOK4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DOK4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DOK4 BINDING SITE, designated SEQ ID:15066, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26811] Another function of GAM179 is therefore inhibition of Docking protein 4 (DOK4, Accession NP_060580.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DOK4.

[26812] Down syndrome critical region gene 1 (DSCR1, Accession NP_004405.2) is another GAM179 target gene, herein designated TARGET GENE. DSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSCR1 BINDING SITE, designated SEQ ID:18056, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26813] Another function of GAM179 is therefore inhibition of Down syndrome critical region gene 1 (DSCR1, Accession NP_004405.2), a gene which inhibits calcineurin- dependent transcriptional responses. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSCR1.

[26814] The function of DSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Ectodermal dysplasia 1, anhidrotic (ED1, Accession NP_001390.1) is another GAM179 target gene, herein designated TARGET GENE. ED1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ED1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ED1 BINDING SITE, designated SEQ ID:7504, to the nucleotide sequence of

GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26815] Another function of GAM179 is therefore inhibition of Ectodermal dysplasia 1, anhidrotic (ED1, Accession NP_001390.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ED1.

[26816] Fibulin 1 (FBLN1, Accession NP_006476.1) is another GAM179 target gene, herein designated TARGET GENE. FBLN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBLN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBLN1 BINDING SITE, designated SEQ ID:9477, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26817] Another function of GAM179 is therefore inhibition of Fibulin 1 (FBLN1, Accession NP_006476.1), a gene which secreted glycoprotein; has EGF- like repeats, similar to anaphylatoxins C3a, C4a, and C5a. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBLN1.

[26818] The function of FBLN1 has been established by previous studies. Fibulin- 1 was first described as an integrin-binding fibulin from human placenta by Argraves et al. (1989), who found that it is a secreted glycoprotein that becomes incorporated into a fibrillar extracellular matrix when expressed in cultured cells or added exogenously to cell monolayers. Preliminary electron microscopic data suggested a rod- like structure for fibulin- 1, consistent with the sequence predictions. Calcium- binding to fibulin- 1 is apparently required to mediate its binding to laminin and nidogen (OMIM Ref. No. 131390). By in situ hybridization of tritium- labeled cDNA probes, Mattei et al. (1994) assigned the human FBLN1 gene to 22q13.2-q13.3 and assigned its counterpart in mouse to the E- F band of chromosome 15. Korenberg et al. (1995) assigned the FBLN1 gene to 22q13.3 by fluorescence in situ hybridization.

[26819]

[26820] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26821] Korenberg, J. R.; Chen, X.- N.; Tran, H.; Argraves, W. S. : Localization of the human gene for fibulin- 1 (FBLN1) to

chromosome band 22q13.3. Cytogenet. Cell Genet. 68: 192- 193, 1995. ; and

[26822] Mattei, M.- G.; Pan, T.- C.; Zhang, R.- Z.; Timpl, R.; Chu, M.- L. : The fibulin- 1 gene (FBLN1) is located on human chromosome 22 and on mouse chromosome 15. Genomics 22: 437- 438, 1994.

[26823] Further studies establishing the function and utilities of FBLN1 are found in John Hopkins OMIM database record ID 135820, and in cited publications listed in Table 5, which are hereby incorporated by reference.FLJ10116 (Accession NP_060470.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ10116 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10116, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10116 BINDING SITE, designated SEQ ID:18159, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26824] Another function of GAM179 is therefore inhibition of FLJ10116 (Accession NP_060470.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ10116.

[26825] FLJ10307 (Accession NP_060523.2) is another GAM179 target gene, herein designated TARGET GENE. FLJ10307 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10307, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10307 BINDING SITE, designated SEQ ID:16190, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26826] Another function of GAM179 is therefore inhibition of FLJ10307 (Accession NP_060523.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10307.

[26827] FLJ10462 (Accession NP_060569.3) is another GAM179 target gene, herein designated TARGET GENE. FLJ10462 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10462, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ10462 BINDING SITE, designated SEQ ID:9026, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26828] Another function of GAM179 is therefore inhibition of FLJ10462 (Accession NP_060569.3) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10462.

[26829] FLJ13215 (Accession NP_079280.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ13215 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13215, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13215 BINDING SITE, designated SEQ ID:11648, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26830] Another function of GAM179 is therefore inhibition of FLJ13215 (Accession NP_079280.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ13215.

[26831] FLJ13615 (Accession NP_079390.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ13615 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13615, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13615 BINDING SITE, designated SEQ ID:10037, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26832] Another function of GAM179 is therefore inhibition of FLJ13615 (Accession NP_079390.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13615.

[26833] FLJ13782 (Accession NP_079191.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ13782 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13782, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ13782 BINDING SITE, designated SEQ ID:9784, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26834] Another function of GAM179 is therefore inhibition of FLJ13782 (Accession NP_079191.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13782.

[26835] FLJ13841 (Accession NP_078978.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ13841 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13841, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13841 BINDING SITE, designated SEQ ID:15474, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26836] Another function of GAM179 is therefore inhibition of FLJ13841 (Accession NP_078978.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13841.

[26837] FLJ20574 (Accession NP_060356.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ20574 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20574, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20574 BINDING SITE, designated SEQ ID:6230, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26838] Another function of GAM179 is therefore inhibition of FLJ20574 (Accession NP_060356.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20574.

[26839] FLJ21870 (Accession NP_075392.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ21870 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21870, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21870 BINDING SITE, designated SEQ ID:4419, to the

nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26840] Another function of GAM179 is therefore inhibition of FLJ21870 (Accession NP_075392.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21870.

[26841] FLJ31300 (Accession NP_653240.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ31300 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31300, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31300 BINDING SITE, designated SEQ ID:792, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26842] Another function of GAM179 is therefore inhibition of FLJ31300 (Accession NP_653240.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31300.

[26843] FLJ32934 (Accession NP_653223.1) is another GAM179

target gene, herein designated TARGET GENE. FLJ32934 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32934, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32934 BINDING SITE, designated SEQ ID:19512, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26844] Another function of GAM179 is therefore inhibition of FLJ32934 (Accession NP_653223.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32934.

[26845] FLJ36000 (Accession NP_787101.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ36000 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36000, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36000 BINDING SITE, designated SEQ ID:6917, to the nucleotide sequence of GAM179 RNA, herein designated

GAM RNA, also designated SEQ ID:300.

[26846] Another function of GAM179 is therefore inhibition of FLJ36000 (Accession NP_787101.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36000.

[26847] FLJ38607 (Accession NP_689867.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ38607 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38607, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38607 BINDING SITE, designated SEQ ID:8910, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26848] Another function of GAM179 is therefore inhibition of FLJ38607 (Accession NP_689867.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38607.

[26849] FLJ39005 (Accession NP_848616.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ39005

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39005, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39005 BINDING SITE, designated SEQ ID:11931, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26850] Another function of GAM179 is therefore inhibition of FLJ39005 (Accession NP_848616.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39005.

[26851] FLJ90798 (Accession NP_699198.1) is another GAM179 target gene, herein designated TARGET GENE. FLJ90798 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90798, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90798 BINDING SITE, designated SEQ ID:660, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26852] Another function of GAM179 is therefore inhibition of FLJ90798 (Accession NP_699198.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90798.

[26853] G protein-coupled receptor 48 (GPR48, Accession NP_060960.1) is another GAM179 target gene, herein designated TARGET GENE. GPR48 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR48, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR48 BINDING SITE, designated SEQ ID:14773, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26854] Another function of GAM179 is therefore inhibition of G protein-coupled receptor 48 (GPR48, Accession NP_060960.1), a gene which binds to follicle- stimulating hormone and thyroid- stimulating hormone. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR48.

[26855] The function of GPR48 has been established by previous studies. By EST database searching with known GPCRs as queries, Hsu et al. (1998) identified ESTs encoding transmembrane domains 4 and 5 of human GPR48, which they called LGR4. By RT- PCR and repeated screening of a rat ovary cDNA library, they isolated a full- length cDNA encoding rat Lgr4. Sequence analysis predicted that the 951- amino acid rat Lgr4 protein contains a signal peptide; N- and C- flanking cysteine- rich sequences separated by 17 LRRs; 5 potential N- glycosylation sites; a transmembrane region; and a 145- residue cytoplasmic tail with multiple phosphorylation sites and a conserved potential protein kinase A (see OMIM Ref. No. 176911) phosphorylation site. Northern blot analysis of human tissues detected a 5.5- kb LGR4 transcript in multiple steroidogenic tissues and in a number of other tissues. Functional analysis showed that expression of a chimeric receptor composed of the extracellular domain of luteinizing hormone receptor (OMIM Ref. No. 152790) with the transmembrane and cytoplasmic domains of Lgr4 resulted in binding of hCG (OMIM Ref. No. 118860) but no increase in basal production of cAMP, suggesting that LGR4 may signal through another mechanism. Loh et al.

(2001) cloned human GPR48. Like rat Lgr4, the deduced human GPR48 protein has 951 amino acids and a similar structure. Northern blot analysis detected wide expression of GPR48 that was highest in pancreas. Within brain, highest expression of GPR48 was in hippocampus and amygdala. Expression of Gpr48 in mouse embryos occurred as early as embryonic day 7 and peaked at day 15.

[26856]

[26857] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26858] Hsu, S. Y.; Liang, S.- G.; Hsueh, A. J. W. : Characterization of two LGR genes homologous to gonadotropin and thyrotropin receptors with extracellular leucine- rich repeats and a G protein- coupled, seven- transmembrane region. Molec. Endocr. 12: 1830- 1845, 1998. ; and

[26859] Loh, E. D.; Broussard, S. R.; Kolakowski, L. F. : Molecular characterization of a novel glycoprotein hormone G- protein- coupled receptor. Biochem. Biophys. Res. Commun. 282: 757- 764, 2001.

[26860] Further studies establishing the function and utilities of GPR48 are found in John Hopkins OMIM database record ID 606666, and in cited publications listed in Table 5,

which are hereby incorporated by reference.Grip1 associated protein 1 (GRIPAP1, Accession NP_064522.2) is another GAM179 target gene, herein designated TARGET GENE. GRIPAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRIPAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRIPAP1 BINDING SITE, designated SEQ ID:19328, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26861] Another function of GAM179 is therefore inhibition of Grip1 associated protein 1 (GRIPAP1, Accession NP_064522.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIPAP1.

[26862] Hyaluronan binding protein 2 (HABP2, Accession NP_004123.1) is another GAM179 target gene, herein designated TARGET GENE. HABP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HABP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HABP2 BINDING SITE, designated SEQ ID:17826, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26863] Another function of GAM179 is therefore inhibition of Hyaluronan binding protein 2 (HABP2, Accession NP_004123.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HABP2.

[26864] Interleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NP_004504.3) is another GAM179 target gene, herein designated TARGET GENE. IL16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL16 BINDING SITE, designated SEQ ID:9723, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26865] Another function of GAM179 is therefore inhibition of Interleukin 16 (lymphocyte chemoattractant factor) (IL16,

Accession NP_004504.3), a gene which modulates T- cell activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL16.

[26866] The function of IL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Interleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NP_757366.1) is another GAM179 target gene, herein designated TARGET GENE. IL16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL16 BINDING SITE, designated SEQ ID:9723, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26867] Another function of GAM179 is therefore inhibition of Interleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NP_757366.1), a gene which modulates T- cell activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical

conditions associated with IL16.

[26868] The function of IL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Interleukin 1, beta (IL1B, Accession NP_000567.1) is another GAM179 target gene, herein designated TARGET GENE. IL1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL1B BINDING SITE, designated SEQ ID:4722, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26869] Another function of GAM179 is therefore inhibition of Interleukin 1, beta (IL1B, Accession NP_000567.1), a gene which stimulates thymocyte proliferation. and therefore may be associated with Gastric cancer risk after h. pylori infection. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of Gastric cancer risk after h. pylori infection, and of other diseases and clinical conditions associated with IL1B.

[26870] The function of IL1B has been established by previous

studies. Interleukin- 1, produced mainly by blood monocytes, mediates the panoply of host reactions collectively known as acute phase response. It is identical to endogenous pyrogen. The multiple biologic activities that define IL1 are properties of a 15- to 18- kD protein that is derived from a 30- to 35- kD precursor. El- Omar et al. (2000) reported that interleukin- 1 gene cluster polymorphisms suspected of enhancing production of interleukin-1- beta are associated with an increased risk of both hypochlorhydria induced by Helicobacter pylori and gastric cancer. Two of these polymorphisms are in near-complete linkage disequilibrium, and 1 is a TATA- box polymorphism that markedly affects DNA- protein interactions in vitro. The association with disease may be explained by the biologic properties of interleukin- 1- beta, which is an important proinflammatory cytokine and a powerful inhibitor of gastric acid secretion. Host genetic factors that affect interleukin- 1- beta may determine why some individuals infected with H. pylori develop gastric cancer while others do not. IL1- beta is upregulated in the presence of H. pylori and is important in initiating and amplifying the inflammatory response to this infection. Three diallelic polymorphisms in IL1B have been reported,

all representing C- to- T base transitions, at positions - 511, - 31, and +3954 basepairs from the transcriptional start site. To determine whether these polymorphisms are important with respect to different outcomes of H. pylori infections, El- Omar et al. (2000) studied their effects on gastric physiology in healthy subjects. Carriers of the ILB - 31T allele (147720.0001) had an age- adjusted odds ratio of 9.1 (95% confidence interval, 2.2- 37) for low acid secretion, and there was little difference between homozygous and heterozygous carriers. The IL1B +3954 genotype was not associated with the risk of hypochlorhydria. Carriers of IL1B - 31T had an increased gastric cancer risk at an odds ratio of 1.9 (95% confidence interval, 1.5- 2.6), with no significant difference between homozygotes and heterozygotes Hamajima et al. (2001) determined that the C- to- T transition at position - 31, creating a TATA box, is associated with vulnerability to persistent H. pylori infection, and that the susceptibility is modified by smoking

[26871] Animal model experiments lend further support to the function of IL1B. Mature IL1- beta levels are a sensitive and specific indicator of caspase- 1 (OMIM Ref. No. 147678) activation. Ona et al. (1999) studied the effect of inhibition of caspase- 1 on the progression of Huntington

disease (OMIM Ref. No. 143100) in the mouse model developed by Mangiarini et al. (1996), which they called R6/2 mice. Ona et al. (1999) crossed R6/2 mice with a well- characterized transgenic mouse strain expressing a dominant- negative mutant of caspase- 1 in the brain (NSE M17Z). Double mutant mice showed extended survival and delayed appearance of neuronal inclusions, neurotransmitter receptor alterations, and onset of symptoms, indicating that caspase- 1 is important in the pathogenesis of Huntington disease. Mature IL1- beta levels in R6/2 mice were elevated to 268% of those in wild-type controls. This increase was significantly inhibited in the R6/2- NSE M17Z mice. IL1- beta levels in the brains of human patients also exhibited significant increases, to 213% of those in normal controls

[26872] It is appreciated that the abovementioned animal model for IL1B is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[26873] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26874] El- Omar, E. M.; Carrington, M.; Chow, W.- H.; McColl, K.

E. L.; Bream, J. H.; Young, H. A.; Herrera, J.; Lissowska, J.; Yuan, C.- C.; Rothman, N.; Lanyon, G.; Martin, M.; Fraumeni, J. F., Jr.; Rabkin, C. S. : Interleukin- 1 polymorphisms associated with increased risk of gastric cancer. Nature 404: 398- 402, 2000. Note: Erratum: Nature 412: 99 only, 2001. ; and

[26875] Ona, V. O.; Li, M.; Vonsattel, J. P. G.; Andrews, L. J.; Khan, S. Q.; Chung, W. M.; Frey, A. S.; Menon, A. S.; Li, X.- J.; Stieg, P. E.; Yuan, J.; Penney, J. B.; Young, A. B.; Cha, J.- H.

[26876] Further studies establishing the function and utilities of IL1B are found in John Hopkins OMIM database record ID 147720, and in cited publications listed in Table 5, which are hereby incorporated by reference.Iq motif containing gtpase activating protein 1 (IQGAP1, Accession NP_003861.1) is another GAM179 target gene, herein designated TARGET GENE. IQGAP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IQGAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IQGAP1 BINDING SITE, designated SEQ ID:17358, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA,

also designated SEQ ID:300.

[26877] Another function of GAM179 is therefore inhibition of Iq motif containing gtpase activating protein 1 (IQGAP1, Accession NP_003861.1), a gene which inhibits GTPase activity of ras family of GTP binding proteins Cdc42Hs and rac. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IQGAP1.

[26878] The function of IQGAP1 has been established by previous studies. Sugimoto et al. (2001) demonstrated that IQGAP1, a negative regulator of cell- cell adhesion, is upregulated by gene amplification at 15q26 in 2 gastric cancer cell lines. Amplification at 15q26 had been found in various malignancies, including breast cancers, and FES (OMIM Ref. No. 190030) and/or IGF1R (OMIM Ref. No. 147370) had been identified as targets for gene amplification in breast cancer, melanoma, and pancreatic adenocarcinoma. In contrast, Sugimoto et al. (2001) found that both genes are located telomeric to the amplicon at 15q26 in the 2 gastric cancer cell lines they studied. Fukata et al. (2002) found that IQGAP1, an effector of RAC1 (OMIM Ref. No. 602048) and CDC42, interacts with CLIP170 (RSN; 179838). In Vero fibroblasts, IQGAP1 local-

ized at the polarized leading edge. Expression of a C- terminal fragment of IQGAP1 that included the CLIP170-binding region delocalized GFP- CLIP170 from the tips of microtubules and altered the microtubule array. The authors found that activated RAC1/CDC42, IQGAP1, and CLIP170 form a tripartite complex. Furthermore, expression of an IQGAP1 mutant defective in RAC1/CDC42 binding induced multiple leading edges. These results indicated that RAC1/CDC42 marks special cortical spots where the IQGAP1 and CLIP170 complex is targeted, leading to a polarized microtubule array and cell polarization

[26879]

[26880] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26881] Fukata, M.; Watanabe, T.; Noritake, J.; Nakagawa, M.; Yamaga, M.; Kuroda, S.; Matsuura, Y.; Iwamatsu, A.; Perez, F.; Kaibuchi, K. : Rac1 and Cdc42 capture microtubules through IQGAP1 and CLIP- 170. Cell 109: 873- 885, 2002. ; and

[26882] Hart, M. J.; Callow, M. G.; Souza, B.; Polakis, P. : IQGAP1, a calmodulin- binding protein with a rasGAP- related domain, is a potential effector for cdc42Hs. EMBO J. 15:

2997- 3005, 1996.

[26883] Further studies establishing the function and utilities of IQGAP1 are found in John Hopkins OMIM database record ID 603379, and in cited publications listed in Table 5, which are hereby incorporated by reference.Potassium channel, subfamily k, member 4 (KCNK4, Accession NP_201567.1) is another GAM179 target gene, herein designated TARGET GENE. KCNK4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNK4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNK4 BINDING SITE, designated SEQ ID:3257, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26884] Another function of GAM179 is therefore inhibition of Potassium channel, subfamily k, member 4 (KCNK4, Accession NP_201567.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK4.

[26885] Potassium channel, subfamily k, member 4 (KCNK4, Accession NP_057695.2) is another GAM179 target gene,

herein designated TARGET GENE. KCNK4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNK4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNK4 BINDING SITE, designated SEQ ID:3257, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26886] Another function of GAM179 is therefore inhibition of Potassium channel, subfamily k, member 4 (KCNK4, Accession NP_057695.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK4.

[26887] Potassium channel, subfamily k, member 4 (KCNK4, Accession NP_201568.1) is another GAM179 target gene, herein designated TARGET GENE. KCNK4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNK4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNK4 BINDING SITE, designated SEQ ID:3257, to the nu-

cleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26888] Another function of GAM179 is therefore inhibition of Potassium channel, subfamily k, member 4 (KCNK4, Accession NP_201568.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK4.

[26889] KIAA0286 (Accession XP_043118.3) is another GAM179 target gene, herein designated TARGET GENE. KIAA0286 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0286, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0286 BINDING SITE, designated SEQ ID:12582, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26890] Another function of GAM179 is therefore inhibition of KIAA0286 (Accession XP_043118.3) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0286.

[26891] KIAA1170 (Accession XP_045907.2) is another GAM179

target gene, herein designated TARGET GENE. KIAA1170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1170 BINDING SITE, designated SEQ ID:14096, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26892] Another function of GAM179 is therefore inhibition of KIAA1170 (Accession XP_045907.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1170.

[26893] LAK (Accession NP_079420.2) is another GAM179 target gene, herein designated TARGET GENE. LAK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAK BINDING SITE, designated SEQ ID:9362, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:300.

[26894] Another function of GAM179 is therefore inhibition of LAK (Accession NP_079420.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAK.

[26895] LOC120105 (Accession XP_061864.2) is another GAM179 target gene, herein designated TARGET GENE. LOC120105 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC120105, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC120105 BINDING SITE, designated SEQ ID:12997, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26896] Another function of GAM179 is therefore inhibition of LOC120105 (Accession XP_061864.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120105.

[26897] LOC125058 (Accession XP_008617.5) is another GAM179 target gene, herein designated TARGET GENE. LOC125058 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC125058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC125058 BINDING SITE, designated SEQ ID:10141, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26898] Another function of GAM179 is therefore inhibition of LOC125058 (Accession XP_008617.5) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125058.

[26899] LOC133926 (Accession XP_059674.1) is another GAM179 target gene, herein designated TARGET GENE. LOC133926 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC133926, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC133926 BINDING SITE, designated SEQ ID:16799, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26900] Another function of GAM179 is therefore inhibition of

LOC133926 (Accession XP_059674.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133926.

[26901] LOC143188 (Accession XP_096387.1) is another GAM179 target gene, herein designated TARGET GENE. LOC143188 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC143188, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143188 BINDING SITE, designated SEQ ID:8192, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26902] Another function of GAM179 is therefore inhibition of LOC143188 (Accession XP_096387.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143188.

[26903] LOC145098 (Accession XP_085022.1) is another GAM179 target gene, herein designated TARGET GENE. LOC145098 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145098, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145098 BINDING SITE, designated SEQ ID:13315, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26904] Another function of GAM179 is therefore inhibition of LOC145098 (Accession XP_085022.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145098.

[26905] LOC148894 (Accession XP_097542.1) is another GAM179 target gene, herein designated TARGET GENE. LOC148894 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148894 BINDING SITE, designated SEQ ID:3771, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26906] Another function of GAM179 is therefore inhibition of LOC148894 (Accession XP_097542.1) . Accordingly, utili-

ties of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148894.

[26907] LOC149837 (Accession XP_097747.1) is another GAM179 target gene, herein designated TARGET GENE. LOC149837 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149837, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149837 BINDING SITE, designated SEQ ID:4055, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26908] Another function of GAM179 is therefore inhibition of LOC149837 (Accession XP_097747.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149837.

[26909] LOC150174 (Accession XP_086802.2) is another GAM179 target gene, herein designated TARGET GENE. LOC150174 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150174, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150174 BINDING SITE, designated SEQ ID:12743, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26910] Another function of GAM179 is therefore inhibition of LOC150174 (Accession XP_086802.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150174.

[26911] LOC150213 (Accession XP_059324.1) is another GAM179 target gene, herein designated TARGET GENE. LOC150213 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150213, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150213 BINDING SITE, designated SEQ ID:12743, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26912] Another function of GAM179 is therefore inhibition of LOC150213 (Accession XP_059324.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC150213.

[26913] LOC151171 (Accession XP_087116.1) is another GAM179 target gene, herein designated TARGET GENE. LOC151171 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151171, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151171 BINDING SITE, designated SEQ ID:7338, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26914] Another function of GAM179 is therefore inhibition of LOC151171 (Accession XP_087116.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151171.

[26915] LOC157556 (Accession XP_098783.1) is another GAM179 target gene, herein designated TARGET GENE. LOC157556 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC157556, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC157556 BINDING SITE, designated SEQ ID:18978, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26916] Another function of GAM179 is therefore inhibition of LOC157556 (Accession XP_098783.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157556.

[26917] LOC220980 (Accession XP_167629.1) is another GAM179 target gene, herein designated TARGET GENE. LOC220980 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC220980, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220980 BINDING SITE, designated SEQ ID:3721, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26918] Another function of GAM179 is therefore inhibition of LOC220980 (Accession XP_167629.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC220980.

[26919] LOC221140 (Accession XP_167908.1) is another GAM179 target gene, herein designated TARGET GENE. LOC221140 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221140 BINDING SITE, designated SEQ ID:3664, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26920] Another function of GAM179 is therefore inhibition of LOC221140 (Accession XP_167908.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221140.

[26921] LOC255736 (Accession XP_170898.2) is another GAM179 target gene, herein designated TARGET GENE. LOC255736 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255736, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC255736 BINDING SITE, designated SEQ ID:14351, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26922] Another function of GAM179 is therefore inhibition of LOC255736 (Accession XP_170898.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255736.

[26923] LOC283016 (Accession XP_208024.1) is another GAM179 target gene, herein designated TARGET GENE. LOC283016 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283016, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283016 BINDING SITE, designated SEQ ID:758, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26924] Another function of GAM179 is therefore inhibition of LOC283016 (Accession XP_208024.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283016.

[26925] LOC283048 (Accession XP_210867.1) is another GAM179 target gene, herein designated TARGET GENE. LOC283048 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283048, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283048 BINDING SITE, designated SEQ ID:15999, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26926] Another function of GAM179 is therefore inhibition of LOC283048 (Accession XP_210867.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283048.

[26927] LOC283168 (Accession XP_210910.1) is another GAM179 target gene, herein designated TARGET GENE. LOC283168 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283168, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283168 BINDING SITE, designated SEQ ID:5476, to

the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26928] Another function of GAM179 is therefore inhibition of LOC283168 (Accession XP_210910.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283168.

[26929] LOC283177 (Accession XP_210903.1) is another GAM179 target gene, herein designated TARGET GENE. LOC283177 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283177 BINDING SITE, designated SEQ ID:2829, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26930] Another function of GAM179 is therefore inhibition of LOC283177 (Accession XP_210903.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283177.

[26931] LOC284124 (Accession XP_294862.1) is another GAM179

target gene, herein designated TARGET GENE. LOC284124 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284124, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284124 BINDING SITE, designated SEQ ID:6917, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26932] Another function of GAM179 is therefore inhibition of LOC284124 (Accession XP_294862.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284124.

[26933] LOC284313 (Accession XP_209116.1) is another GAM179 target gene, herein designated TARGET GENE. LOC284313 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284313, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284313 BINDING SITE, designated SEQ ID:11931, to the nucleotide sequence of GAM179 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:300.

[26934] Another function of GAM179 is therefore inhibition of LOC284313 (Accession XP_209116.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284313.

[26935] LOC284911 (Accession XP_211684.1) is another GAM179 target gene, herein designated TARGET GENE. LOC284911 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284911, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284911 BINDING SITE, designated SEQ ID:9507, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26936] Another function of GAM179 is therefore inhibition of LOC284911 (Accession XP_211684.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284911.

[26937] LOC285193 (Accession XP_209509.1) is another GAM179 target gene, herein designated TARGET GENE. LOC285193

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285193, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285193 BINDING SITE, designated SEQ ID:4970, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26938] Another function of GAM179 is therefore inhibition of LOC285193 (Accession XP_209509.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285193.

[26939] LOC285334 (Accession XP_211844.1) is another GAM179 target gene, herein designated TARGET GENE. LOC285334 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285334 BINDING SITE, designated SEQ ID:800, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26940] Another function of GAM179 is therefore inhibition of LOC285334 (Accession XP_211844.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285334.

[26941] LOC285412 (Accession XP_208319.1) is another GAM179 target gene, herein designated TARGET GENE. LOC285412 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285412, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285412 BINDING SITE, designated SEQ ID:17899, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26942] Another function of GAM179 is therefore inhibition of LOC285412 (Accession XP_208319.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285412.

[26943] LOC285431 (Accession XP_211898.1) is another GAM179 target gene, herein designated TARGET GENE. LOC285431 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC285431, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285431 BINDING SITE, designated SEQ ID:7608, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26944] Another function of GAM179 is therefore inhibition of LOC285431 (Accession XP_211898.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285431.

[26945] LOC285735 (Accession XP_212002.1) is another GAM179 target gene, herein designated TARGET GENE. LOC285735 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285735 BINDING SITE, designated SEQ ID:5912, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26946] Another function of GAM179 is therefore inhibition of

LOC285735 (Accession XP_212002.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285735.

[26947] LOC285827 (Accession XP_212038.1) is another GAM179 target gene, herein designated TARGET GENE. LOC285827 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC285827, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285827 BINDING SITE, designated SEQ ID:13258, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26948] Another function of GAM179 is therefore inhibition of LOC285827 (Accession XP_212038.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285827.

[26949] LOC285827 (Accession XP_212645.1) is another GAM179 target gene, herein designated TARGET GENE. LOC285827 BINDING SITE is a target binding site found in the 5` un-

translated region of multiple transcripts of mRNA encoded by LOC285827, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285827 BINDING SITE, designated SEQ ID:13258, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26950] Another function of GAM179 is therefore inhibition of LOC285827 (Accession XP_212645.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285827.

[26951] LOC285827 (Accession XP_212604.1) is another GAM179 target gene, herein designated TARGET GENE. LOC285827 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC285827, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285827 BINDING SITE, designated SEQ ID:13258, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:300.

[26952] Another function of GAM179 is therefore inhibition of LOC285827 (Accession XP_212604.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285827.

[26953] LOC285931 (Accession NP_777609.1) is another GAM179 target gene, herein designated TARGET GENE. LOC285931 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285931, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285931 BINDING SITE, designated SEQ ID:17124, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26954] Another function of GAM179 is therefore inhibition of LOC285931 (Accession NP_777609.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285931.

[26955] LOC286058 (Accession XP_212158.1) is another GAM179 target gene, herein designated TARGET GENE. LOC286058

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286058 BINDING SITE, designated SEQ ID:17023, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26956] Another function of GAM179 is therefore inhibition of LOC286058 (Accession XP_212158.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286058.

[26957] LOC339808 (Accession XP_295071.1) is another GAM179 target gene, herein designated TARGET GENE. LOC339808 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339808, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339808 BINDING SITE, designated SEQ ID:12230, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26958] Another function of GAM179 is therefore inhibition of LOC339808 (Accession XP_295071.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339808.

[26959] LOC346259 (Accession XP_299387.1) is another GAM179 target gene, herein designated TARGET GENE. LOC346259 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC346259, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC346259 BINDING SITE, designated SEQ ID:16628, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26960] Another function of GAM179 is therefore inhibition of LOC346259 (Accession XP_299387.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC346259.

[26961] LOC347767 (Accession XP_300531.1) is another GAM179 target gene, herein designated TARGET GENE. LOC347767 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC347767, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347767 BINDING SITE, designated SEQ ID:13207, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26962] Another function of GAM179 is therefore inhibition of LOC347767 (Accession XP_300531.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347767.

[26963] LOC348155 (Accession XP_211219.1) is another GAM179 target gene, herein designated TARGET GENE. LOC348155 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348155, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348155 BINDING SITE, designated SEQ ID:12472, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26964] Another function of GAM179 is therefore inhibition of

LOC348155 (Accession XP_211219.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348155.

[26965] LOC348182 (Accession XP_302676.1) is another GAM179 target gene, herein designated TARGET GENE. LOC348182 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348182, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348182 BINDING SITE, designated SEQ ID:15435, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26966] Another function of GAM179 is therefore inhibition of LOC348182 (Accession XP_302676.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348182.

[26967] LOC348371 (Accession XP_300722.1) is another GAM179 target gene, herein designated TARGET GENE. LOC348371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348371, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348371 BINDING SITE, designated SEQ ID:3641, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26968] Another function of GAM179 is therefore inhibition of LOC348371 (Accession XP_300722.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348371.

[26969] LOC348488 (Accession XP_300352.1) is another GAM179 target gene, herein designated TARGET GENE. LOC348488 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348488, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348488 BINDING SITE, designated SEQ ID:8278, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26970] Another function of GAM179 is therefore inhibition of LOC348488 (Accession XP_300352.1) . Accordingly, utili-

ties of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348488.

[26971] LOC349384 (Accession XP_301935.1) is another GAM179 target gene, herein designated TARGET GENE. LOC349384 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349384, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349384 BINDING SITE, designated SEQ ID:10985, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26972] Another function of GAM179 is therefore inhibition of LOC349384 (Accession XP_301935.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349384.

[26973] Mitogen-activated protein kinase 4 (MAPK4, Accession NP_002738.1) is another GAM179 target gene, herein designated TARGET GENE. MAPK4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MAPK4, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPK4 BINDING SITE, designated SEQ ID:11406, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26974] Another function of GAM179 is therefore inhibition of Mitogen-activated protein kinase 4 (MAPK4, Accession NP_002738.1), a gene which phosphorylates microtubule-associated protein- 2 may promote entry into the cell cycle. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK4.

[26975] The function of MAPK4 has been established by previous studies. See MAPK1 (OMIM Ref. No. 176948). Gonzalez et al. (1992) reported the molecular cloning of genes for 4 human proteins with high homology to members of the mitogen- activated protein kinase group of enzymes. Of the 4, 2 probably resulted from alternative processing of transcripts from a single gene. Zhu et al. (1994) stated that p63MAPK, which had been known as ERK3, shares only 73% protein sequence identity with rat ERK3. They suggested that p97MAPK (MAPK6; 602904) is the true

ERK3 homolog, and that p63MAPK is a member of the ERK3 subfamily. Garcia et al. (1996) reported that a gene they referred to as MNK2 is the rat homolog of p63MAPK. The 2 protein sequences are 95% identical. Li et al. (1994) used Southern blotting of DNA from a panel of human hamster cell hybrids and fluorescence in situ hybridization to map the MAPK4 gene to 18q12- q21

[26976]

[26977] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[26978] Garcia, J. I.; Zalba, G.; Detera- Wadleigh, S. D.; de Miguel, C. : Isolation of a cDNA encoding the rat MAP- kinase homolog of human p63mapk. Mammalian Genome 7: 810-814, 1996. ; and

[26979] Li, L.; Wysk, M.; Gonzalez, F. A.; Davis, R. J. : Genomic loci of human mitogen- activated protein kinases. Oncogene 9: 647- 649, 1994.

[26980] Further studies establishing the function and utilities of MAPK4 are found in John Hopkins OMIM database record ID 176949, and in cited publications listed in Table 5, which are hereby incorporated by reference.MBNL1 (Accession NP_066368.1) is another GAM179 target gene,

herein designated TARGET GENE. MBNL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MBNL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MBNL1 BINDING SITE, designated SEQ ID:12912, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26981] Another function of GAM179 is therefore inhibition of MBNL1 (Accession NP_066368.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBNL1.

[26982] Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758866.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide

sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26983] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758866.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[26984] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_722548.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated

GAM RNA, also designated SEQ ID:300.

[26985] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_722548.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[26986] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758868.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26987] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758868.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[26988] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758865.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26989] Another function of GAM179 is therefore inhibition of

Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758865.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[26990] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758867.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26991] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lympho-

cyte cross-reactive antigen) (MCP, Accession NP_758867.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[26992] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758860.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26993] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession

NP_758860.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[26994] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758871.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26995] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758871.1), a gene which may be involved in the regu-

lation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[26996] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758870.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26997] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758870.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of

GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[26998] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758864.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[26999] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758864.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with MCP.

[27000] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758861.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27001] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758861.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[27002] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758863.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27003] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758863.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[27004] The function of MCP and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758862.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27005] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758862.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[27006] The function of MCP and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_002380.3) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27007] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_002380.3), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[27008] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM63.1.Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758869.1) is another GAM179 target gene, herein designated TARGET GENE. MCP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MCP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCP BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27009] Another function of GAM179 is therefore inhibition of Membrane cofactor protein (cd46, trophoblast-lymphocyte cross-reactive antigen) (MCP, Accession NP_758869.1), a gene which may be involved in the regulation of complement activation. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCP.

[27010] The function of MCP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.MGC10986 (Accession NP_085053.1) is an-

other GAM179 target gene, herein designated TARGET GENE. MGC10986 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10986, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10986 BINDING SITE, designated SEQ ID:4521, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27011] Another function of GAM179 is therefore inhibition of MGC10986 (Accession NP_085053.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10986.

[27012] MGC21874 (Accession XP_291105.1) is another GAM179 target gene, herein designated TARGET GENE. MGC21874 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC21874, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC21874 BINDING SITE, designated SEQ ID:2320, to the

nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27013] Another function of GAM179 is therefore inhibition of MGC21874 (Accession XP_291105.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21874.

[27014] MGC26733 (Accession NP_659429.2) is another GAM179 target gene, herein designated TARGET GENE. MGC26733 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC26733, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC26733 BINDING SITE, designated SEQ ID:16246, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27015] Another function of GAM179 is therefore inhibition of MGC26733 (Accession NP_659429.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC26733.

[27016] MGC33371 (Accession NP_653265.1) is another GAM179

target gene, herein designated TARGET GENE. MGC33371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC33371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC33371 BINDING SITE, designated SEQ ID:12923, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27017] Another function of GAM179 is therefore inhibition of MGC33371 (Accession NP_653265.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33371.

[27018] Molybdenum cofactor synthesis 2 (MOCS2, Accession NP_004522.1) is another GAM179 target gene, herein designated TARGET GENE. MOCS2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MOCS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MOCS2 BINDING SITE, designated SEQ ID:19765, to the

nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27019] Another function of GAM179 is therefore inhibition of Molybdenum cofactor synthesis 2 (MOCS2, Accession NP_004522.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOCS2.

[27020] Membrane-spanning 4-domains, subfamily a, member 4 (MS4A4A, Accession NP_683876.1) is another GAM179 target gene, herein designated TARGET GENE. MS4A4A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MS4A4A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MS4A4A BINDING SITE, designated SEQ ID:19413, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27021] Another function of GAM179 is therefore inhibition of Membrane-spanning 4-domains, subfamily a, member 4 (MS4A4A, Accession NP_683876.1), a gene which binds to the fc region of immunoglobulins epsilon. high affinity re-

ceptor. initiating the allergic response. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MS4A4A.

[27022] The function of MS4A4A has been established by previous studies. By EST database searching for homologs of CD20 (MS4A1; 112210), Ishibashi et al. (2001) isolated a cDNA encoding MS4A4A, which they called MS4A4. The deduced 205- amino acid protein has a conserved phosphorylation site at the intracellular loop. Northern blot analysis revealed weak expression in mouse colon and intestine but detected no expression in human tissues. Liang and Tedder (2001) also obtained a cDNA encoding MS4A4A. The predicted 220- amino acid protein is more than 40% identical to its mouse homologs. PCR analysis detected variable expression of MS4A4A in cDNA from multiple hemopoietic cell lines.

[27023]

[27024] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27025] Ishibashi, K.; Suzuki, M.; Sasaki, S.; Imai, M. : Identification of a new multigene four- transmembrane family

(MS4A) related to CD20, HTm4 and beta subunit of the high- affinity IgE receptor. Gene 264: 87- 93, 2001. ; and

[27026] Liang, Y.; Tedder, T. F. : Identification of a CD20-, Fc- epsilon- RI- beta- related gene family: sixteen new MS4A family members expressed in human and mouse. Genomics 72: 119- 127, 2001.

[27027] Further studies establishing the function and utilities of MS4A4A are found in John Hopkins OMIM database record ID 606547, and in cited publications listed in Table 5, which are hereby incorporated by reference.Membrane-spanning 4-domains, subfamily a, member 4 (MS4A4A, Accession NP_076926.2) is another GAM179 target gene, herein designated TARGET GENE. MS4A4A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MS4A4A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MS4A4A BINDING SITE, designated SEQ ID:19413, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27028] Another function of GAM179 is therefore inhibition of

Membrane-spanning 4-domains, subfamily a, member 4 (MS4A4A, Accession NP_076926.2), a gene which binds to the fc region of immunoglobulins epsilon. high affinity receptor. initiating the allergic response. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MS4A4A.

[27029] The function of MS4A4A has been established by previous studies. By EST database searching for homologs of CD20 (MS4A1; 112210), Ishibashi et al. (2001) isolated a cDNA encoding MS4A4A, which they called MS4A4. The deduced 205- amino acid protein has a conserved phosphorylation site at the intracellular loop. Northern blot analysis revealed weak expression in mouse colon and intestine but detected no expression in human tissues. Liang and Tedder (2001) also obtained a cDNA encoding MS4A4A. The predicted 220- amino acid protein is more than 40% identical to its mouse homologs. PCR analysis detected variable expression of MS4A4A in cDNA from multiple hemopoietic cell lines.

[27030]

[27031] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[27032] Ishibashi, K.; Suzuki, M.; Sasaki, S.; Imai, M. : Identification of a new multigene four- transmembrane family (MS4A) related to CD20, HTm4 and beta subunit of the high- affinity IgE receptor. Gene 264: 87- 93, 2001. ; and

[27033] Liang, Y.; Tedder, T. F. : Identification of a CD20-, Fc- epsilon- RI- beta- related gene family: sixteen new MS4A family members expressed in human and mouse. Genomics 72: 119- 127, 2001.

[27034] Further studies establishing the function and utilities of MS4A4A are found in John Hopkins OMIM database record ID 606547, and in cited publications listed in Table 5, which are hereby incorporated by reference.MTH2 (Accession NP_060753.1) is another GAM179 target gene, herein designated TARGET GENE. MTH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTH2 BINDING SITE, designated SEQ ID:19548, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27035] Another function of GAM179 is therefore inhibition of MTH2 (Accession NP_060753.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTH2.

[27036] Myosin ie (MYO1E, Accession NP_004989.1) is another GAM179 target gene, herein designated TARGET GENE. MYO1E BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYO1E, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYO1E BINDING SITE, designated SEQ ID:3663, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27037] Another function of GAM179 is therefore inhibition of Myosin ie (MYO1E, Accession NP_004989.1), a gene which is an unconventional myosin. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYO1E.

[27038] The function of MYO1E has been established by previous studies. Bement et al. (1994) cloned a human unconventional myosin gene, MYO1E, encoding a predicted 127-kD polypeptide of 1,109 amino acids. The gene, which

they designated myosin IC, contains a characteristic N- terminal myosin head, a single 'IQ motif' predicted to bind a single myosin light chain, and a C- terminal tail with a putative membrane- binding site. They also noted the presence of a C- terminal src- homology domain, reminiscent of 'long- tailed' myosins I from amoeboid organisms. By Northern analysis, Bement et al. (1994) detected ubiquitous expression of MYO1E. Hasson et al. (1996) used fluorescence in situ hybridization to map the loci for 4 unconventional myosin loci in humans: MYO1E (formerly MYO1C), MYO1A (OMIM Ref. No. 601478), MYO1F (OMIM Ref. No. 601480), and MYO10 (OMIM Ref. No. 601481). The MYO1E gene was found to be located on 15q21- q22 in the precise location predicted from its location on chromosome 9 of the mouse.

[27039]

[27040] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27041] Bement, W. M.; Wirth, J. A.; Mooseker, M. S. : Cloning and mRNA expression of human unconventional myosin- IC: a homologue of amoeboid myosins- I with a single IQ motif and an SH3 domain. J. Molec. Biol. 243: 356- 363, 1994. ;

and

[27042] Hasson, T.; Skowron, J. F.; Gilbert, D. J.; Avraham, K. B.; Perry, W. L.; Bement, W. M.; Anderson, B. L.; Sherr, E. H.; Chen, Z.- Y.; Greene, L. A.; Ward, D. C.; Corey, D. P.; Mooseker.

[27043] Further studies establishing the function and utilities of MYO1E are found in John Hopkins OMIM database record ID 601479, and in cited publications listed in Table 5, which are hereby incorporated by reference.Nuclear receptor coactivator 1 (NCOA1, Accession NP_671756.1) is another GAM179 target gene, herein designated TARGET GENE. NCOA1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NCOA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA1 BINDING SITE, designated SEQ ID:13930, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27044] Another function of GAM179 is therefore inhibition of Nuclear receptor coactivator 1 (NCOA1, Accession NP_671756.1), a gene which acts as a transcriptional

coactivator for steroid and nuclear hormone receptors. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA1.

[27045] The function of NCOA1 has been established by previous studies. Onate et al. (1995) identified steroid receptor coactivator- 1 (SRC1), a coactivator that is required for full transcriptional activity of the steroid receptor superfamily. They isolated a cDNA encoding SRC1 using the yeast 2-hybrid system to identify proteins that interact with the human progesterone receptor (PGR; 607311). The SRC1 protein has a glutamine- rich region and a serine/threonine- rich region. SRC1 enhances the transcriptional activity of ligand- bound PGR but does not alter the basal activity of the target promoter. SRC1 also enhances estrogen receptor (ESR; 133430), glucocorticoid receptor (GRL; 138040), thyroid hormone receptor (e.g., 190120), and retinoid X receptor (e.g., RXRA; 180245) transcriptional activities through their cognate DNA response elements in the presence of hormone. Studies of the effects of SRC1 on unrelated transactivators showed that SRC1 can enhance the transcriptional activities of SP1 (OMIM Ref. No. 189906) and the chimeric Gal4- VP16 protein, but not

those of E2F (e.g., 189971), E47 (OMIM Ref. No. 147141), or CREB (OMIM Ref. No. 123810). Coexpression of SRC1 with PGR and ESR reversed the ability of ESR to squelch activation by PGR, suggesting that SRC1 is a limiting factor necessary for efficient PGR and ESR transactivation. A C- terminal form of SRC1 containing the receptor- binding region acted as a dominant- negative repressor of endogenous SRC1 function. SRC1 is expressed as 2 mRNAs of approximately 5.5 and 7.5 kb in a variety of human tissues and cell lines. Using a far- Western- based approach to screen a HeLa cell cDNA expression library with bacterially expressed rat thyroid hormone receptor (THRB; 190160), Takeshita et al. (1996) identified a partial SRC1 cDNA. They isolated the remaining sequence by 5- prime RACE. The full- length cDNA encodes a 1,440- amino acid protein with a mass of approximately 160 kD. In vitro binding studies showed that SRC1 can bind to TBP (OMIM Ref. No. 600075) and to TFIIB (OMIM Ref. No. 189963), in addition to a variety of nuclear hormone receptors in a ligand- dependent manner, suggesting that SRC1 may play a role as a bridging molecule between nuclear hormone receptors and general transcription factors. The conserved AF- 2 region of nuclear hormone receptors was

not required for receptor- SRC1 binding

[27046]

[27047] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27048] Onate, S. A.; Tsai, S. Y.; Tsai, M.- J.; O'Malley, B. W. : Sequence and characterization of a coactivator for the steroid hormone receptor superfamily. Science 270: 1354- 1357, 1995. ; and

[27049] Takeshita, A.; Yen, P. M.; Misiti, S.; Cardona, G. R.; Liu, Y.; Chin, W. W. : Molecular cloning and properties of a full-length putative thyroid hormone receptor coactivator. Endocrinol.

[27050] Further studies establishing the function and utilities of NCOA1 are found in John Hopkins OMIM database record ID 602691, and in cited publications listed in Table 5, which are hereby incorporated by reference.NESG1 (Accession NP_036469.1) is another GAM179 target gene, herein designated TARGET GENE. NESG1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NESG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of NESG1 BINDING SITE, designated SEQ ID:3220, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27051] Another function of GAM179 is therefore inhibition of NESG1 (Accession NP_036469.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NESG1.

[27052] NLG1 (Accession NP_115499.1) is another GAM179 target gene, herein designated TARGET GENE. NLG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NLG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NLG1 BINDING SITE, designated SEQ ID:19329, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27053] Another function of GAM179 is therefore inhibition of NLG1 (Accession NP_115499.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NLG1.

[27054] Phosphoinositide-3-kinase, regulatory subunit, polypep-

tide 3 (p55, gamma) (PIK3R3, Accession NP_003620.1) is another GAM179 target gene, herein designated TARGET GENE. PIK3R3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3R3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3R3 BINDING SITE, designated SEQ ID:16643, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27055] Another function of GAM179 is therefore inhibition of Phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma) (PIK3R3, Accession NP_003620.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3R3.

[27056] PILRB (Accession NP_038468.3) is another GAM179 target gene, herein designated TARGET GENE. PILRB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PILRB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of PILRB BINDING SITE, designated SEQ ID:17335, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27057] Another function of GAM179 is therefore inhibition of PILRB (Accession NP_038468.3) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PILRB.

[27058] PILRB (Accession NP_839956.1) is another GAM179 target gene, herein designated TARGET GENE. PILRB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PILRB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PILRB BINDING SITE, designated SEQ ID:17335, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27059] Another function of GAM179 is therefore inhibition of PILRB (Accession NP_839956.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PILRB.

[27060] PILRB (Accession NP_778212.2) is another GAM179 target

gene, herein designated TARGET GENE. PILRB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PILRB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PILRB BINDING SITE, designated SEQ ID:17335, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27061] Another function of GAM179 is therefore inhibition of PILRB (Accession NP_778212.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PILRB.

[27062] Phosphatidylinositol-4-phosphate 5-kinase, type i, beta (PIP5K1B, Accession NP_003549.1) is another GAM179 target gene, herein designated TARGET GENE. PIP5K1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIP5K1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIP5K1B BINDING SITE, designated SEQ ID:11230, to the nucleotide sequence of GAM179 RNA, herein designated

GAM RNA, also designated SEQ ID:300.

[27063] Another function of GAM179 is therefore inhibition of Phosphatidylinositol-4-phosphate 5-kinase, type i, beta (PIP5K1B, Accession NP_003549.1), a gene which catalyses the phosphorylation of phosphatidylinositol- 4- phosphate to form phosphatidylinositol- 4,5- biphosphate . and therefore may be associated with Friedreich ataxia. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of Friedreich ataxia., and of other diseases and clinical conditions associated with PIP5K1B.

[27064] The function of PIP5K1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Plexin c1 (PLXNC1, Accession NP_005752.1) is another GAM179 target gene, herein designated TARGET GENE. PLXNC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLXNC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PLXNC1 BINDING SITE, designated SEQ ID:17920, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ

ID:300.

[27065] Another function of GAM179 is therefore inhibition of Plexin c1 (PLXNC1, Accession NP_005752.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLXNC1.

[27066] PP1628 (Accession NP_079477.1) is another GAM179 target gene, herein designated TARGET GENE. PP1628 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PP1628, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP1628 BINDING SITE, designated SEQ ID:5602, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27067] Another function of GAM179 is therefore inhibition of PP1628 (Accession NP_079477.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1628.

[27068] Palmitoyl-protein thioesterase 2 (PPT2, Accession NP_619731.1) is another GAM179 target gene, herein designated TARGET GENE. PPT2 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPT2 BINDING SITE, designated SEQ ID:5462, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27069] Another function of GAM179 is therefore inhibition of Palmitoyl-protein thioesterase 2 (PPT2, Accession NP_619731.1), a gene which is a palmitoyl- protein thioesterase 2 which possesses a different substrate specificity than PPT1. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPT2.

[27070] The function of PPT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Palmitoyl-protein thioesterase 2 (PPT2, Accession NP_005146.3) is another GAM179 target gene, herein designated TARGET GENE. PPT2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPT2, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPT2 BINDING SITE, designated SEQ ID:5462, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27071] Another function of GAM179 is therefore inhibition of Palmitoyl-protein thioesterase 2 (PPT2, Accession NP_005146.3), a gene which is a palmitoyl- protein thioesterase 2 which possesses a different substrate specificity than PPT1. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPT2.

[27072] The function of PPT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Proline-rich protein bstni subfamily 3 (PRB3, Accession NP_006240.2) is another GAM179 target gene, herein designated TARGET GENE. PRB3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of PRB3 BINDING SITE, designated SEQ ID:6636, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27073] Another function of GAM179 is therefore inhibition of Proline-rich protein bstni subfamily 3 (PRB3, Accession NP_006240.2), a gene which is a salivary proline- rich protein and subunit of the splicing factor sf3a. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRB3.

[27074] The function of PRB3 has been established by previous studies. Azen et al. (1978) found 5 alleles. Linkage with Pr, Db, and Pa was indicated by linkage disequilibrium. These genes presumably arose by gene duplication, in view of the structural similarity of the gene products. They play an important role in inhibiting calcium phosphate precipitation from saliva and the glycoprotein forms part of the acquired dental pellicle and plaque. On the basis of relative degrees of linkage disequilibrium, Azen and Denniston (1980) favored positioning of G1 'outside' Db, to give suggested gene order Pa- Pr- Db- G1. Ikemoto et al. (1979) delineated a polymorphic salivary glycoprotein they

symbolized Ph (salivary parotid heavy protein). The relation to G1 of Azen et al. (1978) was not known. According to the hypothesis of Maeda (1985), as outlined in 168730, 6 loci constituting 2 gene subfamilies code the salivary proline- rich proteins. One subfamily, with 2 genes, codes the acidic proteins; the genes are rich in HaeIII restriction sites and are designated PRH1 and PRH2. The other subfamily, with 4 loci, codes the basic proteins; the genes are rich in BstNI restriction sites and are designated PRB1, PRB2, PRB3, and PRB4. Maeda (1985) concluded that the gene she designated PRB3 probably codes G1. Which ones of the other basic proline- rich proteins are coded by PRB1, 2 and 4 is not yet certain. Sequencing and restriction mapping indicate that the PRP cluster is in a segment of DNA about 500 kb long (Maeda, 1985). There is no information on the order and linkage relationships of the 6 genes. The 2 genes PRH1 (OMIM Ref. No. 168730) and PRH2 (OMIM Ref. No. 168790) have been completely sequenced (Kim and Maeda, 1986). The sequence information confirms the allelic relationship of Db, Pa, and PIF.

[27075]

[27076] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[27077] Kim, H.- S.; Maeda, N. : Structures of two HaeIII- type genes in the human salivary proline- rich protein multigene family. J. Biol. Chem. 261: 6712- 6718, 1986. ; and

[27078] Maeda, N. : Inheritance of the human salivary proline- rich proteins: a reinterpretation in terms of six loci forming two subfamilies. Biochem. Genet. 23: 455- 464, 1985.

[27079] Further studies establishing the function and utilities of PRB3 are found in John Hopkins OMIM database record ID 168840, and in cited publications listed in Table 5, which are hereby incorporated by reference.PRO0461 (Accession NP_112558.1) is another GAM179 target gene, herein designated TARGET GENE. PRO0461 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0461, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0461 BINDING SITE, designated SEQ ID:14706, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27080] Another function of GAM179 is therefore inhibition of PRO0461 (Accession NP_112558.1) . Accordingly, utilities

of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0461.

[27081] Rab5c, member ras oncogene family (RAB5C, Accession NP_004574.1) is another GAM179 target gene, herein designated TARGET GENE. RAB5C BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAB5C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB5C BINDING SITE, designated SEQ ID:590, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27082] Another function of GAM179 is therefore inhibition of Rab5c, member ras oncogene family (RAB5C, Accession NP_004574.1), a gene which is involved in the process of docking and/or fusion of vesicles with their correct acceptor compartment. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB5C.

[27083] The function of RAB5C has been established by previous studies. Members of the Rab protein family are small GTPases of the Ras superfamily that are thought to ensure fi-

delity in the process of docking and/or fusion of vesicles with their correct acceptor compartment. Han et al. (1996) isolated fetal lung cDNAs encoding a RAB protein that they designated RABL (RAB5- like). The predicted 216-amino acid RABL protein shares 86% identity with RAB5A (OMIM Ref. No. 179512) and RAB5B (OMIM Ref. No. 179514) and contains the conserved GTP- binding site characteristic of RAS proteins. RT- PCR analysis revealed that RABL is expressed ubiquitously. By analysis of cloned segments, Albertsen et al. (1994) determined that the RABL gene, which they called BC1- 16, is located in the BRCA1 (OMIM Ref. No. 113705) gene region on chromosome 17q12- q21. Han et al. (1996) refined the map position to 17q21.2 using FISH.

[27084]

[27085] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27086] Albertsen, H. M.; Smith, S. A.; Mazoyer, S.; Fujimoto, E.; Stevens, J.; Williams, B.; Rodriguez, P.; Cropp, C. S.; Slijepcevic, P.; Carlson, M.; Robertson, M.; Bradley, P.; and 9 others : A physical map and candidate genes in the BRCA1 region on chromosome 17q12- 21. Nature Genet. 7: 472-

479, 1994. ; and

[27087] Han, H.- J.; Sudo, K.; Inazawa, J.; Nakamura, Y. : Isolation and mapping of a human gene (RABL) encoding a small GTP- binding protein homologous to the Ras- related RAB gene. Cytogenet. Cel.

[27088] Further studies establishing the function and utilities of RAB5C are found in John Hopkins OMIM database record ID 604037, and in cited publications listed in Table 5, which are hereby incorporated by reference.Rad9 homolog (s. pombe) (RAD9, Accession NP_004575.1) is another GAM179 target gene, herein designated TARGET GENE. RAD9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAD9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD9 BINDING SITE, designated SEQ ID:16284, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27089] Another function of GAM179 is therefore inhibition of Rad9 homolog (s. pombe) (RAD9, Accession NP_004575.1), a gene which may function as a cell cycle checkpoint protein. Accordingly, utilities of GAM179 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD9.

[27090] The function of RAD9 has been established by previous studies. In S. pombe, rad9 is one of 6 genes essential for both the incomplete DNA replication (S- M) and DNA damage checkpoints. See HUS1 (OMIM Ref. No. 603760). By searching an EST database, Lieberman et al. (1996) identified a partial cDNA encoding HRAD9, a human rad9 homolog. The authors used the partial cDNA to recover additional human RAD9 cDNAs corresponding to the entire coding region. The predicted 391- amino acid human protein is 25% identical to S. pombe rad9. The human RAD9 gene partially complemented the hydroxyurea sensitivity, radiosensitivity, and checkpoint defects of rad9-null mutant cells. On immunoblots of mammalian cell extracts, Volkmer and Karnitz (1999) found that human RAD9 migrated at 70 kD, even though it has a predicted molecular mass of 45 kD. The authors attributed this discrepancy to complex posttranslational modifications. In vivo, the human RAD9 protein was phosphorylated in response to DNA damage, suggesting that it participates in a DNA damage- inducible signaling pathway. Immunoprecipitation studies demonstrated that the fully modified

form of RAD9 interacts selectively with RAD1 (OMIM Ref. No. 603153) and HUS1 in a stable complex. Volkmer and Karnitz (1999) concluded that these 3 proteins are central components of a DNA damage- responsive protein complex in human cells.

[27091]

[27092] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27093] Lieberman, H. B.; Hopkins, K. M.; Nass, M.; Demetrick, D.; Davey, S. : A human homolog of the Schizosaccharomyces pombe rad9+ checkpoint control gene. Proc. Nat. Acad. Sci. 93: 13890- 13895, 1996. ; and

[27094] Volkmer, E.; Karnitz, L. M. : Human homologs of Schizosaccharomyces pombe Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J. Biol. Chem. 274: 567- 570, 1999.

[27095] Further studies establishing the function and utilities of RAD9 are found in John Hopkins OMIM database record ID 603761, and in cited publications listed in Table 5, which are hereby incorporated by reference.Retinoblastoma binding protein 2 (RBBP2, Accession NP_005047.1) is another GAM179 target gene, herein designated TARGET

GENE. RBBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RBBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RBBP2 BINDING SITE, designated SEQ ID:19420, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27096] Another function of GAM179 is therefore inhibition of Retinoblastoma binding protein 2 (RBBP2, Accession NP_005047.1), a gene which interacts with the vital protein- binding domain of the retinoblastoma protein. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP2.

[27097] The function of RBBP2 has been established by previous studies. Baens et al. (1995) characterized 117 cDNAs isolated by direct cDNA selection using pools of human chromosome 12p cosmids. Of these, 3 matched previously determined cDNA sequences, including the retinoblastoma- binding protein- 2 (RBBP2) gene. STSs were developed for all cosmids. Regional assignment of the STSs by PCR analysis with somatic cell hybrids and

fluorescence in situ hybridization showed that the loci mapped to 12p11. To identify proteins that may modulate the activity of RBTN2 (LMO2; 180385), Mao et al. (1997) employed the yeast 2- hybrid assay to screen a human lymphocyte cDNA library using the RBTN2 LIM domain region as bait. They isolated a cDNA encoding the C- terminal region of RBBP2. The authors confirmed the interaction between RBTN2 and RBBP2 using in vitro binding assays and by coimmunoprecipitation of the 2 proteins. Deletion analysis showed that the second LIM domain of RBTN2 was necessary and sufficient for binding to the last 69 amino acids of RBBP2. The interaction between RBTN2 and RBBP2 had a functional consequence: the combination of RBBP2 and RBTN2 resulted in a higher level of transcription than RBTN2 alone in an in vitro assay. Mao et al. (1997) stated that the interaction of RBTN2 with RBBP2 suggests that RBTN2 may directly affect the activity of RBBP2 and/or RBTN2 may indirectly modulate the functions of the retinoblastoma protein (RB1; 180200) by binding to RBBP2.

[27098]

[27099] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[27100] Baens, M.; Aerssens, J.; Van Zand, K.; Van den Berghe, H.; Marynen, P. : Isolation and regional assignment of human chromosome 12p cDNAs. Genomics 29: 44- 52, 1995. ; and

[27101] Mao, S.; Neale, G. A. M.; Goorha, R. M. : T- cell oncogene rhombotin- 2 interacts with retinoblastoma- binding protein 2. Oncogene 14: 1531- 1539, 1997.

[27102] Further studies establishing the function and utilities of RBBP2 are found in John Hopkins OMIM database record ID 180202, and in cited publications listed in Table 5, which are hereby incorporated by reference.Regenerating islet-derived-like, pancreatic stone protein-like, pancreatic thread protein-like (rat) (REGL, Accession NP_006499.1) is another GAM179 target gene, herein designated TARGET GENE. REGL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by REGL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of REGL BINDING SITE, designated SEQ ID:12552, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ

ID:300.

[27103] Another function of GAM179 is therefore inhibition of Regenerating islet-derived-like, pancreatic stone protein-like, pancreatic thread protein-like (rat) (REGL, Accession NP_006499.1), a gene which is a member of REG family with unknown function. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with REGL.

[27104] The function of REGL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.SAE1 (Accession NP_005491.1) is another GAM179 target gene, herein designated TARGET GENE. SAE1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SAE1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SAE1 BINDING SITE, designated SEQ ID:17602, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27105] Another function of GAM179 is therefore inhibition of SAE1 (Accession NP_005491.1) . Accordingly, utilities of

GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SAE1.

[27106] Sh3-domain binding protein 1 (SH3BP1, Accession NP_061830.2) is another GAM179 target gene, herein designated TARGET GENE. SH3BP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SH3BP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SH3BP1 BINDING SITE, designated SEQ ID:14730, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27107] Another function of GAM179 is therefore inhibition of Sh3-domain binding protein 1 (SH3BP1, Accession NP_061830.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BP1.

[27108] Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_775323.1) is another GAM179 target gene, herein designated TARGET GENE. SIAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of

mRNA encoded by SIAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIAT1 BINDING SITE, designated SEQ ID:10204, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27109] Another function of GAM179 is therefore inhibition of Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_775323.1), a gene which transfers sialic acid from the donor of substrate cmp- sialic acid to galactose containing acceptor substrates. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIAT1.

[27110] The function of SIAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.2.Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_003023.1) is another GAM179 target gene, herein designated TARGET GENE. SIAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of

mRNA encoded by SIAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIAT1 BINDING SITE, designated SEQ ID:10204, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27111] Another function of GAM179 is therefore inhibition of Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_003023.1), a gene which transfers sialic acid from the donor of substrate cmp- sialic acid to galactose containing acceptor substrates. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIAT1.

[27112] The function of SIAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.2.Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_775324.1) is another GAM179 target gene, herein designated TARGET GENE. SIAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of

mRNA encoded by SIAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIAT1 BINDING SITE, designated SEQ ID:10204, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27113] Another function of GAM179 is therefore inhibition of Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_775324.1), a gene which transfers sialic acid from the donor of substrate cmp- sialic acid to galactose containing acceptor substrates. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIAT1.

[27114] The function of SIAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.2.Solute carrier family 12 (potassium/chloride transporters), member 7 (SLC12A7, Accession NP_006589.1) is another GAM179 target gene, herein designated TARGET GENE. SLC12A7 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by SLC12A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC12A7 BINDING SITE, designated SEQ ID:15230, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27115] Another function of GAM179 is therefore inhibition of Solute carrier family 12 (potassium/chloride transporters), member 7 (SLC12A7, Accession NP_006589.1), a gene which is a potassium/chloride- cotransporter. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC12A7.

[27116] The function of SLC12A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM105.1.SLC37A3 (Accession NP_115671.1) is another GAM179 target gene, herein designated TARGET GENE. SLC37A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC37A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC37A3 BINDING SITE, designated SEQ ID:14888, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27117] Another function of GAM179 is therefore inhibition of SLC37A3 (Accession NP_115671.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC37A3.

[27118] Smcx homolog, x chromosome (mouse) (SMCX, Accession NP_004178.1) is another GAM179 target gene, herein designated TARGET GENE. SMCX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SMCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMCX BINDING SITE, designated SEQ ID:8263, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27119] Another function of GAM179 is therefore inhibition of Smcx homolog, x chromosome (mouse) (SMCX, Accession NP_004178.1), a gene which escapes X inactivation. Ac-

cordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMCX.

[27120] The function of SMCX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Spondin 1, (f-spondin) extracellular matrix protein (SPON1, Accession NP_006099.1) is another GAM179 target gene, herein designated TARGET GENE. SPON1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPON1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPON1 BINDING SITE, designated SEQ ID:16909, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27121] Another function of GAM179 is therefore inhibition of Spondin 1, (f-spondin) extracellular matrix protein (SPON1, Accession NP_006099.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPON1.

[27122] Serine palmitoyltransferase, long chain base subunit 2

(SPTLC2, Accession NP_004854.1) is another GAM179 target gene, herein designated TARGET GENE. SPTLC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPTLC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPTLC2 BINDING SITE, designated SEQ ID:16724, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27123] Another function of GAM179 is therefore inhibition of Serine palmitoyltransferase, long chain base subunit 2 (SPTLC2, Accession NP_004854.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPTLC2.

[27124] Stromal antigen 3 (STAG3, Accession NP_076975.1) is another GAM179 target gene, herein designated TARGET GENE. STAG3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by STAG3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of STAG3 BINDING SITE, designated SEQ ID:5382, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27125] Another function of GAM179 is therefore inhibition of Stromal antigen 3 (STAG3, Accession NP_076975.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAG3.

[27126] Synaptotagmin-like 2 (SYTL2, Accession NP_116561.1) is another GAM179 target gene, herein designated TARGET GENE. SYTL2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SYTL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYTL2 BINDING SITE, designated SEQ ID:7702, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27127] Another function of GAM179 is therefore inhibition of Synaptotagmin-like 2 (SYTL2, Accession NP_116561.1) . Accordingly, utilities of GAM179 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with SYTL2.

[27128] Tenascin r (restrictin, janusin) (TNR, Accession NP_003276.2) is another GAM179 target gene, herein designated TARGET GENE. TNR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNR BINDING SITE, designated SEQ ID:19266, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27129] Another function of GAM179 is therefore inhibition of Tenascin r (restrictin, janusin) (TNR, Accession NP_003276.2), a gene which has a role in axonal path finding during embryonic development. Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNR.

[27130] The function of TNR has been established by previous studies. The tenascin (TN) gene family includes at least 3 genes in mammals: TN- C (or hexabrachion; 187380),

TN- X (TNXA; 600261), and TN- R (Erickson, 1993). The genes are expressed in distinct tissues at different times during embyronic development and are present in adult tissues. Carnemolla et al. (1996) and Leprini et al. (1996) stated that TN- R has been detected predominantly in the central nervous system and is localized around motor neurons and on motor axons in the spinal cord, cerebellum, hippocampus, and olfactory bulb. It is detectable at embryonic days 6 to 16, but is barely detectable in the adult. This time- restricted distribution suggests an involvement of TN- R in central nervous system development Erickson (1997) provided a diagram of the individual members of the tenascin family, including TN- Y, a new member discovered in chicken. Each tenascin subunit has an N- terminal segment that connects into trimers or hexamers, a series of EGF domains, a series of FN- III domains, and a fibrinogen- like domain at the C terminus; see Figure 1 of Erickson (1997).

[27131]

[27132] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27133] Carnemolla, B.; Leprini, A.; Borsi, L.; Querze, G.; Urbini, S.;

Zardi, L. : Human tenascin- R: complete primary structure, pre- mRNA alternative splicing and gene localization on chromosome 1q23- q24. J. Biol. Chem. 271: 8157- 8160, 1996. ; and

[27134] Erickson, H. P. : A tenascin knockout with a phenotype. Nature Genet. 17: 5- 7, 1997.

[27135] Further studies establishing the function and utilities of TNR are found in John Hopkins OMIM database record ID 601995, and in cited publications listed in Table 5, which are hereby incorporated by reference.Tyro protein tyrosine kinase binding protein (TYROBP, Accession NP_003323.1) is another GAM179 target gene, herein designated TARGET GENE. TYROBP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TYROBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TYROBP BINDING SITE, designated SEQ ID:12609, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27136] Another function of GAM179 is therefore inhibition of Tyro protein tyrosine kinase binding protein (TYROBP, Ac-

cession NP_003323.1) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TYROBP.

[27137] Upstream binding protein 1 (lbp-1a) (UBP1, Accession NP_055332.2) is another GAM179 target gene, herein designated TARGET GENE. UBP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBP1 BINDING SITE, designated SEQ ID:17947, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27138] Another function of GAM179 is therefore inhibition of Upstream binding protein 1 (lbp-1a) (UBP1, Accession NP_055332.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBP1.

[27139] WBP3 (Accession NP_783863.2) is another GAM179 target gene, herein designated TARGET GENE. WBP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WBP3, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBP3 BINDING SITE, designated SEQ ID:18927, to the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, also designated SEQ ID:300.

[27140] Another function of GAM179 is therefore inhibition of WBP3 (Accession NP_783863.2) . Accordingly, utilities of GAM179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBP3.

[27141]

[27142] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 180 (GAM180), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[27143] GAM180 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM180 was detected is described hereinabove with reference to Figs. 8-15.

[27144] GAM180 gene, herein designated GAM GENE, and GAM180 target gene, herein designated TARGET GENE,

are human genes contained in the human genome.

[27145] GAM180 gene encodes a GAM180 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM180 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM180 precursor RNA is designated SEQ ID:107, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:107 is located at position 128815436 relative to chromosome 11.

[27146] GAM180 precursor RNA folds onto itself, forming GAM180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27147] GAM180 precursor RNA folds onto itself, forming GAM180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin struc-

ture`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[27148] Nucleotide sequence of GAM180 precursor RNA, designated SEQ-ID: 107, and a schematic representation of a predicted secondary folding of GAM180 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[27149] An enzyme complex designated DICER COMPLEX, `dices` the GAM180 folded precursor RNA into GAM180 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: B) nucleotide sequence of GAM180 RNA is designated SEQ ID:214, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[27150] GAM180 target gene, herein designated TARGET GENE,

encodes a corresponding messenger RNA, GAM180 target RNA, herein designated GAM TARGET RNA. GAM180 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[27151] GAM180 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM180 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM180 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM180 RNA may have a different number of target binding sites in untranslated regions of a GAM180 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[27152] The complementary binding of GAM180 RNA, herein designated GAM RNA, to target binding sites on GAM180 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM180 target RNA into GAM180 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[27153] It is appreciated that GAM180 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM180 target genes. The mRNA of each one of this plurality of GAM180 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM180 RNA, herein designated GAM RNA, and which when bound by GAM180 RNA causes inhibition of translation of respective one or more GAM180 target proteins.

[27154] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM180 gene, herein designated GAM GENE, on one or more GAM180 target genes, herein collectively designated

TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27155] It is appreciated that specific functions and accordingly utilities of GAM180 correlate with, and may be deduced from, the identity of the target genes which GAM180 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[27156]

[27157]

[27158] 3PAP (Accession NP_061934.2) is a GAM180 target gene, herein designated TARGET GENE. 3PAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by 3PAP, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of 3PAP BINDING SITE, designated SEQ ID:9183, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27159] A function of GAM180 is therefore inhibition of 3PAP (Accession NP_061934.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 3PAP.

[27160] ACK1 (Accession NP_005772.2) is another GAM180 target gene, herein designated TARGET GENE. ACK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACK1 BINDING SITE, designated SEQ ID:18640, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27161] Another function of GAM180 is therefore inhibition of ACK1 (Accession NP_005772.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with ACK1.

[27162] Acid phosphatase 2, lysosomal (ACP2, Accession NP_001601.1) is another GAM180 target gene, herein designated TARGET GENE. ACP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACP2 BINDING SITE, designated SEQ ID:16613, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27163] Another function of GAM180 is therefore inhibition of Acid phosphatase 2, lysosomal (ACP2, Accession NP_001601.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACP2.

[27164] A disintegrin and metalloproteinase domain 8 (ADAM8, Accession NP_001100.1) is another GAM180 target gene, herein designated TARGET GENE. ADAM8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAM8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAM8 BINDING SITE, designated SEQ ID:19901, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27165] Another function of GAM180 is therefore inhibition of A disintegrin and metalloproteinase domain 8 (ADAM8, Accession NP_001100.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM8.

[27166] Adenylate cyclase 5 (ADCY5, Accession XP_171048.2) is another GAM180 target gene, herein designated TARGET GENE. ADCY5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ADCY5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY5 BINDING SITE, designated SEQ ID:9867, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27167] Another function of GAM180 is therefore inhibition of Adenylate cyclase 5 (ADCY5, Accession XP_171048.2) . Accordingly, utilities of GAM180 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with ADCY5.

[27168] A kinase (prka) anchor protein 7 (AKAP7, Accession NP_619539.1) is another GAM180 target gene, herein designated TARGET GENE. AKAP7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AKAP7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKAP7 BINDING SITE, designated SEQ ID:662, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27169] Another function of GAM180 is therefore inhibition of A kinase (prka) anchor protein 7 (AKAP7, Accession NP_619539.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP7.

[27170] A kinase (prka) anchor protein 7 (AKAP7, Accession NP_057461.1) is another GAM180 target gene, herein designated TARGET GENE. AKAP7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AKAP7, correspond-

ing to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKAP7 BINDING SITE, designated SEQ ID:662, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27171] Another function of GAM180 is therefore inhibition of A kinase (prka) anchor protein 7 (AKAP7, Accession NP_057461.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP7.

[27172] A kinase (prka) anchor protein 7 (AKAP7, Accession NP_004833.1) is another GAM180 target gene, herein designated TARGET GENE. AKAP7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AKAP7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKAP7 BINDING SITE, designated SEQ ID:662, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27173] Another function of GAM180 is therefore inhibition of A

kinase (prka) anchor protein 7 (AKAP7, Accession NP_004833.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP7.

[27174] ALK7 (Accession NP_660302.1) is another GAM180 target gene, herein designated TARGET GENE. ALK7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALK7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALK7 BINDING SITE, designated SEQ ID:4668, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27175] Another function of GAM180 is therefore inhibition of ALK7 (Accession NP_660302.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALK7.

[27176] ANKFY1 (Accession NP_057460.2) is another GAM180 target gene, herein designated TARGET GENE. ANKFY1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ANKFY1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANKFY1 BINDING SITE, designated SEQ ID:13680, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27177] Another function of GAM180 is therefore inhibition of ANKFY1 (Accession NP_057460.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKFY1.

[27178] AP1S3 (Accession NP_848929.1) is another GAM180 target gene, herein designated TARGET GENE. AP1S3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1S3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1S3 BINDING SITE, designated SEQ ID:10369, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27179] Another function of GAM180 is therefore inhibition of

AP1S3 (Accession NP_848929.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1S3.

[27180] Ariadne homolog 2 (drosophila) (ARIH2, Accession NP_006312.1) is another GAM180 target gene, herein designated TARGET GENE. ARIH2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ARIH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARIH2 BINDING SITE, designated SEQ ID:6107, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27181] Another function of GAM180 is therefore inhibition of Ariadne homolog 2 (drosophila) (ARIH2, Accession NP_006312.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARIH2.

[27182] Additional sex combs like 1 (drosophila) (ASXL1, Accession NP_056153.2) is another GAM180 target gene, herein designated TARGET GENE. ASXL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASXL1, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASXL1 BINDING SITE, designated SEQ ID:6136, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27183] Another function of GAM180 is therefore inhibition of Additional sex combs like 1 (drosophila) (ASXL1, Accession NP_056153.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASXL1.

[27184] Arginine vasopressin receptor 1b (AVPR1B, Accession NP_000698.1) is another GAM180 target gene, herein designated TARGET GENE. AVPR1B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AVPR1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AVPR1B BINDING SITE, designated SEQ ID:10287, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27185] Another function of GAM180 is therefore inhibition of Arginine vasopressin receptor 1b (AVPR1B, Accession

NP_000698.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AVPR1B.

[27186] Btb and cnc homology 1, basic leucine zipper transcription factor 2 (BACH2, Accession NP_068585.1) is another GAM180 target gene, herein designated TARGET GENE. BACH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BACH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACH2 BINDING SITE, designated SEQ ID:9027, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27187] Another function of GAM180 is therefore inhibition of Btb and cnc homology 1, basic leucine zipper transcription factor 2 (BACH2, Accession NP_068585.1), a gene which acts as repressor or activator, binds to maf recognition elements and therefore may be associated with Non-hodgkin lymphoma. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of Non-hodgkin lymphoma, and of other diseases and clinical conditions associated with BACH2.

[27188] The function of BACH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.Blood vessel epicardial substance (BVES, Accession NP_671488.1) is another GAM180 target gene, herein designated TARGET GENE. BVES BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BVES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BVES BINDING SITE, designated SEQ ID:12682, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27189] Another function of GAM180 is therefore inhibition of Blood vessel epicardial substance (BVES, Accession NP_671488.1), a gene which plays an important role in vertebrate heart development. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BVES.

[27190] The function of BVES has been established by previous studies. Reese et al. (1999) cloned chick and mouse bves and showed by immunolocalization that bves protein is

expressed in the progenitors of coronary artery smooth muscle cells as well as in differentiated smooth muscle cells. Using a probe obtained by low stringency PCR with mouse bves to screen a human heart cDNA library, Reese and Bader (1999) identified a cDNA for human BVES. BVES encodes a deduced 334- amino acid protein that is 75% identical to the 357- amino acid chick bves. Sequence analysis predicts 3 transmembrane helices with an extracellular C terminus. Northern blot analysis revealed that expression of an approximately 5.5- kb BVES transcript is restricted to skeletal muscle and adult and fetal heart. In an independent search for transcripts preferentially expressed during chick heart development, Andree et al. (2000) isolated chick, mouse, and human BVES, which they called Popeye protein- 1 (POP1). They found that BVES encodes a deduced 41- kD, 359- amino acid protein that shares sequence homology with the Popeye genes POP2 (OMIM Ref. No. 605823) and POP3 (OMIM Ref. No. 605824). By screening heart and total embryo cDNA libraries, Andree et al. (2000) isolated 4 different transcripts of BVES, which differ in their tissue specificity. Using in situ hybridization, they detected BVES expression in the developing heart of both chicken and mouse. After

transfection of BVES into COS- 7 cells, Andree et al. (2000) observed perinuclear distribution of BVES protein and concluded that POP proteins are associated with membranes. Based on the conservation and expression pattern of the 3 Popeye genes in mouse, chicken, and human, Andree et al. (2000) concluded that POP genes play an important role in vertebrate heart development.

[27191]

[27192] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27193] Reese, D. E.; Zavaljevski, M.; Streiff, N. L.; Bader, D. : Bves: a novel gene expressed during coronary blood vessel development. Dev. Biol. 209: 159- 171, 1999. ; and

[27194] Andree, B.; Hillemann, T.; Kessler- Ieckson, G.; Schmitt-John, T.; Jockusch, H.; Arnold, H.- H.; Brand, T. : Isolation and characterization of the novel Popeye gene family expressed in s.

[27195] Further studies establishing the function and utilities of BVES are found in John Hopkins OMIM database record ID 604577, and in cited publications listed in Table 5, which are hereby incorporated by reference.Chromosome 1 open reading frame 16 (C1orf16, Accession NP_055652.2) is

another GAM180 target gene, herein designated TARGET GENE. C1orf16 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C1orf16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf16 BINDING SITE, designated SEQ ID:9607, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27196] Another function of GAM180 is therefore inhibition of Chromosome 1 open reading frame 16 (C1orf16, Accession NP_055652.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf16.

[27197] Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) is another GAM180 target gene, herein designated TARGET GENE. C1orf24 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C1orf24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:9821, to the

nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27198] Another function of GAM180 is therefore inhibition of Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24.

[27199] Chromosome 1 open reading frame 24 (C1orf24, Accession NP_071366.1) is another GAM180 target gene, herein designated TARGET GENE. C1orf24 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C1orf24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:9821, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27200] Another function of GAM180 is therefore inhibition of Chromosome 1 open reading frame 24 (C1orf24, Accession NP_071366.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24.

[27201] Complement component 1, q subcomponent, receptor 1 (C1QR1, Accession NP_036204.1) is another GAM180 target gene, herein designated TARGET GENE. C1QR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1QR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1QR1 BINDING SITE, designated SEQ ID:6733, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27202] Another function of GAM180 is therefore inhibition of Complement component 1, q subcomponent, receptor 1 (C1QR1, Accession NP_036204.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QR1.

[27203] Chromosome 20 open reading frame 28 (C20orf28, Accession NP_056232.1) is another GAM180 target gene, herein designated TARGET GENE. C20orf28 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf28, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of C20orf28 BINDING SITE, designated SEQ ID:15921, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27204] Another function of GAM180 is therefore inhibition of Chromosome 20 open reading frame 28 (C20orf28, Accession NP_056232.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf28.

[27205] Chromosome 20 open reading frame 70 (C20orf70, Accession XP_114180.1) is another GAM180 target gene, herein designated TARGET GENE. C20orf70 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf70, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf70 BINDING SITE, designated SEQ ID:9329, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27206] Another function of GAM180 is therefore inhibition of Chromosome 20 open reading frame 70 (C20orf70, Accession XP_114180.1) . Accordingly, utilities of GAM180

include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf70.

[27207] Carbonic anhydrase xiv (CA14, Accession NP_036245.1) is another GAM180 target gene, herein designated TARGET GENE. CA14 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CA14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CA14 BINDING SITE, designated SEQ ID:11029, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27208] Another function of GAM180 is therefore inhibition of Carbonic anhydrase xiv (CA14, Accession NP_036245.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CA14.

[27209] Calmodulin 1 (phosphorylase kinase, delta) (CALM1, Accession NP_008819.1) is another GAM180 target gene, herein designated TARGET GENE. CALM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CALM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CALM1 BINDING SITE, designated SEQ ID:13087, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27210] Another function of GAM180 is therefore inhibition of Calmodulin 1 (phosphorylase kinase, delta) (CALM1, Accession NP_008819.1), a gene which plays roles in growth and the cell cycle as well as in signal transduction and the synthesis and release of neurotransmitters. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALM1.

[27211] The function of CALM1 has been established by previous studies. Calmodulin is the archetype of the family of calcium- modulated proteins of which nearly 20 members have been found. They are identified by their occurrence in the cytosol or on membranes facing the cytosol and by a high affinity for calcium. Calmodulin contains 149 amino acids and has 4 calcium- binding domains. Its functions include roles in growth and the cell cycle as well as in signal transduction and the synthesis and release of neurotransmitters. To determine how calcium/calmodulin

activates calcium/calmodulin- dependent protein kinase I (CAMK1; 604998), Chin et al. (1997) characterized CAMK1 activation by calmodulin mutants with substitutions at hydrophobic residues. They found that CAMK1 activity is dependent on met124 within the C- terminal domain of calmodulin as well as on N- terminal hydrophobic residues of calmodulin.

[27212]

[27213] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27214] Rhyner, J. A.; Ottiger, M.; Wicki, R.; Greenwood, T. M.; Strehler, E. E. : Structure of the human CALM1 calmodulin gene and identification of two CALM1- related pseudogenes CALM1P1 and CALM1P2. Europ. J. Biochem. 225: 71- 82, 1994. ; and

[27215] Chin, D.; Winkler, K. E.; Means, A. R. : Characterization of substrate phosphorylation and use of calmodulin mutants to address implications from the enzyme crystal structure of calmodul.

[27216] Further studies establishing the function and utilities of CALM1 are found in John Hopkins OMIM database record ID 114180, and in cited publications listed in Table 5,

which are hereby incorporated by reference.Calumenin (CALU, Accession NP_001210.1) is another GAM180 target gene, herein designated TARGET GENE. CALU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CALU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CALU BINDING SITE, designated SEQ ID:544, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27217] Another function of GAM180 is therefore inhibition of Calumenin (CALU, Accession NP_001210.1), a gene which binds 7 calcium ions with a low affinity with unidtified function. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALU.

[27218] The function of CALU has been established by previous studies. Many calcium- binding proteins are reported to be localized in the endoplasmic reticulum (ER) and involved in such ER functions as protein folding and sorting. Among these are RCN1 (OMIM Ref. No. 602735), RCN2 (OMIM Ref. No. 602584), and calumenin (CALU), which

form a novel family of calcium- binding proteins in the ER and Golgi apparatus. By searching sequence databases with a mouse Calu cDNA sequence (Yabe et al., 1997), Yabe et al. (1998) identified a human CALU EST, which they used to clone a full- length CALU cDNA. The cDNA encodes a deduced 315- amino acid protein containing 6 EF- hand motifs, 1 potential N- glycosylation site, and a C- terminal ER retention signal. The human and mouse CALU proteins are 98% identical. Northern blot analysis demonstrated that the 3.4- kb CALU mRNA is ubiquitously expressed in human tissues. Southern blot analysis using a human CALU cDNA probe detected bands in a variety of species. Yabe et al. (1997) mapped the mouse Calu gene to the proximal portion of chromosome 7. By fluorescence in situ hybridization, Yabe et al. (1998) localized the human CALU gene to 7q32, which was an unexpected result due to the homology of synteny between proximal mouse chromosome 7 and human 19q13.2-q13.3.

[27219]

[27220] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27221] Yabe, D.; Nakamura, T.; Kanazawa, N.; Tashiro, K.; Honjo, T. : Calumenin, a Ca(2+)- binding protein retained in the endoplasmic reticulum with a novel carboxyl- terminal sequence, HDEF. J. Biol. Chem. 272: 18232- 18239, 1997. ; and

[27222] Yabe, D.; Taniwaki, M.; Nakamura, T.; Kanazawa, N.; Tashiro, K.; Honjo, T. : Human calumenin gene (CALU): cDNA isolation and chromosomal mapping to 7q32. Genomics 49: 331- 333, 1998.

[27223] Further studies establishing the function and utilities of CALU are found in John Hopkins OMIM database record ID 603420, and in cited publications listed in Table 5, which are hereby incorporated by reference.Caspase recruitment domain family, member 9 (CARD9, Accession NP_434700.1) is another GAM180 target gene, herein designated TARGET GENE. CARD9 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CARD9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CARD9 BINDING SITE, designated SEQ ID:11302, to the nucleotide sequence of GAM180 RNA, herein designated

GAM RNA, also designated SEQ ID:214.

[27224] Another function of GAM180 is therefore inhibition of Caspase recruitment domain family, member 9 (CARD9, Accession NP_434700.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD9.

[27225] Caspase recruitment domain family, member 9 (CARD9, Accession NP_071747.2) is another GAM180 target gene, herein designated TARGET GENE. CARD9 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CARD9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CARD9 BINDING SITE, designated SEQ ID:11302, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27226] Another function of GAM180 is therefore inhibition of Caspase recruitment domain family, member 9 (CARD9, Accession NP_071747.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD9.

[27227] Caspase recruitment domain family, member 9 (CARD9,

Accession NP_434701.1) is another GAM180 target gene, herein designated TARGET GENE. CARD9 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CARD9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CARD9 BINDING SITE, designated SEQ ID:11302, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27228] Another function of GAM180 is therefore inhibition of Caspase recruitment domain family, member 9 (CARD9, Accession NP_434701.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD9.

[27229] Chemokine (c-c motif) ligand 11 (CCL11, Accession NP_002977.1) is another GAM180 target gene, herein designated TARGET GENE. CCL11 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CCL11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL11 BINDING SITE, designated

SEQ ID:4942, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27230] Another function of GAM180 is therefore inhibition of Chemokine (c-c motif) ligand 11 (CCL11, Accession NP_002977.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL11.

[27231] Chemokine (c-c motif) ligand 8 (CCL8, Accession NP_005614.2) is another GAM180 target gene, herein designated TARGET GENE. CCL8 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CCL8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL8 BINDING SITE, designated SEQ ID:6343, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27232] Another function of GAM180 is therefore inhibition of Chemokine (c-c motif) ligand 8 (CCL8, Accession NP_005614.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL8.

[27233] Cd22 antigen (CD22, Accession NP_001762.1) is another

GAM180 target gene, herein designated TARGET GENE. CD22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD22 BINDING SITE, designated SEQ ID:5550, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27234] Another function of GAM180 is therefore inhibition of Cd22 antigen (CD22, Accession NP_001762.1), a gene which is an antigen expressed specifically in B lymphocytes (Cd22 antigen) and may act in cell- cell interactions. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD22.

[27235] The function of CD22 has been established by previous studies. Nonhuman mammalian cells express N- acetylneuraminic acid (OMIM Ref. No. Neu5Ac) and N- glycolylneuraminic acid (OMIM Ref. No. Neu5Gc). Human cells contain only Neu5Ac because of an exon deletion/ frameshift mutation in cytidine monophospho- sialic acid hydroxylase (CMAH; 603209), which converts Neu5Ac to

Neu5Gc. Sialic acid- binding immunoglobulin- like lectins, or SIGLECs, such as CD22 (SIGLEC2), recognize sialic acids. Brinkman- Van der Linden et al. (2000) showed that human SIGLEC1 (SN; 600751) strongly prefers Neu5Ac over Neu5Gc. Sequence analysis of SIGLEC2 cDNA found that while the chimpanzee sequence is 97% homologous to human, bonobo and gorilla are only 96% homologous, and the orangutan is only 93% homologous. Using regions of SIGLEC2 proteins from mouse, chimpanzee, orangutan, and human fused to the Fc region of human IgG, and flow cytometry analysis, Brinkman- Van der Linden et al. (2000) showed that all bound well to chimpanzee Epstein-Barr virus (EBV)- transformed B cells, which expressed high levels of Neu5Gc. Except for mouse, all bound well to human EBV- transformed B cells, which expressed high levels of Neu5Ac.

[27236] Animal model experiments lend further support to the function of CD22. O'Keefe et al. (1996) made observations in mice with a targeted disruption of the CD22 gene indicating that CD22 is a negative regulator of antigen receptor signaling whose onset of expression at the mature B cell stage may serve to raise the antigen concentration threshold required for B cell triggering. Splenic B cells

from CD22 knockout mice were found to be hyperresponsive to receptor signaling. Heightened calcium fluxes and cell proliferation were obtained at lower ligand concentrations. The mice gave augmented immune response, had an expanded peritoneal B- 1 cell population, and contained increased serum titers of autoantibody.

[27237] It is appreciated that the abovementioned animal model for CD22 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[27238] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27239] O'Keefe, T. L.; Williams, G. T.; Davies, S. L.; Neuberger, M. S. : Hyperresponsive B cells in CD22- deficient mice. Science 274: 798- 801, 1996. ; and

[27240] Brinkman- Van der Linden, E. C. M.; Sjoberg, E. R.; Juneja, L. R.; Crocker, P. R.; Varki, N.; Varki, A. : Loss of N- glycolylneuraminic acid in human evolution: implications for sialic aci.

[27241] Further studies establishing the function and utilities of CD22 are found in John Hopkins OMIM database record ID 107266, and in cited publications listed in Table 5, which

are hereby incorporated by reference.Cdk5 regulatory subunit associated protein 3 (CDK5RAP3, Accession NP_079473.2) is another GAM180 target gene, herein designated TARGET GENE. CDK5RAP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDK5RAP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDK5RAP3 BINDING SITE, designated SEQ ID:3530, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27242] Another function of GAM180 is therefore inhibition of Cdk5 regulatory subunit associated protein 3 (CDK5RAP3, Accession NP_079473.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDK5RAP3.

[27243] Cdk5 regulatory subunit associated protein 3 (CDK5RAP3, Accession NP_788275.1) is another GAM180 target gene, herein designated TARGET GENE. CDK5RAP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by

CDK5RAP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDK5RAP3 BINDING SITE, designated SEQ ID:3530, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27244] Another function of GAM180 is therefore inhibition of Cdk5 regulatory subunit associated protein 3 (CDK5RAP3, Accession NP_788275.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDK5RAP3.

[27245] Chitinase 3-like 2 (CHI3L2, Accession NP_003991.1) is another GAM180 target gene, herein designated TARGET GENE. CHI3L2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHI3L2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHI3L2 BINDING SITE, designated SEQ ID:13391, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ

ID:214.

[27246] Another function of GAM180 is therefore inhibition of Chitinase 3-like 2 (CHI3L2, Accession NP_003991.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHI3L2.

[27247] Carbohydrate (chondroitin 6) sulfotransferase 3 (CHST3, Accession NP_004264.2) is another GAM180 target gene, herein designated TARGET GENE. CHST3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHST3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHST3 BINDING SITE, designated SEQ ID:19995, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27248] Another function of GAM180 is therefore inhibition of Carbohydrate (chondroitin 6) sulfotransferase 3 (CHST3, Accession NP_004264.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST3.

[27249] Carbohydrate (n-acetylglucosamine 6-o) sulfotransferase

5 (CHST5, Accession NP_036258.1) is another GAM180 target gene, herein designated TARGET GENE. CHST5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CHST5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHST5 BINDING SITE, designated SEQ ID:6807, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27250] Another function of GAM180 is therefore inhibition of Carbohydrate (n-acetylglucosamine 6-o) sulfotransferase 5 (CHST5, Accession NP_036258.1), a gene which may be involved in sulfation of glycoproteins and proteoglycans. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST5.

[27251] The function of CHST5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.1.Collagen, type iv, alpha 4 (COL4A4, Accession NP_000083.1) is another GAM180 target gene, herein designated TARGET GENE. COL4A4 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by COL4A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL4A4 BINDING SITE, designated SEQ ID:5844, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27252] Another function of GAM180 is therefore inhibition of Collagen, type iv, alpha 4 (COL4A4, Accession NP_000083.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A4.

[27253] Doublecortin and cam kinase-like 1 (DCAMKL1, Accession NP_004725.1) is another GAM180 target gene, herein designated TARGET GENE. DCAMKL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DCAMKL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCAMKL1 BINDING SITE, designated SEQ ID:2905, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA,

also designated SEQ ID:214.

[27254] Another function of GAM180 is therefore inhibition of Doublecortin and cam kinase-like 1 (DCAMKL1, Accession NP_004725.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCAMKL1.

[27255] DKFZP434F011 (Accession XP_291159.1) is another GAM180 target gene, herein designated TARGET GENE. DKFZP434F011 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F011, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434F011 BINDING SITE, designated SEQ ID:7730, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27256] Another function of GAM180 is therefore inhibition of DKFZP434F011 (Accession XP_291159.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F011.

[27257] DKFZP564O0423 (Accession XP_166254.2) is another

GAM180 target gene, herein designated TARGET GENE. DKFZP564O0423 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O0423, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564O0423 BINDING SITE, designated SEQ ID:8990, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27258] Another function of GAM180 is therefore inhibition of DKFZP564O0423 (Accession XP_166254.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564O0423.

[27259] DKFZP586I2223 (Accession NP_542768.1) is another GAM180 target gene, herein designated TARGET GENE. DKFZP586I2223 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by DKFZP586I2223, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DK-

FZP586I2223 BINDING SITE, designated SEQ ID:11679, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27260] Another function of GAM180 is therefore inhibition of DKFZP586I2223 (Accession NP_542768.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586I2223.

[27261] DKFZP586I2223 (Accession NP_056253.2) is another GAM180 target gene, herein designated TARGET GENE. DKFZP586I2223 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by DKFZP586I2223, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586I2223 BINDING SITE, designated SEQ ID:11679, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27262] Another function of GAM180 is therefore inhibition of DKFZP586I2223 (Accession NP_056253.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

DKFZP586I2223.

[27263] DKFZp761K1423 (Accession NP_060892.1) is another GAM180 target gene, herein designated TARGET GENE. DKFZp761K1423 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761K1423, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761K1423 BINDING SITE, designated SEQ ID:10603, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27264] Another function of GAM180 is therefore inhibition of DKFZp761K1423 (Accession NP_060892.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761K1423.

[27265] DKFZP761M1511 (Accession XP_295135.1) is another GAM180 target gene, herein designated TARGET GENE. DKFZP761M1511 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP761M1511, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP761M1511 BINDING SITE, designated SEQ ID:898, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27266] Another function of GAM180 is therefore inhibition of DKFZP761M1511 (Accession XP_295135.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761M1511.

[27267] DKFZp762E1312 (Accession NP_060880.2) is another GAM180 target gene, herein designated TARGET GENE. DKFZp762E1312 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp762E1312, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762E1312 BINDING SITE, designated SEQ ID:19364, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27268] Another function of GAM180 is therefore inhibition of DKFZp762E1312 (Accession NP_060880.2) . Accordingly,

utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762E1312.

[27269] Dopamine receptor d2 (DRD2, Accession NP_000786.1) is another GAM180 target gene, herein designated TARGET GENE. DRD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DRD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DRD2 BINDING SITE, designated SEQ ID:8911, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27270] Another function of GAM180 is therefore inhibition of Dopamine receptor d2 (DRD2, Accession NP_000786.1), a gene which has a key role in the control of movement. and therefore may be associated with Hereditary autosomal dominant myoclonus dystonia. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of Hereditary autosomal dominant myoclonus dystonia, and of other diseases and clinical conditions associated with DRD2.

[27271] The function of DRD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM148.1.Dopamine receptor d2 (DRD2, Accession NP_057658.2) is another GAM180 target gene, herein designated TARGET GENE. DRD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DRD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DRD2 BINDING SITE, designated SEQ ID:8911, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27272] Another function of GAM180 is therefore inhibition of Dopamine receptor d2 (DRD2, Accession NP_057658.2), a gene which has a key role in the control of movement. and therefore may be associated with Hereditary autosomal dominant myoclonus dystonia. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of Hereditary autosomal dominant myoclonus dystonia, and of other diseases and clinical conditions associated with DRD2.

[27273] The function of DRD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM148.1.Dual specificity phosphatase 2 (DUSP2, Accession NP_004409.1) is another GAM180 target gene, herein designated TARGET GENE. DUSP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DUSP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP2 BINDING SITE, designated SEQ ID:13525, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27274] Another function of GAM180 is therefore inhibition of Dual specificity phosphatase 2 (DUSP2, Accession NP_004409.1), a gene which regulates mitogenic signal transduction. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP2.

[27275] The function of DUSP2 has been established by previous studies. Mitogenic stimulation of quiescent cells leads to the rapid and reversible activation of mitogen- activated

protein (MAP) kinases via dual phosphorylation within a thr- glu- tyr motif. Following activation, MAP kinases translocate into the nucleus where they phosphorylate several signal transduction targets. The dual- specificity phosphatases can reverse MAP kinase activation by de-phosphorylating phosphotyrosine and phosphothreonine residues. Rohan et al. (1993) isolated mouse and human cDNAs encoding PAC1, a mitogen- induced 32- kD protein that contains a sequence that is associated with enzymatic activity in previously identified protein phosphotyrosine phosphatases. The predicted human PAC1 protein has 314 amino acids. Northern blot analysis of human cell lines and mouse tissues revealed that PAC1 is expressed predominantly in hematopoietic tissues. By immunofluorescence of transfected cells and mitogen- stimulated T cells, Rohan et al. (1993) localized PAC1 to the nucleus. Ward et al. (1994) demonstrated that PAC1 is a dual- specific thr/tyr phosphatase that is a physiologically relevant MAP kinase phosphatase. Yi et al. (1995) determined that the PAC1, or DUSP2, gene contains 4 exons that span approximately 2.3 kb. By somatic cell hybrid analysis, linkage analysis, and in situ hybridization, Yi et al. (1995) mapped the PAC1 gene to 2p11.2- q11. Using

fluorescence in situ hybridization, Martell et al. (1994) refined the localization of the PAC1 gene to 2q11.

[27276]

[27277] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27278] Rohan, P. J.; Davis, P.; Moskaluk, C. A.; Kearns, M.; Krutzsch, H.; Siebenlist, U.; Kelly, K. : PAC- 1: a mitogen-induced nuclear protein tyrosine phosphatase. Science 259: 1763- 1766, 1993. ; and

[27279] Yi, H.; Morton, C. C.; Weremowicz, S.; McBride, O. W.; Kelly, K. : Genomic organization and chromosomal localization of the DUSP2 gene, encoding a MAP kinase phosphatase, to human 2p11.

[27280] Further studies establishing the function and utilities of DUSP2 are found in John Hopkins OMIM database record ID 603068, and in cited publications listed in Table 5, which are hereby incorporated by reference.Ephrin-a3 (EFNA3, Accession NP_004943.1) is another GAM180 target gene, herein designated TARGET GENE. EFNA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EFNA3, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EFNA3 BINDING SITE, designated SEQ ID:19601, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27281] Another function of GAM180 is therefore inhibition of Ephrin-a3 (EFNA3, Accession NP_004943.1), a gene which is a ligand of Eph- related receptor tyrosine kinases. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFNA3.

[27282] The function of EFNA3 has been established by previous studies. Proteins in the LERK subfamily of ligands, called ephrins, bind to members of the EPH group of receptor tyrosine kinases. The various ephrins are characterized by sequence similarities and the fact that they are attached to the cell membrane by glycosylphosphatidylinositol (GPI) anchors or by a single transmembrane domain. See 179610 for additional information on ephrins and the Eph receptor family. By fluorescence in situ hybridization, Cerretti et al. (1996) mapped the EPLG3 gene to a cluster on chromosome 1q21- q22, together with EPLG1 (EFNA1; 191164) and EPLG4 (EFNA4; 601380). By interspecific

backcross analysis, they mapped the mouse EPLG3 homolog (Epl3) to the central region of mouse chromosome 3. Cerretti and Nelson (1998) reported that the mouse Efna3 gene has 5 exons. The gene structures of human EFNA2 (OMIM Ref. No. 602756) and mouse Efna3, Efna4 (OMIM Ref. No. 601380), and Efnb1 (OMIM Ref. No. 300035) are conserved through the first 3 exons.

[27283]

[27284] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27285] Cerretti, D. P.; Lyman, S. D.; Kozlosky, C. J.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Valentine, V.; Kirstein, M. N.; Shapiro, D. N.; Morris, S. W. : The genes encoding the Eph- related receptor tyrosine kinase ligands LERK- 1 (EPLG1, Epl1), LERK- 3 (EPLG3, Epl3), and LERK- 4 (EPLG4, Epl4) are clustered on human chromosome 1 and mouse chromosome 3. Genomics 33: 277- 282, 1996. ; and

[27286] Cerretti, D. P.; Nelson, N. : Characterization of the genes for mouse LERK- 3/Ephrin- A3 (Epl3), mouse LERK- 4/Ephrin- A4 (Epl4), and human LERK- 6/Ephrin- A2 (EPLG6): conservation of intron/e.

[27287] Further studies establishing the function and utilities of

EFNA3 are found in John Hopkins OMIM database record ID 601381, and in cited publications listed in Table 5, which are hereby incorporated by reference.ELKS (Accession NP_055879.1) is another GAM180 target gene, herein designated TARGET GENE. ELKS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ELKS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ELKS BINDING SITE, designated SEQ ID:787, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27288] Another function of GAM180 is therefore inhibition of ELKS (Accession NP_055879.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELKS.

[27289] Ellis van creveld syndrome (EVC, Accession NP_055371.1) is another GAM180 target gene, herein designated TARGET GENE. EVC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EVC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:5644, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27290] Another function of GAM180 is therefore inhibition of Ellis van creveld syndrome (EVC, Accession NP_055371.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC.

[27291] Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075598.1) is another GAM180 target gene, herein designated TARGET GENE. FGFR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE, designated SEQ ID:5084, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27292] Another function of GAM180 is therefore inhibition of Fibroblast growth factor receptor 1 (fms-related tyrosine

kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075598.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1.

[27293] FHX (Accession NP_060886.1) is another GAM180 target gene, herein designated TARGET GENE. FHX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FHX BINDING SITE, designated SEQ ID:12381, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27294] Another function of GAM180 is therefore inhibition of FHX (Accession NP_060886.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHX.

[27295] FKSG42 (Accession NP_114421.1) is another GAM180 target gene, herein designated TARGET GENE. FKSG42 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FKSG42, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FKSG42 BINDING SITE, designated SEQ ID:17992, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27296] Another function of GAM180 is therefore inhibition of FKSG42 (Accession NP_114421.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKSG42.

[27297] FLJ10648 (Accession NP_060637.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ10648 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10648, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10648 BINDING SITE, designated SEQ ID:4717, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27298] Another function of GAM180 is therefore inhibition of FLJ10648 (Accession NP_060637.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ10648.

[27299] FLJ10970 (Accession NP_060756.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ10970 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10970, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10970 BINDING SITE, designated SEQ ID:13268, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27300] Another function of GAM180 is therefore inhibition of FLJ10970 (Accession NP_060756.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10970.

[27301] FLJ11700 (Accession NP_079168.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ11700 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11700, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ11700 BINDING SITE, designated SEQ ID:3258, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27302] Another function of GAM180 is therefore inhibition of FLJ11700 (Accession NP_079168.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11700.

[27303] FLJ12577 (Accession NP_112187.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ12577 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12577, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12577 BINDING SITE, designated SEQ ID:7536, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27304] Another function of GAM180 is therefore inhibition of FLJ12577 (Accession NP_112187.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12577.

[27305] FLJ12587 (Accession NP_071925.2) is another GAM180 target gene, herein designated TARGET GENE. FLJ12587 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12587 BINDING SITE, designated SEQ ID:1658, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27306] Another function of GAM180 is therefore inhibition of FLJ12587 (Accession NP_071925.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12587.

[27307] FLJ13902 (Accession NP_078929.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ13902 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13902, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13902 BINDING SITE, designated SEQ ID:19221, to the

nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27308] Another function of GAM180 is therefore inhibition of FLJ13902 (Accession NP_078929.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13902.

[27309] FLJ14166 (Accession NP_078841.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ14166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14166 BINDING SITE, designated SEQ ID:3589, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27310] Another function of GAM180 is therefore inhibition of FLJ14166 (Accession NP_078841.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14166.

[27311] FLJ14249 (Accession NP_567825.1) is another GAM180

target gene, herein designated TARGET GENE. FLJ14249 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ14249, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14249 BINDING SITE, designated SEQ ID:14831, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27312] Another function of GAM180 is therefore inhibition of FLJ14249 (Accession NP_567825.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14249.

[27313] FLJ14249 (Accession NP_071905.2) is another GAM180 target gene, herein designated TARGET GENE. FLJ14249 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ14249, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14249 BINDING SITE, designated

SEQ ID:14831, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27314] Another function of GAM180 is therefore inhibition of FLJ14249 (Accession NP_071905.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14249.

[27315] FLJ14936 (Accession NP_115660.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ14936 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ14936, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14936 BINDING SITE, designated SEQ ID:6933, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27316] Another function of GAM180 is therefore inhibition of FLJ14936 (Accession NP_115660.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14936.

[27317] FLJ20174 (Accession NP_060169.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ20174 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20174, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20174 BINDING SITE, designated SEQ ID:4747, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27318] Another function of GAM180 is therefore inhibition of FLJ20174 (Accession NP_060169.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20174.

[27319] FLJ20297 (Accession NP_060421.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ20297 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ20297, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20297 BINDING SITE, designated

SEQ ID:1321, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27320] Another function of GAM180 is therefore inhibition of FLJ20297 (Accession NP_060421.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20297.

[27321] FLJ20297 (Accession NP_060221.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ20297 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ20297, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20297 BINDING SITE, designated SEQ ID:1321, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27322] Another function of GAM180 is therefore inhibition of FLJ20297 (Accession NP_060221.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20297.

[27323] FLJ20298 (Accession NP_060222.1) is another GAM180

target gene, herein designated TARGET GENE. FLJ20298 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20298, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20298 BINDING SITE, designated SEQ ID:11216, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27324] Another function of GAM180 is therefore inhibition of FLJ20298 (Accession NP_060222.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20298.

[27325] FLJ20511 (Accession NP_060323.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ20511 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20511, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20511 BINDING SITE, designated SEQ ID:14414, to the nucleotide sequence of GAM180 RNA, herein designated

GAM RNA, also designated SEQ ID:214.

[27326] Another function of GAM180 is therefore inhibition of FLJ20511 (Accession NP_060323.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20511.

[27327] FLJ20573 (Accession XP_033853.2) is another GAM180 target gene, herein designated TARGET GENE. FLJ20573 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20573, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20573 BINDING SITE, designated SEQ ID:11877, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27328] Another function of GAM180 is therefore inhibition of FLJ20573 (Accession XP_033853.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20573.

[27329] FLJ20666 (Accession NP_060392.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ20666

BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ20666, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20666 BINDING SITE, designated SEQ ID:8314, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27330] Another function of GAM180 is therefore inhibition of FLJ20666 (Accession NP_060392.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20666.

[27331] FLJ22167 (Accession NP_078809.2) is another GAM180 target gene, herein designated TARGET GENE. FLJ22167 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22167 BINDING SITE, designated SEQ ID:6807, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27332] Another function of GAM180 is therefore inhibition of FLJ22167 (Accession NP_078809.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22167.

[27333] FLJ22578 (Accession NP_079140.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ22578 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22578, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22578 BINDING SITE, designated SEQ ID:8608, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27334] Another function of GAM180 is therefore inhibition of FLJ22578 (Accession NP_079140.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22578.

[27335] FLJ23074 (Accession NP_079328.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ23074 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ23074, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23074 BINDING SITE, designated SEQ ID:16835, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27336] Another function of GAM180 is therefore inhibition of FLJ23074 (Accession NP_079328.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23074.

[27337] FLJ23462 (Accession NP_079119.2) is another GAM180 target gene, herein designated TARGET GENE. FLJ23462 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23462, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23462 BINDING SITE, designated SEQ ID:7500, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27338] Another function of GAM180 is therefore inhibition of

FLJ23462 (Accession NP_079119.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23462.

[27339] FLJ30679 (Accession NP_694562.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ30679 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30679, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30679 BINDING SITE, designated SEQ ID:2972, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27340] Another function of GAM180 is therefore inhibition of FLJ30679 (Accession NP_694562.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30679.

[27341] FLJ32452 (Accession NP_653177.2) is another GAM180 target gene, herein designated TARGET GENE. FLJ32452 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32452, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32452 BINDING SITE, designated SEQ ID:2212, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27342] Another function of GAM180 is therefore inhibition of FLJ32452 (Accession NP_653177.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32452.

[27343] FLJ34658 (Accession NP_689617.2) is another GAM180 target gene, herein designated TARGET GENE. FLJ34658 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ34658, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34658 BINDING SITE, designated SEQ ID:4616, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27344] Another function of GAM180 is therefore inhibition of FLJ34658 (Accession NP_689617.2) . Accordingly, utilities

of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34658.

[27345] FLJ34817 (Accession NP_689516.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ34817 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ34817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34817 BINDING SITE, designated SEQ ID:1005, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27346] Another function of GAM180 is therefore inhibition of FLJ34817 (Accession NP_689516.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34817.

[27347] FLJ39957 (Accession NP_689749.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ39957 BINDING SITE1 and FLJ39957 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ39957, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39957 BINDING SITE1 and FLJ39957 BINDING SITE2, designated SEQ ID:12852 and SEQ ID:2358 respectively, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27348] Another function of GAM180 is therefore inhibition of FLJ39957 (Accession NP_689749.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39957.

[27349] FLJ40235 (Accession NP_775906.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ40235 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ40235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ40235 BINDING SITE, designated SEQ ID:4486, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27350] Another function of GAM180 is therefore inhibition of

FLJ40235 (Accession NP_775906.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ40235.

[27351] FLJ90798 (Accession NP_699198.1) is another GAM180 target gene, herein designated TARGET GENE. FLJ90798 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90798, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90798 BINDING SITE, designated SEQ ID:14320, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27352] Another function of GAM180 is therefore inhibition of FLJ90798 (Accession NP_699198.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90798.

[27353] Forkhead box p1 (FOXP1, Accession NP_116071.2) is another GAM180 target gene, herein designated TARGET GENE. FOXP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FOXP1,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXP1 BINDING SITE, designated SEQ ID:19853, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27354] Another function of GAM180 is therefore inhibition of Forkhead box p1 (FOXP1, Accession NP_116071.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXP1.

[27355] Formyl peptide receptor 1 (FPR1, Accession NP_002020.1) is another GAM180 target gene, herein designated TARGET GENE. FPR1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FPR1 BINDING SITE, designated SEQ ID:2325, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27356] Another function of GAM180 is therefore inhibition of Formyl peptide receptor 1 (FPR1, Accession NP_002020.1)

. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FPR1.

[27357] Formyl peptide receptor-like 2 (FPRL2, Accession NP_002021.2) is another GAM180 target gene, herein designated TARGET GENE. FPRL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FPRL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FPRL2 BINDING SITE, designated SEQ ID:13294, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27358] Another function of GAM180 is therefore inhibition of Formyl peptide receptor-like 2 (FPRL2, Accession NP_002021.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FPRL2.

[27359] Fucosyltransferase 3 (galactoside 3(4)-l-fucosyltransferase, lewis blood group included) (FUT3, Accession NP_000140.1) is another GAM180 target gene, herein designated TARGET GENE. FUT3 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FUT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FUT3 BINDING SITE, designated SEQ ID:2915, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27360] Another function of GAM180 is therefore inhibition of Fucosyltransferase 3 (galactoside 3(4)-l-fucosyltransferase, lewis blood group included) (FUT3, Accession NP_000140.1), a gene which may catalyze alpha- 1,3 and alpha- 1,4 glycosidic linkages involved in the expression of vim- 2, lewis a, lewis b, sialyl lewis x and lewis x/ssea-1 antigens. and therefore may be associated with Lewis-negative disease. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of Lewis- negative disease., and of other diseases and clinical conditions associated with FUT3.

[27361] The function of FUT3 has been established by previous studies. The Lewis system involves genetically variable antigens in the body fluids and only secondarily are the antigens absorbed to red cells. Grollman et al. (1969)

showed that Lewis- negative women lack a specific fucosyltransferase which is present in the milk of Lewis- positive women. The enzyme is apparently required for synthesis of the structural determinants of both Lewis (a) and Lewis (b) specificity. The same enzyme is involved in the synthesis of milk oligosaccharides, because 2 oligosaccharides containing the relevant linkage were absent from the milk of Lewis- negative women. Grubb (1953) provided the ingenious interpretation of the interactions between the Les locus determining presence/absence of Lewis substance in the saliva and on red cells and the Se locus (OMIM Ref. No. 182100) determining secretion of ABH blood group substances in the saliva and Le(a) or Le(b) expression in red cells. In transfusion medicine, it has been found that some individuals who type as Lewis-positive on erythrocytes can change their erythrocyte phenotype to Lewis- negative during diseases or during pregnancy. Orntoft et al. (1996) noted that these patients have been named non- genuine Lewis- negative individuals as they have alpha- 1- 4 fucosyltransferase activity in saliva. Due to this phenomenon, the Lewis- negative phenotype is more common among cancer patients (approximately 20%) than among healthy individuals (approximately 8%).

Orntoft et al. (1996) examined the mutational spectrum of the Lewis gene in Denmark and found 6 different mutations. Five, 59T- G (L20R; 111100.0001), 202T- C (W68R), 314C- T (T105M), 508G- A (G170S; 111100.0001), and 1067T- A (I356K), were frequent, and 1, 445C- A (L146M), was only detected in 1 of 40 individuals. The authors demonstrated that the nucleotide 202 and 314 mutations were located on the same allele. COS- 7 cells transfected with an allele having the 202/314 mutations lacked enzyme activity. Lewis- negative patients, whose erythrocytes converted from Lewis- positive to Lewis- negative during their disease, showed FUT3 heterozygosity significantly more often than did others (p less than 0.05). Pang et al. (1998) identified 5 novel missense mutations in the FUT3 gene in African (Xhosa) and Caucasian subjects in South Africa.

[27362]

[27363] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27364] Grollman, E. F.; Kobata, A.; Ginsburg, V. : An enzymatic basis for Lewis blood types in man. J. Clin. Invest. 48: 1489- 1494, 1969. ; and

[27365] Orntoft, T. F.; Vestergaard, E. M.; Holmes, E.; Jakobsen, J. S.; Grunnet, N.; Mortensen, M.; Johnson, P.; Bross, P.; Gregersen, N.; Skorstengaard, K.; Jensen, U. B.; Bolund, L.; Wolf, H.

[27366] Further studies establishing the function and utilities of FUT3 are found in John Hopkins OMIM database record ID 111100, and in cited publications listed in Table 5, which are hereby incorporated by reference.Fucosyltransferase 5 (alpha (1,3) fucosyltransferase) (FUT5, Accession NP_002025.1) is another GAM180 target gene, herein designated TARGET GENE. FUT5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FUT5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FUT5 BINDING SITE, designated SEQ ID:2915, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27367] Another function of GAM180 is therefore inhibition of Fucosyltransferase 5 (alpha (1,3) fucosyltransferase) (FUT5, Accession NP_002025.1), a gene which may catalyse alpha- 1,3 glycosidic linkages involved in the expression of vim- 2, lewis x/ssea- 1 and sialyl lewis x antigens. Ac-

cordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUT5.

[27368] The function of FUT5 has been established by previous studies. Weston et al. (1992) isolated a human alpha- 3-fucosyltransferase gene homologous to but distinct from 2 previously reported fucosyltransferase genes: alpha-3,4- fucosyltransferase, thought to represent the human Lewis blood group locus (FUT3; 111100), and an alpha-3- fucosyltransferase expressed in the myeloid lineage (FUT4; 104230). The new enzyme shared 91% amino acid sequence identity with the Lewis blood group fucosyltransferase, yet exhibited only trace amounts of alpha- 4-fucosyltransferase activity. By PCR analysis of somatic cell hybrid DNAs, Weston et al. (1992) demonstrated that the gene is located on chromosome 19. They concluded that the gene encodes a 'plasma type' of alpha- 3- fucosyltransferase. McCurley et al. (1995) mapped FUT5 to 19p13.3 by fluorescence in situ hybridization using cosmids containing FUT6 (OMIM Ref. No. 136836) and FUT5. The results indicated that FUT6 lies approximately 70 kb telomeric of FUT5. McCurley et al. (1995) used conventional and pulsed field gel electrophoresis mapping to to-

tal genomic DNA and large genomic clones in order to generate a fine map of the cluster of 19p FUT genes. A P1 clone indicated the gene order: cen- - FUT5- - FUT3- - FUT6- - tel. FUT5 and FUT3 are separated by 23 kb and FUT3 and FUT6 are separated by 14 kb; these data placed FUT5 and FUT6 closer together than was estimated by fluorescence in situ hybridization. The close proximity and tandem orientation of the 3 genes suggests coordinate regulation. The direction of transcription is toward the telomere in the case of all 3 genes

[27369]

[27370] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27371] McCurley, R. S.; Recinos, A., III; Olsen, A. S.; Gingrich, J. C.; Szczepaniak, D.; Cameron, H. S.; Krauss, R.; Weston, B. W. : Physical maps of human alpha(1,3)fucosyltransferase genes FUT3- FUT6 on chromosomes 19p13.3 and 11q21. Genomics 26: 142- 146, 1995. ; and

[27372] Weston, B. W.; Nair, R. P.; Larsen, R. D.; Lowe, J. B. : Isolation of a novel human alpha(1,3)fucosyltransferase gene and molecular comparison to the human Lewis blood group alpha(1,3/1.

[27373] Further studies establishing the function and utilities of FUT5 are found in John Hopkins OMIM database record ID 136835, and in cited publications listed in Table 5, which are hereby incorporated by reference.Fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6, Accession NP_000141.1) is another GAM180 target gene, herein designated TARGET GENE. FUT6 BINDING SITE1 and FUT6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FUT6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FUT6 BINDING SITE1 and FUT6 BINDING SITE2, designated SEQ ID:5353 and SEQ ID:7499 respectively, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27374] Another function of GAM180 is therefore inhibition of Fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6, Accession NP_000141.1), a gene which is involved in the biosynthesis of the e- selectin ligand, sialyl- lewis x. catalyzes the transfer of fucose from gdp- beta- fucose to alpha- 2,3 sialylated substrates. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with FUT6.

[27375] The function of FUT6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Fxyd domain containing ion transport regulator 3 (FXYD3, Accession NP_005962.1) is another GAM180 target gene, herein designated TARGET GENE. FXYD3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FXYD3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FXYD3 BINDING SITE, designated SEQ ID:3047, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27376] Another function of GAM180 is therefore inhibition of Fxyd domain containing ion transport regulator 3 (FXYD3, Accession NP_005962.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FXYD3.

[27377] Fxyd domain containing ion transport regulator 3 (FXYD3, Accession NP_068710.1) is another GAM180 target gene, herein designated TARGET GENE. FXYD3 BINDING SITE is a

target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FXYD3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FXYD3 BINDING SITE, designated SEQ ID:3047, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27378] Another function of GAM180 is therefore inhibition of Fxyd domain containing ion transport regulator 3 (FXYD3, Accession NP_068710.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FXYD3.

[27379] Gamma-aminobutyric acid (gaba) b receptor, 1 (GABBR1, Accession NP_068705.1) is another GAM180 target gene, herein designated TARGET GENE. GABBR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GABBR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GABBR1 BINDING SITE, designated SEQ ID:7008, to the nucleotide sequence of GAM180 RNA, herein designated

GAM RNA, also designated SEQ ID:214.

[27380] Another function of GAM180 is therefore inhibition of Gamma-aminobutyric acid (gaba) b receptor, 1 (GABBR1, Accession NP_068705.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABBR1.

[27381] GAC1 (Accession NP_006329.1) is another GAM180 target gene, herein designated TARGET GENE. GAC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAC1 BINDING SITE, designated SEQ ID:7458, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27382] Another function of GAM180 is therefore inhibition of GAC1 (Accession NP_006329.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAC1.

[27383] Glycoprotein a repetitions predominant (GARP, Accession NP_005503.1) is another GAM180 target gene, herein designated TARGET GENE. GARP BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by GARP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GARP BINDING SITE, designated SEQ ID:10909, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27384] Another function of GAM180 is therefore inhibition of Glycoprotein a repetitions predominant (GARP, Accession NP_005503.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GARP.

[27385] Glucocorticoid induced transcript 1 (GLCCI1, Accession XP_166529.2) is another GAM180 target gene, herein designated TARGET GENE. GLCCI1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLCCI1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GLCCI1 BINDING SITE, designated SEQ ID:14024, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:214.

[27386] Another function of GAM180 is therefore inhibition of Glucocorticoid induced transcript 1 (GLCCI1, Accession XP_166529.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLCCI1.

[27387] Glutamate-ammonia ligase (glutamine synthase) (GLUL, Accession NP_002056.2) is another GAM180 target gene, herein designated TARGET GENE. GLUL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLUL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GLUL BINDING SITE, designated SEQ ID:661, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27388] Another function of GAM180 is therefore inhibition of Glutamate-ammonia ligase (glutamine synthase) (GLUL, Accession NP_002056.2), a gene which catalyzes the condensation of glutamate and ammonia to form glutamine. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with GLUL.

[27389] The function of GLUL has been established by previous studies. Glutamine synthetase (EC 6.3.1.2), also called glutamate- ammonia ligase (GLUL), is expressed throughout the body and plays an important role in controlling body pH and in removing ammonia from the circulation. The enzyme clears L- glutamate, the major neurotransmitter in the central nervous system, from neuronal synapses (see OMIM Ref. No. references in Clancy et al., 1996). Gibbs et al. (1987) reported the complete 1,119-bp coding sequence of glutamine synthetase, which they determined from a liver- derived cDNA. Pesole et al. (1991) suggested that glutamine synthetase is a good molecular clock for determining times of divergence even as great as that which occurred between eukaryotes and prokaryotes. One conclusion reached by Pesole et al. (1991) was that organelle- specific enzymes, such as those of the mitochondria, may have originated from a duplication of nuclear genes. The endosymbiotic hypothesis suggests that a transfer of prokaryotic genes to nuclei occurred during the evolution of the primitive eukaryotic cell. In some cases, it is likely that the old prokaryotic gene could not be active in the new nuclear genome envi-

ronment and was totally lost because its function in the organelle could be dispensed with. Subsequently, a new organelle- specific enzyme could have originated to serve specialized metabolic functions. The presence of glutamine synthetase in mitochondria is linked to the nitrogen metabolism of the species, and in particular to the need for glutamine as a source of ammonia and for particular biochemical pathways for ammonia detoxification.

[27390]

[27391] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27392] Gibbs, C. S.; Campbell, K. E.; Wilson, R. H. : Sequence of a human glutamine synthetase cDNA. Nucleic Acids Res. 15: 6293 only, 1987. ; and

[27393] Pesole, G.; Bozzetti, M. P.; Lanave, C.; Preparata, G.; Saccone, C. : Glutamine synthetase gene evolution: a good molecular clock. Proc. Nat. Acad. Sci. 88: 522- 526, 1991.

[27394] Further studies establishing the function and utilities of GLUL are found in John Hopkins OMIM database record ID 138290, and in cited publications listed in Table 5, which are hereby incorporated by reference.gm117 (Accession XP_086187.1) is another GAM180 target gene, herein

designated TARGET GENE. gm117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by gm117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of gm117 BINDING SITE, designated SEQ ID:1842, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27395] Another function of GAM180 is therefore inhibition of gm117 (Accession XP_086187.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with gm117.

[27396] GPR124 (Accession NP_116166.6) is another GAM180 target gene, herein designated TARGET GENE. GPR124 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR124, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR124 BINDING SITE, designated SEQ ID:14853, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27397] Another function of GAM180 is therefore inhibition of

GPR124 (Accession NP_116166.6) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR124.

[27398] Hyaluronan synthase 3 (HAS3, Accession NP_005320.2) is another GAM180 target gene, herein designated TARGET GENE. HAS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by HAS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HAS3 BINDING SITE, designated SEQ ID:17871, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27399] Another function of GAM180 is therefore inhibition of Hyaluronan synthase 3 (HAS3, Accession NP_005320.2), a gene which plays a role in hyaluronan/hyaluronic acid (ha) synthesis. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAS3.

[27400] The function of HAS3 has been established by previous studies. Hyaluronan (HA) is an unbranched glycosamino-

glycan composed of repeating disaccharide units. It is a major constituent of the extracellular matrix and has been implicated in development, tumorigenesis, and several diseases. HA is synthesized at the inner face of the plasma membrane and is subsequently extruded to the outside of the cell. By degenerate PCR, Spicer et al. (1997) isolated a genomic fragment of human HA synthase- 3 (HAS3) and genomic and cDNA clones of mouse Has3. The amino acid sequences encoded by the partial HAS3 fragment and the corresponding region of Has3 are 99% conserved. The authors noted that the high degree of sequence conservation between specific human and mouse HASs contrasts with the lower level of identity between HASs within a species, suggesting an evolutionary conservation of functionally important residues and differences in the mode of action of the various HASs. The predicted 554- amino acid Has3 has several consensus HA- binding motifs and multiple transmembrane domains, with 2 at the N terminus and a cluster at the C terminus. Expression of Has3 in COS- 1 cells led to high levels of HA biosynthesis. Northern blot analysis of the mouse embryo showed that Has3 is predominantly expressed at late gestation as a major, approximately 6.0- to 6.5- kb transcript and a minor, ap-

proximately 4.0- kb transcript. By PCR screening somatic cell hybrid DNAs and a YAC contig, Spicer et al. (1997) localized the human HAS3 gene to 16q22.1. By interspecific backcross analysis, they mapped the mouse Has3 gene to chromosome 8. Since HAS1 (OMIM Ref. No. 601463), HAS2 (OMIM Ref. No. 601636), and HAS3 are located on different autosomes, Spicer et al. (1997) suggested that the HAS gene family arose comparatively early in vertebrate evolution by sequential duplication of an ancestral HAS gene.

[27401]

[27402] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27403] Spicer, A. P.; Olson, J. S.; McDonald, J. A. : Molecular cloning and characterization of a cDNA encoding the third putative mammalian hyaluronan synthase. J. Biol. Chem. 272: 8957- 8961, 1997. ; and

[27404] Spicer, A. P.; Seldin, M. F.; Olsen, A. S.; Brown, N.; Wells, D. E.; Doggett, N. A.; Itano, N.; Kimata, K.; Inazawa, J.; McDonald, J. A. : Chromosomal localization of the human and mous.

[27405] Further studies establishing the function and utilities of

HAS3 are found in John Hopkins OMIM database record ID 602428, and in cited publications listed in Table 5, which are hereby incorporated by reference.Huntingtin (huntington disease) (HD, Accession NP_002102.2) is another GAM180 target gene, herein designated TARGET GENE. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HD BINDING SITE, designated SEQ ID:4516, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27406] Another function of GAM180 is therefore inhibition of Huntingtin (huntington disease) (HD, Accession NP_002102.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HD.

[27407] Huntingtin interacting protein 1 (HIP1, Accession NP_005329.2) is another GAM180 target gene, herein designated TARGET GENE. HIP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HIP1, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIP1 BINDING SITE, designated SEQ ID:17634, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27408] Another function of GAM180 is therefore inhibition of Huntingtin interacting protein 1 (HIP1, Accession NP_005329.2), a gene which is a membrane protein and interacts with huntingtin. and therefore may be associated with Huntington disease. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of Huntington disease, and of other diseases and clinical conditions associated with HIP1.

[27409] The function of HIP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Hiv-1 tat interactive protein, 60kda (HTATIP, Accession NP_006379.1) is another GAM180 target gene, herein designated TARGET GENE. HTATIP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTATIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTATIP BINDING SITE, designated SEQ ID:20106, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27410] Another function of GAM180 is therefore inhibition of Hiv-1 tat interactive protein, 60kda (HTATIP, Accession NP_006379.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTATIP.

[27411] Interleukin 4 induced 1 (IL4I1, Accession NP_690863.1) is another GAM180 target gene, herein designated TARGET GENE. IL4I1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by IL4I1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL4I1 BINDING SITE, designated SEQ ID:17359, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27412] Another function of GAM180 is therefore inhibition of Interleukin 4 induced 1 (IL4I1, Accession NP_690863.1) .

Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL4I1.

[27413] KIAA0258 (Accession NP_055600.1) is another GAM180 target gene, herein designated TARGET GENE. KIAA0258 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0258, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0258 BINDING SITE, designated SEQ ID:10239, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27414] Another function of GAM180 is therefore inhibition of KIAA0258 (Accession NP_055600.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0258.

[27415] KIAA0513 (Accession NP_055547.1) is another GAM180 target gene, herein designated TARGET GENE. KIAA0513 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0513, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE, designated SEQ ID:931, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27416] Another function of GAM180 is therefore inhibition of KIAA0513 (Accession NP_055547.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513.

[27417] KIAA0682 (Accession NP_055667.1) is another GAM180 target gene, herein designated TARGET GENE. KIAA0682 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA0682, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0682 BINDING SITE, designated SEQ ID:12275, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27418] Another function of GAM180 is therefore inhibition of KIAA0682 (Accession NP_055667.1) . Accordingly, utilities

of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0682.

[27419] KIAA0753 (Accession NP_055619.1) is another GAM180 target gene, herein designated TARGET GENE. KIAA0753 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0753, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0753 BINDING SITE, designated SEQ ID:10688, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27420] Another function of GAM180 is therefore inhibition of KIAA0753 (Accession NP_055619.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0753.

[27421] KIAA0935 (Accession XP_052620.6) is another GAM180 target gene, herein designated TARGET GENE. KIAA0935 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0935, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0935 BINDING SITE, designated SEQ ID:17230, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27422] Another function of GAM180 is therefore inhibition of KIAA0935 (Accession XP_052620.6) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0935.

[27423] KIAA1111 (Accession XP_171233.1) is another GAM180 target gene, herein designated TARGET GENE. KIAA1111 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1111, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1111 BINDING SITE, designated SEQ ID:15309, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27424] Another function of GAM180 is therefore inhibition of KIAA1111 (Accession XP_171233.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA1111.

[27425] KIAA1194 (Accession NP_056270.2) is another GAM180 target gene, herein designated TARGET GENE. KIAA1194 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1194 BINDING SITE, designated SEQ ID:5209, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27426] Another function of GAM180 is therefore inhibition of KIAA1194 (Accession NP_056270.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1194.

[27427] KIAA1268 (Accession XP_291055.1) is another GAM180 target gene, herein designated TARGET GENE. KIAA1268 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA1268 BINDING SITE, designated SEQ ID:16742, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27428] Another function of GAM180 is therefore inhibition of KIAA1268 (Accession XP_291055.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1268.

[27429] KIAA1765 (Accession XP_047355.1) is another GAM180 target gene, herein designated TARGET GENE. KIAA1765 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1765, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1765 BINDING SITE, designated SEQ ID:15863, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27430] Another function of GAM180 is therefore inhibition of KIAA1765 (Accession XP_047355.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1765.

[27431] KIAA2001 (Accession XP_291322.1) is another GAM180 target gene, herein designated TARGET GENE. KIAA2001 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA2001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA2001 BINDING SITE, designated SEQ ID:16865, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27432] Another function of GAM180 is therefore inhibition of KIAA2001 (Accession XP_291322.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2001.

[27433] KIAA2024 (Accession NP_742067.1) is another GAM180 target gene, herein designated TARGET GENE. KIAA2024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA2024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA2024 BINDING SITE, designated SEQ ID:9621, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27434] Another function of GAM180 is therefore inhibition of KIAA2024 (Accession NP_742067.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2024.

[27435] Karyopherin (importin) beta 1 (KPNB1, Accession NP_002256.2) is another GAM180 target gene, herein designated TARGET GENE. KPNB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KPNB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KPNB1 BINDING SITE, designated SEQ ID:15603, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27436] Another function of GAM180 is therefore inhibition of Karyopherin (importin) beta 1 (KPNB1, Accession NP_002256.2), a gene which is required for nuclear protein import and mediates docking of import substrate to

distinct nucleoporins. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KPNB1.

[27437] The function of KPNB1 has been established by previous studies. The import of proteins into the nucleus proceeds through the nuclear pore complex. Cytoplasmic proteins with a nuclear localization signal (NLS) bind to an importin- alpha/importin- beta heterodimer. The trimeric complex docks to the cytoplasmic periphery of the nuclear pore complex and is subsequently translocated through as a single entity. The import reaction is terminated by the direct binding of RAN (OMIM Ref. No. 601179) to KPNB, which dissociates the importin heterodimer. Gorlich et al. (1995) purified a 90- kD subunit of importin (importin-90) from Xenopus egg extracts and obtained a 188-amino acid partial protein sequence from internal peptides. Using the partial amino acid sequence, they isolated cDNAs encoding human importin- 90, or KPNB1, from a HeLa cell cDNA library. The sequence of the predicted 876- amino acid human KPNB1 protein is 93% identical to the 188- amino acid partial sequence of Xenopus importin- 90. Gorlich et al. (1995) showed that Xenopus importin- 60 and importin- 90 cooperate to form an import

receptor that distinguishes functional NLSs from nonfunctional ones and selectively binds import substrates to the nuclear envelope. Independently, Chi et al. (1995) identified cDNAs encoding human KPNB1. Based on the 97- kD product of in vitro translation, they designated the protein p97. Using a monoclonal antibody against bovine p97, Chi et al. (1995) localized p97 to the cytoplasm and nuclear envelope of bovine kidney cells. These authors found that recombinant human p97 binds zinc and that a bound metal ion is required for nuclear envelope- binding activity. Kutay et al. (1997) identified the regions of KPNB1 that interact with RAN, importin- alpha, and the nuclear pore complex. Bayliss et al. (2000) described the crystal structure of a complex between KPNB1 residues 1 to 442 and 5 tandem FxFG nucleoporin repeats from yeast Nsp1. By fluorescence in situ hybridization, Ayala- Madrigal et al. (2000) mapped the KPNB1 gene to chromosome 17q21. By FISH, Matsuda et al. (1996) mapped the mouse Kpnb1 gene to the proximal end of chromosome 11D.

[27438]

[27439] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27440] Ayala- Madrigal, M. L.; Doerr, S.; Ramirez- Duenas, M. L.; Hansmann, I. : Assignment of KPNA4 and KPNB1 encoding karyopherin alpha 4 and beta 1 to human chromosome bands 11q22 and 17q21 respectively, by in situ hybridization. Cytogenet. Cell Genet. 89: 258- 259, 2000. ; and

[27441] Bayliss, R.; Littlewood, T.; Stewart, M. : Structural basis for the interaction between FxFG nucleoporin repeats and importin- beta in nuclear trafficking. Cell 102: 99- 108, 2000.

[27442] Further studies establishing the function and utilities of KPNB1 are found in John Hopkins OMIM database record ID 602738, and in cited publications listed in Table 5, which are hereby incorporated by reference.LOC114987 (Accession NP_660284.1) is another GAM180 target gene, herein designated TARGET GENE. LOC114987 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC114987, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC114987 BINDING SITE, designated SEQ ID:1173, to the nucleotide sequence of GAM180 RNA, herein designated

GAM RNA, also designated SEQ ID:214.

[27443] Another function of GAM180 is therefore inhibition of LOC114987 (Accession NP_660284.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC114987.

[27444] LOC116437 (Accession XP_058185.1) is another GAM180 target gene, herein designated TARGET GENE. LOC116437 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC116437, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC116437 BINDING SITE, designated SEQ ID:1933, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27445] Another function of GAM180 is therefore inhibition of LOC116437 (Accession XP_058185.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116437.

[27446] LOC126162 (Accession XP_064964.5) is another GAM180 target gene, herein designated TARGET GENE. LOC126162

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC126162, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126162 BINDING SITE, designated SEQ ID:16559, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27447] Another function of GAM180 is therefore inhibition of LOC126162 (Accession XP_064964.5) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126162.

[27448] LOC126767 (Accession XP_060167.4) is another GAM180 target gene, herein designated TARGET GENE. LOC126767 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC126767, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126767 BINDING SITE, designated SEQ ID:8959, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27449] Another function of GAM180 is therefore inhibition of LOC126767 (Accession XP_060167.4) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126767.

[27450] LOC129198 (Accession XP_072197.3) is another GAM180 target gene, herein designated TARGET GENE. LOC129198 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC129198, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC129198 BINDING SITE, designated SEQ ID:13916, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27451] Another function of GAM180 is therefore inhibition of LOC129198 (Accession XP_072197.3) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129198.

[27452] LOC142941 (Accession XP_096363.1) is another GAM180 target gene, herein designated TARGET GENE. LOC142941 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC142941, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC142941 BINDING SITE, designated SEQ ID:788, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27453] Another function of GAM180 is therefore inhibition of LOC142941 (Accession XP_096363.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142941.

[27454] LOC143310 (Accession XP_084485.1) is another GAM180 target gene, herein designated TARGET GENE. LOC143310 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC143310, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143310 BINDING SITE, designated SEQ ID:10414, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27455] Another function of GAM180 is therefore inhibition of

LOC143310 (Accession XP_084485.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143310.

[27456] LOC143916 (Accession XP_084664.1) is another GAM180 target gene, herein designated TARGET GENE. LOC143916 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC143916, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143916 BINDING SITE, designated SEQ ID:7055, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27457] Another function of GAM180 is therefore inhibition of LOC143916 (Accession XP_084664.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143916.

[27458] LOC144017 (Accession XP_096520.1) is another GAM180 target gene, herein designated TARGET GENE. LOC144017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144017, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144017 BINDING SITE, designated SEQ ID:2879, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27459] Another function of GAM180 is therefore inhibition of LOC144017 (Accession XP_096520.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144017.

[27460] LOC147804 (Accession XP_085901.1) is another GAM180 target gene, herein designated TARGET GENE. LOC147804 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147804, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147804 BINDING SITE, designated SEQ ID:1554, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27461] Another function of GAM180 is therefore inhibition of LOC147804 (Accession XP_085901.1) . Accordingly, utili-

ties of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147804.

[27462] LOC147975 (Accession XP_097351.2) is another GAM180 target gene, herein designated TARGET GENE. LOC147975 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147975 BINDING SITE, designated SEQ ID:19458, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27463] Another function of GAM180 is therefore inhibition of LOC147975 (Accession XP_097351.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147975.

[27464] LOC148490 (Accession XP_086210.2) is another GAM180 target gene, herein designated TARGET GENE. LOC148490 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148490, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148490 BINDING SITE, designated SEQ ID:16289, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27465] Another function of GAM180 is therefore inhibition of LOC148490 (Accession XP_086210.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148490.

[27466] LOC150225 (Accession XP_097870.1) is another GAM180 target gene, herein designated TARGET GENE. LOC150225 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150225, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150225 BINDING SITE, designated SEQ ID:18952, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27467] Another function of GAM180 is therefore inhibition of LOC150225 (Accession XP_097870.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC150225.

[27468] LOC150776 (Accession XP_032542.1) is another GAM180 target gene, herein designated TARGET GENE. LOC150776 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150776, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150776 BINDING SITE, designated SEQ ID:1321, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27469] Another function of GAM180 is therefore inhibition of LOC150776 (Accession XP_032542.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150776.

[27470] LOC151568 (Accession NP_612492.1) is another GAM180 target gene, herein designated TARGET GENE. LOC151568 BINDING SITE1 and LOC151568 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC151568, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151568 BINDING SITE1 and LOC151568 BINDING SITE2, designated SEQ ID:15467 and SEQ ID:5239 respectively, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27471] Another function of GAM180 is therefore inhibition of LOC151568 (Accession NP_612492.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151568.

[27472] LOC152445 (Accession XP_098231.1) is another GAM180 target gene, herein designated TARGET GENE. LOC152445 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE, designated SEQ ID:10081, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27473] Another function of GAM180 is therefore inhibition of LOC152445 (Accession XP_098231.1) . Accordingly, utili-

ties of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152445.

[27474] LOC162083 (Accession XP_091339.2) is another GAM180 target gene, herein designated TARGET GENE. LOC162083 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC162083, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162083 BINDING SITE, designated SEQ ID:9824, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27475] Another function of GAM180 is therefore inhibition of LOC162083 (Accession XP_091339.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162083.

[27476] LOC164091 (Accession XP_089356.1) is another GAM180 target gene, herein designated TARGET GENE. LOC164091 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC164091, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC164091 BINDING SITE, designated SEQ ID:7693, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27477] Another function of GAM180 is therefore inhibition of LOC164091 (Accession XP_089356.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164091.

[27478] LOC165257 (Accession XP_092478.3) is another GAM180 target gene, herein designated TARGET GENE. LOC165257 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC165257, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC165257 BINDING SITE, designated SEQ ID:1432, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27479] Another function of GAM180 is therefore inhibition of LOC165257 (Accession XP_092478.3) . Accordingly, utilities of GAM180 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC165257.

[27480] LOC200609 (Accession XP_117256.1) is another GAM180 target gene, herein designated TARGET GENE. LOC200609 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC200609, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200609 BINDING SITE, designated SEQ ID:1876, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27481] Another function of GAM180 is therefore inhibition of LOC200609 (Accession XP_117256.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200609.

[27482] LOC201562 (Accession XP_114343.2) is another GAM180 target gene, herein designated TARGET GENE. LOC201562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC201562 BINDING SITE, designated SEQ ID:12642, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27483] Another function of GAM180 is therefore inhibition of LOC201562 (Accession XP_114343.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201562.

[27484] LOC219918 (Accession XP_166197.1) is another GAM180 target gene, herein designated TARGET GENE. LOC219918 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC219918, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219918 BINDING SITE, designated SEQ ID:5660, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27485] Another function of GAM180 is therefore inhibition of LOC219918 (Accession XP_166197.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC219918.

[27486] LOC220071 (Accession XP_167848.1) is another GAM180 target gene, herein designated TARGET GENE. LOC220071 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC220071, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220071 BINDING SITE, designated SEQ ID:5660, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27487] Another function of GAM180 is therefore inhibition of LOC220071 (Accession XP_167848.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220071.

[27488] LOC220758 (Accession XP_165466.1) is another GAM180 target gene, herein designated TARGET GENE. LOC220758 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC220758, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC220758 BINDING SITE, designated SEQ ID:1949, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27489] Another function of GAM180 is therefore inhibition of LOC220758 (Accession XP_165466.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220758.

[27490] LOC220763 (Accession XP_055551.1) is another GAM180 target gene, herein designated TARGET GENE. LOC220763 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC220763, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220763 BINDING SITE, designated SEQ ID:5457, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27491] Another function of GAM180 is therefore inhibition of LOC220763 (Accession XP_055551.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220763.

[27492] LOC221584 (Accession XP_168132.1) is another GAM180 target gene, herein designated TARGET GENE. LOC221584 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221584, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221584 BINDING SITE, designated SEQ ID:13096, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27493] Another function of GAM180 is therefore inhibition of LOC221584 (Accession XP_168132.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221584.

[27494] LOC253044 (Accession XP_172924.2) is another GAM180 target gene, herein designated TARGET GENE. LOC253044 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253044, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253044 BINDING SITE, designated SEQ ID:11944, to

the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27495] Another function of GAM180 is therefore inhibition of LOC253044 (Accession XP_172924.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253044.

[27496] LOC253263 (Accession XP_173102.1) is another GAM180 target gene, herein designated TARGET GENE. LOC253263 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC253263, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253263 BINDING SITE, designated SEQ ID:12769, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27497] Another function of GAM180 is therefore inhibition of LOC253263 (Accession XP_173102.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253263.

[27498] LOC283038 (Accession XP_302599.1) is another GAM180

target gene, herein designated TARGET GENE. LOC283038 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283038, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283038 BINDING SITE, designated SEQ ID:4836, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27499] Another function of GAM180 is therefore inhibition of LOC283038 (Accession XP_302599.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283038.

[27500] LOC283087 (Accession XP_208509.1) is another GAM180 target gene, herein designated TARGET GENE. LOC283087 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283087, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283087 BINDING SITE, designated SEQ ID:7112, to the nucleotide sequence of GAM180 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:214.

[27501] Another function of GAM180 is therefore inhibition of LOC283087 (Accession XP_208509.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283087.

[27502] LOC283140 (Accession XP_210911.1) is another GAM180 target gene, herein designated TARGET GENE. LOC283140 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283140 BINDING SITE, designated SEQ ID:11320, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27503] Another function of GAM180 is therefore inhibition of LOC283140 (Accession XP_210911.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283140.

[27504] LOC283298 (Accession XP_208606.1) is another GAM180 target gene, herein designated TARGET GENE. LOC283298

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283298, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283298 BINDING SITE, designated SEQ ID:11643, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27505] Another function of GAM180 is therefore inhibition of LOC283298 (Accession XP_208606.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283298.

[27506] LOC283337 (Accession XP_300560.1) is another GAM180 target gene, herein designated TARGET GENE. LOC283337 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283337, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283337 BINDING SITE, designated SEQ ID:8912, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27507] Another function of GAM180 is therefore inhibition of LOC283337 (Accession XP_300560.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283337.

[27508] LOC283570 (Accession XP_211118.1) is another GAM180 target gene, herein designated TARGET GENE. LOC283570 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283570, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283570 BINDING SITE, designated SEQ ID:12808, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27509] Another function of GAM180 is therefore inhibition of LOC283570 (Accession XP_211118.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283570.

[27510] LOC283574 (Accession XP_211099.1) is another GAM180 target gene, herein designated TARGET GENE. LOC283574 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC283574, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283574 BINDING SITE, designated SEQ ID:1593, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27511] Another function of GAM180 is therefore inhibition of LOC283574 (Accession XP_211099.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283574.

[27512] LOC283810 (Accession XP_208853.1) is another GAM180 target gene, herein designated TARGET GENE. LOC283810 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283810, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283810 BINDING SITE, designated SEQ ID:3590, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27513] Another function of GAM180 is therefore inhibition of

LOC283810 (Accession XP_208853.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283810.

[27514] LOC283831 (Accession XP_211224.1) is another GAM180 target gene, herein designated TARGET GENE. LOC283831 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283831, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283831 BINDING SITE, designated SEQ ID:4669, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27515] Another function of GAM180 is therefore inhibition of LOC283831 (Accession XP_211224.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283831.

[27516] LOC283911 (Accession XP_211259.2) is another GAM180 target gene, herein designated TARGET GENE. LOC283911 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283911, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283911 BINDING SITE, designated SEQ ID:11417, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27517] Another function of GAM180 is therefore inhibition of LOC283911 (Accession XP_211259.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283911.

[27518] LOC283922 (Accession XP_208908.1) is another GAM180 target gene, herein designated TARGET GENE. LOC283922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283922 BINDING SITE, designated SEQ ID:15803, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27519] Another function of GAM180 is therefore inhibition of LOC283922 (Accession XP_208908.1) . Accordingly, utili-

ties of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283922.

[27520] LOC283929 (Accession XP_208905.2) is another GAM180 target gene, herein designated TARGET GENE. LOC283929 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283929, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283929 BINDING SITE, designated SEQ ID:10481, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27521] Another function of GAM180 is therefore inhibition of LOC283929 (Accession XP_208905.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283929.

[27522] LOC283982 (Accession XP_208954.1) is another GAM180 target gene, herein designated TARGET GENE. LOC283982 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283982, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283982 BINDING SITE, designated SEQ ID:6204, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27523] Another function of GAM180 is therefore inhibition of LOC283982 (Accession XP_208954.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283982.

[27524] LOC284045 (Accession XP_210776.1) is another GAM180 target gene, herein designated TARGET GENE. LOC284045 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284045 BINDING SITE, designated SEQ ID:15106, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27525] Another function of GAM180 is therefore inhibition of LOC284045 (Accession XP_210776.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284045.

[27526] LOC284220 (Accession XP_211391.1) is another GAM180 target gene, herein designated TARGET GENE. LOC284220 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284220, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284220 BINDING SITE, designated SEQ ID:16999, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27527] Another function of GAM180 is therefore inhibition of LOC284220 (Accession XP_211391.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284220.

[27528] LOC284360 (Accession XP_211433.1) is another GAM180 target gene, herein designated TARGET GENE. LOC284360 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284360, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC284360 BINDING SITE, designated SEQ ID:1154, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27529] Another function of GAM180 is therefore inhibition of LOC284360 (Accession XP_211433.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284360.

[27530] LOC284549 (Accession XP_211514.1) is another GAM180 target gene, herein designated TARGET GENE. LOC284549 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284549, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284549 BINDING SITE, designated SEQ ID:2382, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27531] Another function of GAM180 is therefore inhibition of LOC284549 (Accession XP_211514.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284549.

[27532] LOC284585 (Accession XP_209277.2) is another GAM180 target gene, herein designated TARGET GENE. LOC284585 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284585, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284585 BINDING SITE, designated SEQ ID:1916, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27533] Another function of GAM180 is therefore inhibition of LOC284585 (Accession XP_209277.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284585.

[27534] LOC284773 (Accession XP_209353.1) is another GAM180 target gene, herein designated TARGET GENE. LOC284773 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284773, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284773 BINDING SITE, designated SEQ ID:16000, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27535] Another function of GAM180 is therefore inhibition of LOC284773 (Accession XP_209353.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284773.

[27536] LOC284947 (Accession XP_211705.1) is another GAM180 target gene, herein designated TARGET GENE. LOC284947 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284947, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284947 BINDING SITE, designated SEQ ID:11231, to

the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27537] Another function of GAM180 is therefore inhibition of LOC284947 (Accession XP_211705.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284947.

[27538] LOC285026 (Accession XP_209440.1) is another GAM180 target gene, herein designated TARGET GENE. LOC285026 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285026, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285026 BINDING SITE, designated SEQ ID:6831, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27539] Another function of GAM180 is therefore inhibition of LOC285026 (Accession XP_209440.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285026.

[27540] LOC285029 (Accession XP_211741.1) is another GAM180

target gene, herein designated TARGET GENE. LOC285029 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285029, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285029 BINDING SITE, designated SEQ ID:12677, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27541] Another function of GAM180 is therefore inhibition of LOC285029 (Accession XP_211741.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285029.

[27542] LOC285056 (Accession XP_208283.1) is another GAM180 target gene, herein designated TARGET GENE. LOC285056 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285056, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285056 BINDING SITE, designated SEQ ID:10528, to the nucleotide sequence of GAM180 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:214.

[27543] Another function of GAM180 is therefore inhibition of LOC285056 (Accession XP_208283.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285056.

[27544] LOC285286 (Accession XP_211834.1) is another GAM180 target gene, herein designated TARGET GENE. LOC285286 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285286, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285286 BINDING SITE, designated SEQ ID:555, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27545] Another function of GAM180 is therefore inhibition of LOC285286 (Accession XP_211834.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285286.

[27546] LOC285376 (Accession XP_211864.1) is another GAM180 target gene, herein designated TARGET GENE. LOC285376

BINDING SITE1 and LOC285376 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285376, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285376 BINDING SITE1 and LOC285376 BINDING SITE2, designated SEQ ID:15389 and SEQ ID:1613 respectively, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27547] Another function of GAM180 is therefore inhibition of LOC285376 (Accession XP_211864.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285376.

[27548] LOC285786 (Accession XP_208349.1) is another GAM180 target gene, herein designated TARGET GENE. LOC285786 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285786, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285786 BINDING SITE, designated SEQ ID:7150, to

the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27549] Another function of GAM180 is therefore inhibition of LOC285786 (Accession XP_208349.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285786.

[27550] LOC285999 (Accession XP_212120.1) is another GAM180 target gene, herein designated TARGET GENE. LOC285999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285999 BINDING SITE, designated SEQ ID:8264, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27551] Another function of GAM180 is therefore inhibition of LOC285999 (Accession XP_212120.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285999.

[27552] LOC338708 (Accession XP_294683.1) is another GAM180

target gene, herein designated TARGET GENE. LOC338708 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338708 BINDING SITE, designated SEQ ID:17540, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27553] Another function of GAM180 is therefore inhibition of LOC338708 (Accession XP_294683.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338708.

[27554] LOC338987 (Accession XP_290664.1) is another GAM180 target gene, herein designated TARGET GENE. LOC338987 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338987, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338987 BINDING SITE, designated SEQ ID:5719, to the nucleotide sequence of GAM180 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:214.

[27555] Another function of GAM180 is therefore inhibition of LOC338987 (Accession XP_290664.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338987.

[27556] LOC339186 (Accession XP_294845.1) is another GAM180 target gene, herein designated TARGET GENE. LOC339186 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339186 BINDING SITE, designated SEQ ID:11297, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27557] Another function of GAM180 is therefore inhibition of LOC339186 (Accession XP_294845.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339186.

[27558] LOC339240 (Accession XP_294880.1) is another GAM180 target gene, herein designated TARGET GENE. LOC339240

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339240, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339240 BINDING SITE, designated SEQ ID:11297, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27559] Another function of GAM180 is therefore inhibition of LOC339240 (Accession XP_294880.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339240.

[27560] LOC339258 (Accession XP_294886.1) is another GAM180 target gene, herein designated TARGET GENE. LOC339258 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339258, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339258 BINDING SITE, designated SEQ ID:11297, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27561] Another function of GAM180 is therefore inhibition of LOC339258 (Accession XP_294886.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339258.

[27562] LOC339751 (Accession XP_295053.1) is another GAM180 target gene, herein designated TARGET GENE. LOC339751 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339751, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339751 BINDING SITE, designated SEQ ID:9131, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27563] Another function of GAM180 is therefore inhibition of LOC339751 (Accession XP_295053.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339751.

[27564] LOC339899 (Accession XP_295096.1) is another GAM180 target gene, herein designated TARGET GENE. LOC339899 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC339899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339899 BINDING SITE, designated SEQ ID:2376, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27565] Another function of GAM180 is therefore inhibition of LOC339899 (Accession XP_295096.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339899.

[27566] LOC340090 (Accession XP_295154.1) is another GAM180 target gene, herein designated TARGET GENE. LOC340090 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340090, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340090 BINDING SITE, designated SEQ ID:13639, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27567] Another function of GAM180 is therefore inhibition of

LOC340090 (Accession XP_295154.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340090.

[27568] LOC342346 (Accession XP_296817.2) is another GAM180 target gene, herein designated TARGET GENE. LOC342346 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC342346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC342346 BINDING SITE, designated SEQ ID:11373, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27569] Another function of GAM180 is therefore inhibition of LOC342346 (Accession XP_296817.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC342346.

[27570] LOC347546 (Accession XP_298101.2) is another GAM180 target gene, herein designated TARGET GENE. LOC347546 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347546, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347546 BINDING SITE, designated SEQ ID:3508, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27571] Another function of GAM180 is therefore inhibition of LOC347546 (Accession XP_298101.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347546.

[27572] LOC347648 (Accession XP_300226.1) is another GAM180 target gene, herein designated TARGET GENE. LOC347648 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC347648, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347648 BINDING SITE, designated SEQ ID:2916, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27573] Another function of GAM180 is therefore inhibition of LOC347648 (Accession XP_300226.1) . Accordingly, utili-

ties of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347648.

[27574] LOC347884 (Accession XP_302617.1) is another GAM180 target gene, herein designated TARGET GENE. LOC347884 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC347884, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347884 BINDING SITE, designated SEQ ID:5296, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27575] Another function of GAM180 is therefore inhibition of LOC347884 (Accession XP_302617.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347884.

[27576] LOC348112 (Accession XP_302657.1) is another GAM180 target gene, herein designated TARGET GENE. LOC348112 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348112, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348112 BINDING SITE, designated SEQ ID:14248, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27577] Another function of GAM180 is therefore inhibition of LOC348112 (Accession XP_302657.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348112.

[27578] LOC348452 (Accession XP_300742.1) is another GAM180 target gene, herein designated TARGET GENE. LOC348452 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348452 BINDING SITE, designated SEQ ID:1711, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27579] Another function of GAM180 is therefore inhibition of LOC348452 (Accession XP_300742.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348452.

[27580] LOC349094 (Accession XP_300945.1) is another GAM180 target gene, herein designated TARGET GENE. LOC349094 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349094, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349094 BINDING SITE, designated SEQ ID:7090, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27581] Another function of GAM180 is therefore inhibition of LOC349094 (Accession XP_300945.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349094.

[27582] LOC349097 (Accession XP_300940.1) is another GAM180 target gene, herein designated TARGET GENE. LOC349097 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349097, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC349097 BINDING SITE, designated SEQ ID:7090, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27583] Another function of GAM180 is therefore inhibition of LOC349097 (Accession XP_300940.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349097.

[27584] LOC349138 (Accession XP_300960.1) is another GAM180 target gene, herein designated TARGET GENE. LOC349138 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349138 BINDING SITE, designated SEQ ID:7090, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27585] Another function of GAM180 is therefore inhibition of LOC349138 (Accession XP_300960.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC349138.

[27586] LOC349305 (Accession XP_301019.1) is another GAM180 target gene, herein designated TARGET GENE. LOC349305 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349305, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349305 BINDING SITE, designated SEQ ID:1916, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27587] Another function of GAM180 is therefore inhibition of LOC349305 (Accession XP_301019.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349305.

[27588] LOC351228 (Accession XP_304390.1) is another GAM180 target gene, herein designated TARGET GENE. LOC351228 BINDING SITE1 through LOC351228 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC351228, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of LOC351228 BINDING SITE1 through LOC351228 BINDING SITE3, designated SEQ ID:1629, SEQ ID:17782 and SEQ ID:5030 respectively, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27589] Another function of GAM180 is therefore inhibition of LOC351228 (Accession XP_304390.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC351228.

[27590] LOC92235 (Accession XP_043739.2) is another GAM180 target gene, herein designated TARGET GENE. LOC92235 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92235 BINDING SITE, designated SEQ ID:11492, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27591] Another function of GAM180 is therefore inhibition of LOC92235 (Accession XP_043739.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC92235.

[27592] LOC92710 (Accession XP_046811.2) is another GAM180 target gene, herein designated TARGET GENE. LOC92710 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92710, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92710 BINDING SITE, designated SEQ ID:17389, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27593] Another function of GAM180 is therefore inhibition of LOC92710 (Accession XP_046811.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92710.

[27594] Lymphocyte antigen 6 complex, locus h (LY6H, Accession NP_002338.1) is another GAM180 target gene, herein designated TARGET GENE. LY6H BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LY6H, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LY6H BINDING SITE, designated SEQ ID:16930, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27595] Another function of GAM180 is therefore inhibition of Lymphocyte antigen 6 complex, locus h (LY6H, Accession NP_002338.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LY6H.

[27596] Lysophospholipase 3 (lysosomal phospholipase a2) (LYPLA3, Accession NP_036452.1) is another GAM180 target gene, herein designated TARGET GENE. LYPLA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LYPLA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LYPLA3 BINDING SITE, designated SEQ ID:10576, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27597] Another function of GAM180 is therefore inhibition of Lysophospholipase 3 (lysosomal phospholipase a2)

(LYPLA3, Accession NP_036452.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LY-PLA3.

[27598] MGC10334 (Accession XP_300761.1) is another GAM180 target gene, herein designated TARGET GENE. MGC10334 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MGC10334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10334 BINDING SITE, designated SEQ ID:1711, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27599] Another function of GAM180 is therefore inhibition of MGC10334 (Accession XP_300761.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10334.

[27600] MGC10334 (Accession NP_085052.1) is another GAM180 target gene, herein designated TARGET GENE. MGC10334 BINDING SITE is a target binding site found in the 5` un-

translated region of multiple transcripts of mRNA encoded by MGC10334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10334 BINDING SITE, designated SEQ ID:1711, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27601] Another function of GAM180 is therefore inhibition of MGC10334 (Accession NP_085052.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10334.

[27602] MGC34680 (Accession NP_689559.1) is another GAM180 target gene, herein designated TARGET GENE. MGC34680 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC34680, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34680 BINDING SITE, designated SEQ ID:4811, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27603] Another function of GAM180 is therefore inhibition of MGC34680 (Accession NP_689559.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34680.

[27604] MGC40042 (Accession NP_689726.2) is another GAM180 target gene, herein designated TARGET GENE. MGC40042 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC40042, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40042 BINDING SITE, designated SEQ ID:15660, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27605] Another function of GAM180 is therefore inhibition of MGC40042 (Accession NP_689726.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40042.

[27606] MGC41906 (Accession NP_689687.1) is another GAM180 target gene, herein designated TARGET GENE. MGC41906 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC41906, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC41906 BINDING SITE, designated SEQ ID:5085, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27607] Another function of GAM180 is therefore inhibition of MGC41906 (Accession NP_689687.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC41906.

[27608] MGC4767 (Accession NP_115690.1) is another GAM180 target gene, herein designated TARGET GENE. MGC4767 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC4767, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4767 BINDING SITE, designated SEQ ID:8947, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27609] Another function of GAM180 is therefore inhibition of

MGC4767 (Accession NP_115690.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4767.

[27610] MPRA (Accession NP_848509.1) is another GAM180 target gene, herein designated TARGET GENE. MPRA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MPRA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPRA BINDING SITE, designated SEQ ID:7693, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27611] Another function of GAM180 is therefore inhibition of MPRA (Accession NP_848509.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPRA.

[27612] Membrane-spanning 4-domains, subfamily a, member 6a (MS4A6A, Accession NP_690590.1) is another GAM180 target gene, herein designated TARGET GENE. MS4A6A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded

by MS4A6A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MS4A6A BINDING SITE, designated SEQ ID:14166, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27613] Another function of GAM180 is therefore inhibition of Membrane-spanning 4-domains, subfamily a, member 6a (MS4A6A, Accession NP_690590.1), a gene which binds to the fc region of immunoglobulins epsilon. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MS4A6A.

[27614] The function of MS4A6A has been established by previous studies. By EST database searching for homologs of CD20 (MS4A1; 112210), Ishibashi et al. (2001) isolated a cDNA encoding MS4A6A, which they termed MS4A6. The deduced 178- amino acid protein has 4 potential phosphorylation sites, including 1 at the intracellular loop, and a nonhydrophilic C terminus. Northern blot analysis revealed low- level expression of a 1.3- kb transcript in mouse kidney and small intestine and a 1.0- kb transcript

in mouse heart; no expression was detected in human tissues. Liang and Tedder (2001) also obtained a cDNA encoding MS4A6A. The predicted 248- amino acid protein is more than 50% identical to its mouse homologs. PCR analysis detected variable expression of MS4A6A in cDNA from some B- cell, myelomonocytic, and erythroleukemia cell lines. The authors identified likely polymorphisms in the MS4A6A gene.

[27615]

[27616] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27617] Ishibashi, K.; Suzuki, M.; Sasaki, S.; Imai, M. : Identification of a new multigene four- transmembrane family (MS4A) related to CD20, HTm4 and beta subunit of the high- affinity IgE receptor. Gene 264: 87- 93, 2001. ; and

[27618] Liang, Y.; Tedder, T. F. : Identification of a CD20-, Fc- epsilon- RI- beta- related gene family: sixteen new MS4A family members expressed in human and mouse. Genomics 72: 119- 127, 2001.

[27619] Further studies establishing the function and utilities of MS4A6A are found in John Hopkins OMIM database record ID 606548, and in cited publications listed in Table 5,

which are hereby incorporated by reference.Membrane-spanning 4-domains, subfamily a, member 6a (MS4A6A, Accession NP_690591.1) is another GAM180 target gene, herein designated TARGET GENE. MS4A6A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MS4A6A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MS4A6A BINDING SITE, designated SEQ ID:14166, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27620] Another function of GAM180 is therefore inhibition of Membrane-spanning 4-domains, subfamily a, member 6a (MS4A6A, Accession NP_690591.1), a gene which binds to the fc region of immunoglobulins epsilon. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MS4A6A.

[27621] The function of MS4A6A has been established by previous studies. By EST database searching for homologs of CD20 (MS4A1; 112210), Ishibashi et al. (2001) isolated a cDNA

encoding MS4A6A, which they termed MS4A6. The deduced 178- amino acid protein has 4 potential phosphorylation sites, including 1 at the intracellular loop, and a nonhydrophilic C terminus. Northern blot analysis revealed low- level expression of a 1.3- kb transcript in mouse kidney and small intestine and a 1.0- kb transcript in mouse heart; no expression was detected in human tissues. Liang and Tedder (2001) also obtained a cDNA encoding MS4A6A. The predicted 248- amino acid protein is more than 50% identical to its mouse homologs. PCR analysis detected variable expression of MS4A6A in cDNA from some B- cell, myelomonocytic, and erythroleukemia cell lines. The authors identified likely polymorphisms in the MS4A6A gene.

[27622]

[27623] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27624] Ishibashi, K.; Suzuki, M.; Sasaki, S.; Imai, M. : Identification of a new multigene four- transmembrane family (MS4A) related to CD20, HTm4 and beta subunit of the high- affinity IgE receptor. Gene 264: 87- 93, 2001. ; and

[27625] Liang, Y.; Tedder, T. F. : Identification of a CD20-, Fc- ep-

silon- RI- beta- related gene family: sixteen new MS4A family members expressed in human and mouse. Genomics 72: 119- 127, 2001.

[27626] Further studies establishing the function and utilities of MS4A6A are found in John Hopkins OMIM database record ID 606548, and in cited publications listed in Table 5, which are hereby incorporated by reference.NCAG1 (Accession NP_115536.1) is another GAM180 target gene, herein designated TARGET GENE. NCAG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCAG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCAG1 BINDING SITE, designated SEQ ID:18626, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27627] Another function of GAM180 is therefore inhibition of NCAG1 (Accession NP_115536.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCAG1.

[27628] NET-7 (Accession NP_036471.1) is another GAM180 target gene, herein designated TARGET GENE. NET-7 BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NET-7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NET-7 BINDING SITE, designated SEQ ID:11703, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27629] Another function of GAM180 is therefore inhibition of NET-7 (Accession NP_036471.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NET-7.

[27630] Nuclear factor i/b (NFIB, Accession NP_005587.1) is another GAM180 target gene, herein designated TARGET GENE. NFIB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NFIB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NFIB BINDING SITE, designated SEQ ID:13925, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27631] Another function of GAM180 is therefore inhibition of Nu-

clear factor i/b (NFIB, Accession NP_005587.1), a gene which recognizes and binds the palindromic sequence 5'-ttggcnnnnngccaa- 3' present in viral and cellular promoters. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFIB.

[27632] The function of NFIB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.NMNAT2 (Accession NP_055854.1) is another GAM180 target gene, herein designated TARGET GENE. NMNAT2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NMNAT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NMNAT2 BINDING SITE, designated SEQ ID:8057, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27633] Another function of GAM180 is therefore inhibition of NMNAT2 (Accession NP_055854.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with NM-NAT2.

[27634] Nitric oxide synthase 1 (neuronal) (NOS1, Accession NP_000611.1) is another GAM180 target gene, herein designated TARGET GENE. NOS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOS1 BINDING SITE, designated SEQ ID:17856, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27635] Another function of GAM180 is therefore inhibition of Nitric oxide synthase 1 (neuronal) (NOS1, Accession NP_000611.1), a gene which produces nitric oxide (no) which is a messenger molecule with diverse functions throughout the body. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOS1.

[27636] The function of NOS1 has been established by previous studies. Bredt et al. (1991) cloned a cDNA for the neuronal form of nitric oxide (NO) synthase and studied its expres-

sion. The only mammalian protein with close sequence similarity was cytochrome P450 reductase. Magee et al. (1996) used PCR to clone a novel form of neuronal NOS from rat penile RNA. This NOS cDNA was termed PnNOS for 'penile neuronal NOS.' Sequencing revealed that the PnNOS cDNA was identical to rat cerebellar neuronal NOS1 except for a 102- bp insertion in PnNOS, indicating that PnNOS is a novel isoform. PCR of a human penile cDNA library confirmed that this insert is present in human DNA at the same location. Repetition of RT- PCR showed PnNOS to be the only form of NOS1 expressed in rat penis, urethra, prostate, and skeletal muscle. The PnNOS form was also present in rat cerebellum, liver, and pelvic plexus, although less abundantly than the shorter isoform. The authors postulated that PnNOS may be responsible for the synthesis of nitric oxide during penile erection and may be involved in control of the tone of the urethra, prostate, and bladder.

[27637] Animal model experiments lend further support to the function of NOS1. Mice with targeted disruption of neuronal NO synthase display grossly normal appearance, locomotor activity, breeding, long- term potentiation, and long- term depression. NOS1- deficient mice are resistant

to neural stroke damage following middle cerebral artery ligation. Nelson et al. (1995) reported a large increase in aggressive behavior and excessive, inappropriate sexual behavior in NOS1 'knockout' mice. Initial observations indicated that male NOS1- deficient mice engaged in chronic aggressive behavior, not apparent among NOS1-deficient female mice or wildtype male or female mice housed together. Relevance of the observations to human behavior was suggested.

[27638] It is appreciated that the abovementioned animal model for NOS1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[27639] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27640] Magee, T.; Fuentes, A. M.; Garban, H.; Rajavashisth, T.; Marquez, D.; Rodriguez, J. A.; Rajfer, J.; Gonzalez- Cadavid, N. F. : Cloning of a novel neuronal nitric oxide synthase expressed in penis and lower urinary tract. Biochem. Biophys. Res. Commun. 226: 145- 151, 1996. ; and

[27641] Nelson, R. J.; Demas, G. E.; Huang, P. L.; Fishman, M. C.; Dawson, V. L.; Dawson, T. M.; Snyder, S. H. : Behavioural

abnormalities in male mice lacking neuronal nitric oxide synthase. N.

[27642] Further studies establishing the function and utilities of NOS1 are found in John Hopkins OMIM database record ID 163731, and in cited publications listed in Table 5, which are hereby incorporated by reference.Natriuretic peptide receptor c/guanylate cyclase c (atrionatriuretic peptide receptor c) (NPR3, Accession NP_000899.1) is another GAM180 target gene, herein designated TARGET GENE. NPR3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPR3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPR3 BINDING SITE, designated SEQ ID:9247, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27643] Another function of GAM180 is therefore inhibition of Natriuretic peptide receptor c/guanylate cyclase c (atrionatriuretic peptide receptor c) (NPR3, Accession NP_000899.1), a gene which is required for timing of endochondral ossification. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with NPR3.

[27644] The function of NPR3 has been established by previous studies. Using a bovine ANP C- type receptor cDNA as a hybridization probe, Porter et al. (1990) cloned cDNA encoding the human atrial natriuretic peptide clearance receptor (ANPRC; gene symbol = NPR3) from human placental and kidney cDNA libraries. The ANPC receptor mediates the internalization and metabolic clearance of ANP. The human sequence was shown to be highly homologous to the bovine sequence. Corresponding mRNA was expressed in human placenta, adult and fetal kidney, and fetal heart. Lowe et al. (1990) reported the sequence of the cDNA.

[27645] Animal model experiments lend further support to the function of NPR3. It is thought that atrial natriuretic peptide released from the heart in response to atrial stretch binds to a guanylyl cyclase- coupled receptor, which Lopez et al. (1995) symbolized GC- A, in the kidney to mediate natriuresis and diuresis, and to the same receptor in the vasculature to mediate relaxation. Lopez et al. (1995) reported that disruption of the GC- A gene by transfection of mouse embryonic stem cells resulted in mice with chronic elevations of blood pressure on a nor-

mal salt diet. Pressure was elevated by 27.4 mm Hg in homozygotes and 10.5 mm Hg in heterozygotes. Unexpectedly, the blood pressure remained elevated and unchanged in response to either minimal salt diet or high salt diet. Aldosterone and ANP concentrations were not affected by the genotype. Thus, the authors speculated that mutations in the receptor gene could explain some salt- resistant forms of essential hypertension in humans. Coupled with other work, this also suggested that the GC-A signaling pathway dominates at the level of peripheral resistance, where it can operate independently of ANP.

[27646] It is appreciated that the abovementioned animal model for NPR3 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[27647] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27648] Lopez, M. J.; Wong, S. K.- F.; Kishimoto, I.; Dubois, S.; Mach, V.; Friesen, J.; Garbers, D. L.; Beuve, A. : Salt- resistant hypertension in mice lacking the guanylyl cyclase- A receptor for atrial natriuretic peptide. Nature 378: 65- 68, 1995. ; and

[27649] Porter, J. G.; Arfsten, A.; Fuller, F.; Miller, J. A.; Gregory, L. C.; Lewicki, J. A. : Isolation and functional expression of the human atrial natriuretic peptide clearance receptor c.

[27650] Further studies establishing the function and utilities of NPR3 are found in John Hopkins OMIM database record ID 108962, and in cited publications listed in Table 5, which are hereby incorporated by reference.NRLN1 (Accession NP_660277.1) is another GAM180 target gene, herein designated TARGET GENE. NRLN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NRLN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRLN1 BINDING SITE, designated SEQ ID:15259, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27651] Another function of GAM180 is therefore inhibition of NRLN1 (Accession NP_660277.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRLN1.

[27652] Oxidative-stress responsive 1 (OSR1, Accession NP_660303.1) is another GAM180 target gene, herein

designated TARGET GENE. OSR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSR1 BINDING SITE, designated SEQ ID:18887, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27653] Another function of GAM180 is therefore inhibition of Oxidative-stress responsive 1 (OSR1, Accession NP_660303.1), a gene which mediats stress- activated signals. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSR1.

[27654] The function of OSR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM133.1.P8 (Accession NP_036517.1) is another GAM180 target gene, herein designated TARGET GENE. P8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P8, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P8 BINDING SITE, designated SEQ ID:9958, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27655] Another function of GAM180 is therefore inhibition of P8 (Accession NP_036517.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P8.

[27656] Phosphodiesterase 8b (PDE8B, Accession NP_003710.1) is another GAM180 target gene, herein designated TARGET GENE. PDE8B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDE8B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDE8B BINDING SITE, designated SEQ ID:17979, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27657] Another function of GAM180 is therefore inhibition of Phosphodiesterase 8b (PDE8B, Accession NP_003710.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with PDE8B.

[27658] Peroxisome biogenesis factor 10 (PEX10, Accession NP_722540.1) is another GAM180 target gene, herein designated TARGET GENE. PEX10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PEX10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PEX10 BINDING SITE, designated SEQ ID:13341, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27659] Another function of GAM180 is therefore inhibition of Peroxisome biogenesis factor 10 (PEX10, Accession NP_722540.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEX10.

[27660] Peroxisome biogenesis factor 10 (PEX10, Accession NP_002608.1) is another GAM180 target gene, herein designated TARGET GENE. PEX10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PEX10, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PEX10 BINDING SITE, designated SEQ ID:13341, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27661] Another function of GAM180 is therefore inhibition of Peroxisome biogenesis factor 10 (PEX10, Accession NP_002608.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEX10.

[27662] Prefoldin 5 (PFDN5, Accession NP_665903.1) is another GAM180 target gene, herein designated TARGET GENE. PFDN5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PFDN5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PFDN5 BINDING SITE, designated SEQ ID:11809, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27663] Another function of GAM180 is therefore inhibition of Prefoldin 5 (PFDN5, Accession NP_665903.1) . Accord-

ingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFDN5.

[27664] Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) is another GAM180 target gene, herein designated TARGET GENE. PNMA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PNMA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PNMA2 BINDING SITE, designated SEQ ID:10910, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27665] Another function of GAM180 is therefore inhibition of Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNMA2.

[27666] Protein phosphatase 1f (pp2c domain containing) (PPM1F, Accession NP_055449.1) is another GAM180 target gene, herein designated TARGET GENE. PPM1F BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by PPM1F, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPM1F BINDING SITE, designated SEQ ID:5913, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27667] Another function of GAM180 is therefore inhibition of Protein phosphatase 1f (pp2c domain containing) (PPM1F, Accession NP_055449.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPM1F.

[27668] Protein phosphatase 1, regulatory (inhibitor) subunit 1b (dopamine and camp regulated phosphoprotein, darpp-32) (PPP1R1B, Accession NP_852606.1) is another GAM180 target gene, herein designated TARGET GENE. PPP1R1B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R1B BINDING SITE, designated SEQ ID:8599, to the nucleotide sequence of

GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27669] Another function of GAM180 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 1b (dopamine and camp regulated phosphoprotein, darpp-32) (PPP1R1B, Accession NP_852606.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R1B.

[27670] Protein phosphatase 1, regulatory (inhibitor) subunit 1b (dopamine and camp regulated phosphoprotein, darpp-32) (PPP1R1B, Accession NP_115568.2) is another GAM180 target gene, herein designated TARGET GENE. PPP1R1B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R1B BINDING SITE, designated SEQ ID:8599, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27671] Another function of GAM180 is therefore inhibition of

Protein phosphatase 1, regulatory (inhibitor) subunit 1b (dopamine and camp regulated phosphoprotein, darpp-32) (PPP1R1B, Accession NP_115568.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R1B.

[27672] PRO2086 (Accession NP_054830.1) is another GAM180 target gene, herein designated TARGET GENE. PRO2086 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO2086, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO2086 BINDING SITE, designated SEQ ID:15425, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27673] Another function of GAM180 is therefore inhibition of PRO2086 (Accession NP_054830.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2086.

[27674] Periaxin (PRX, Accession NP_066007.1) is another GAM180 target gene, herein designated TARGET GENE.

PRX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRX BINDING SITE, designated SEQ ID:15552, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27675] Another function of GAM180 is therefore inhibition of Periaxin (PRX, Accession NP_066007.1), a gene which seems to be required for maintenance of peripheral nerve myelin sheath. may have a role in axon- glial interactions, possibly by interacting with the cytoplasmic domains of integral membrane proteins such as myelin- associated glycoprotein in the periaxonal regions of the schwann cell plasma membrane. may have a role in the early phases of myelin deposition and therefore is associated with Dejerine- sottas neuropathy, autosomal recessive. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of Dejerine- sottas neuropathy, autosomal recessive, and of other diseases and clinical conditions associated with PRX.

[27676] The function of PRX and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Proline-serine-threonine phosphatase interacting protein 1 (PSTPIP1, Accession NP_003969.2) is another GAM180 target gene, herein designated TARGET GENE. PSTPIP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSTPIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSTPIP1 BINDING SITE, designated SEQ ID:1021, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27677] Another function of GAM180 is therefore inhibition of Proline-serine-threonine phosphatase interacting protein 1 (PSTPIP1, Accession NP_003969.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSTPIP1.

[27678] Rab17, member ras oncogene family (RAB17, Accession NP_071894.1) is another GAM180 target gene, herein designated TARGET GENE. RAB17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by RAB17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB17 BINDING SITE, designated SEQ ID:17352, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27679] Another function of GAM180 is therefore inhibition of Rab17, member ras oncogene family (RAB17, Accession NP_071894.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB17.

[27680] Retinoic acid induced 14 (RAI14, Accession NP_056392.1) is another GAM180 target gene, herein designated TARGET GENE. RAI14 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAI14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI14 BINDING SITE, designated SEQ ID:15321, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27681] Another function of GAM180 is therefore inhibition of Retinoic acid induced 14 (RAI14, Accession NP_056392.1), a gene which is required for protein transport from the er to the golgi complex. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI14.

[27682] The function of RAI14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Retinal degeneration, slow (retinitis pigmentosa 7) (RDS, Accession NP_000313.1) is another GAM180 target gene, herein designated TARGET GENE. RDS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RDS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RDS BINDING SITE, designated SEQ ID:14017, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27683] Another function of GAM180 is therefore inhibition of Retinal degeneration, slow (retinitis pigmentosa 7) (RDS, Accession NP_000313.1), a gene which may function as an

adhesion molecule involved in stabilization and compaction of outer segment disks or in the maintenance of the curvature of the rim and therefore is associated with Autosomal dominant retinitis pigmentosa. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of Autosomal dominant retinitis pigmentosa, and of other diseases and clinical conditions associated with RDS.

[27684] The function of RDS has been established by previous studies. Kohl et al. (1997) screened 76 independent families with various forms of mostly central retinal dystrophies for mutations in the RDS gene. Two nonsense mutations, 5 missense mutations, and 1 single base insertion were detected. All of these were in heterozygous state. Kohl et al. (1997) commented on the remarkable variation in phenotype and disease expression between and within families.

[27685] Animal model experiments lend further support to the function of RDS. A common feature of peripherin- related retinitis pigmentosa and macular dystrophy in the human and the rds mutation in mouse is the loss of photoreceptor function. It is characterized by complete failure to develop photoreceptor discs and outer segments, downreg-

ulation of rhodopsin (OMIM Ref. No. 180380), and apoptotic loss of photoreceptor cells. Ali et al. (2000) demonstrated that subretinal injection of recombinant adeno-associated virus encoding a Prph2 transgene resulted in stable generation of outer segment structures and formation of new stacks of discs containing both peripherin- 2 and rhodopsin, which in many cases were morphologically similar to normal outer segments. Moreover, the reestablishment of the structural integrity of the photoreceptor layer resulted in electrophysiologic correction. These studies demonstrated for the first time that a complex ultrastructural cell defect can be corrected both morphologically and functionally by in vivo gene transfer. Sarra et al. (2001) extended the analysis and demonstrated that the potential for ultrastructural improvement is dependent upon the age at which animals are treated, but the effect of a single injection on photoreceptor ultrastructure may be long- term. However, there was no significant effect on photoreceptor cell loss, irrespective of the date of administration, despite the improvements in morphology and function. These findings suggested that successful gene therapy in patients with photoreceptor defects may ultimately depend upon intervention in early stages of dis-

ease and upon accurate control of transgene expression.

[27686] It is appreciated that the abovementioned animal model for RDS is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[27687] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27688] Kohl, S.; Christ- Adler, M.; Apfelstedt- Sylla, E.; Kellner, U.; Eckstein, A.; Zrenner, E.; Wissinger, B. : RDS/peripherin gene mutations are frequent causes of central retinal dystrophies. J. Med. Genet. 34: 620- 626, 1997. ; and

[27689] Sarra, G.- M.; Stephens, C.; de Alwis, M.; Bainbridge, J. W. B.; Smith, A. J.; Thrasher, A. J.; Ali, R. R. : Gene replacement therapy in the retinal degeneration slow (rds) mouse: the ef.

[27690] Further studies establishing the function and utilities of RDS are found in John Hopkins OMIM database record ID 179605, and in cited publications listed in Table 5, which are hereby incorporated by reference.Arginine-glutamic acid dipeptide (re) repeats (RERE, Accession NP_036234.2) is another GAM180 target gene, herein designated TARGET GENE. RERE BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by RERE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RERE BINDING SITE, designated SEQ ID:1004, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27691] Another function of GAM180 is therefore inhibition of Arginine-glutamic acid dipeptide (re) repeats (RERE, Accession NP_036234.2), a gene which binds DRPLA and locates in the nucleus and therefore may be associated with Dentatorubral- pallidoluysian atrophy. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of Dentatorubral- pallidoluysian atrophy, and of other diseases and clinical conditions associated with RERE.

[27692] The function of RERE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Rhesus blood group, c glycoprotein (RHCG, Accession NP_057405.1) is another GAM180 target gene, herein designated TARGET GENE. RHCG BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by RHCG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHCG BINDING SITE, designated SEQ ID:9363, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27693] Another function of GAM180 is therefore inhibition of Rhesus blood group, c glycoprotein (RHCG, Accession NP_057405.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHCG.

[27694] RNAHP (Accession NP_031398.1) is another GAM180 target gene, herein designated TARGET GENE. RNAHP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNAHP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNAHP BINDING SITE, designated SEQ ID:13198, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27695] Another function of GAM180 is therefore inhibition of

RNAHP (Accession NP_031398.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNAHP.

[27696] RODH-4 (Accession NP_003699.2) is another GAM180 target gene, herein designated TARGET GENE. RODH-4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RODH-4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RODH-4 BINDING SITE, designated SEQ ID:8216, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27697] Another function of GAM180 is therefore inhibition of RODH-4 (Accession NP_003699.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RODH-4.

[27698] Sal-like 2 (drosophila) (SALL2, Accession XP_300608.1) is another GAM180 target gene, herein designated TARGET GENE. SALL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SALL2, corresponding to a target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SALL2 BINDING SITE, designated SEQ ID:12473, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27699] Another function of GAM180 is therefore inhibition of Sal-like 2 (drosophila) (SALL2, Accession XP_300608.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SALL2.

[27700] SBP1 (Accession NP_835222.1) is another GAM180 target gene, herein designated TARGET GENE. SBP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SBP1 BINDING SITE, designated SEQ ID:19335, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27701] Another function of GAM180 is therefore inhibition of SBP1 (Accession NP_835222.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with SBP1.

[27702] SDNSF (Accession NP_644808.1) is another GAM180 target gene, herein designated TARGET GENE. SDNSF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SDNSF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SDNSF BINDING SITE, designated SEQ ID:5177, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27703] Another function of GAM180 is therefore inhibition of SDNSF (Accession NP_644808.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDNSF.

[27704] Serum deprivation response (phosphatidylserine binding protein) (SDPR, Accession NP_004648.1) is another GAM180 target gene, herein designated TARGET GENE. SDPR BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SDPR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

SDPR BINDING SITE, designated SEQ ID:5176, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27705] Another function of GAM180 is therefore inhibition of Serum deprivation response (phosphatidylserine binding protein) (SDPR, Accession NP_004648.1), a gene which substrate for protein_kinase_C (assists in localizing PKC to invaginations of the plasma membrane. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDPR.

[27706] The function of SDPR has been established by previous studies. Gustincich et al. (1999) cloned SDPR from a human liver cDNA library using the murine homolog cloned by Gustincich and Schneider (1993) as probe. The SDPR cDNA encodes a deduced 425- amino acid peptide with a calculated molecular mass of 47.2 kD. The human and mouse proteins share 84% sequence identity; both contain a leucine zipper- like domain with 7 repeats and 2 putative protein kinase C phosphorylation sites. Northern blot analysis of various human tissues showed nearly ubiquitous expression of a 3.1- kb transcript, which was always coexpressed with a shorter transcript. Highest expression

was detected in heart and lung. Gustincich et al. (1999) also found that SDPR mRNA was detectable in asynchronously growing human fibroblast cells and was significantly upregulated after serum deprivation but not after density- dependent growth inhibition. Gustincich et al. (1999) determined that SDPR is the same as PS- p68, a phosphatidylserine- binding protein purified from human platelets by Burgener et al. (1990). SDPR localizes to the cytoplasm (Burgener et al., 1990; Gustincich et al., 1999). Using in vitro translation of histidine- tagged recombinant SDPR, Gustincich et al. (1999) found that SDPR is able to bind PS liposomes in a calcium- independent manner. Burgener et al. (1990) identified SDPR as the major PS-binding protein in platelets. They also found that SDPR was able to bind PKC in a cell- free assay in the presence of PS and calcium, resulting in SDPR phosphorylation.

[27707]

[27708] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27709] Burgener, R.; Wolf, M.; Ganz, T.; Baggiolini, M. : Purification and characterization of a major phosphatidylserine-binding phosphoprotein from human platelets. Biochem. J.

269: 729- 734, 1990. ; and

[27710] Gustincich, S.; Vatta, P.; Goruppi, S.; Wolf, M.; Saccone, S.; Della Valle, G.; Baggiolini, M.; Schneider, C. : The human serum deprivation response gene (SDPR) maps to 2q32-q33 and cod.

[27711] Further studies establishing the function and utilities of SDPR are found in John Hopkins OMIM database record ID 606728, and in cited publications listed in Table 5, which are hereby incorporated by reference.Solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10, Accession NP_061063.2) is another GAM180 target gene, herein designated TARGET GENE. SLC16A10 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC16A10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A10 BINDING SITE, designated SEQ ID:2213, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27712] Another function of GAM180 is therefore inhibition of Solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10, Accession NP_061063.2) . Ac-

cordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A10.

[27713] Solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10, Accession NP_071341.1) is another GAM180 target gene, herein designated TARGET GENE. SLC4A10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC4A10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC4A10 BINDING SITE, designated SEQ ID:7776, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27714] Another function of GAM180 is therefore inhibition of Solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10, Accession NP_071341.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC4A10.

[27715] Solute carrier family 4, sodium bicarbonate cotransporter, member 5 (SLC4A5, Accession NP_201580.2) is another GAM180 target gene, herein designated TARGET GENE.

SLC4A5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLC4A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC4A5 BINDING SITE, designated SEQ ID:15696, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27716] Another function of GAM180 is therefore inhibition of Solute carrier family 4, sodium bicarbonate cotransporter, member 5 (SLC4A5, Accession NP_201580.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC4A5.

[27717] Solute carrier family 5 (sodium/glucose cotransporter), member 2 (SLC5A2, Accession NP_003032.1) is another GAM180 target gene, herein designated TARGET GENE. SLC5A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC5A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of SLC5A2 BINDING SITE, designated SEQ ID:3698, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27718] Another function of GAM180 is therefore inhibition of Solute carrier family 5 (sodium/glucose cotransporter), member 2 (SLC5A2, Accession NP_003032.1), a gene which is a sodium - glucose cotransporter. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC5A2.

[27719] The function of SLC5A2 has been established by previous studies. Wells et al. (1992) isolated from a human kidney library a cDNA with 59% amino acid similarity to intestinal Na+/glucose cotransporter (OMIM Ref. No. 182380) and with significant similarity to other members of the Na+/cotransporter family. Uptake experiments using cRNA- injected Xenopus oocytes showed specific uptake of glucose and alpha- methyl glucopyranoside at up to three times background. This uptake was saturable, suggesting that the cDNA corresponds to a low- affinity kidney sodium- glucose transporter. It was therefore referred to as sodium- glucose cotransporter 2, or SGLT2. By Southern blot analysis of genomic DNA from 16 somatic

cell hybrids, Wells et al. (1993) localized the SGLT2 gene to chromosome 16. Analysis of 3 additional hybrids that selectively retained all or part of human chromosome 16 demonstrated localization of the gene to 16p11.2. Kanai et al. (1994) characterized the previously cloned (Wells et al., 1992) human kidney cDNA that codes for a protein with 59% identity to the high affinity Na(+)/glucose co-transporter (SGLT1; 182380). Using expression studies with Xenopus laevis oocytes, they demonstrated that SGLT2 mediates saturable Na(+)- dependent and phlo-rizin- sensitive transport with K(m) values consistent with low affinity Na(+)/glucose cotransport. In contrast to SGLT1, SGLT2 does not transport D- galactose. Using combined in situ hybridization and immunocytochemistry with tubule segment specific marker antibodies, Kanai et al. (1994) demonstrated an extremely high level of SGLT2 message in proximal tubule S1 segments. This level of expression was also evident on Northern blots and likely confers the high capacity of this glucose transport system. Kanai et al. (1994) suggested that the defect in renal gly-cosuria (OMIM Ref. No. 233100) may reside in the SGLT2 gene.

[27720]

[27721] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27722] Wells, R. G.; Mohandas, T. K.; Hediger, M. A. : Localization of the Na+/glucose cotransporter gene SGLT2 to human chromosome 16 close to the centromere. Genomics 17: 787- 789, 1993. ; and

[27723] Kanai, Y.; Lee, W.- S.; You, G.; Brown, D.; Hediger, M. A. : The human kidney low affinity Na(+)/glucose cotransporter SGLT2: delineation of the major renal reabsorptive mechanism for D- gluc.

[27724] Further studies establishing the function and utilities of SLC5A2 are found in John Hopkins OMIM database record ID 182381, and in cited publications listed in Table 5, which are hereby incorporated by reference.Smith-magenis syndrome chromosome region, candidate 7 (SMCR7, Accession NP_631901.2) is another GAM180 target gene, herein designated TARGET GENE. SMCR7 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMCR7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of SMCR7 BINDING SITE, designated SEQ ID:15179, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27725] Another function of GAM180 is therefore inhibition of Smith-magenis syndrome chromosome region, candidate 7 (SMCR7, Accession NP_631901.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMCR7.

[27726] Smith-magenis syndrome chromosome region, candidate 7 (SMCR7, Accession NP_683684.1) is another GAM180 target gene, herein designated TARGET GENE. SMCR7 BINDING SITE is a target binding site found in the 5` un-translated region of multiple transcripts of mRNA encoded by SMCR7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-cleotide sequences of SMCR7 BINDING SITE, designated SEQ ID:15179, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27727] Another function of GAM180 is therefore inhibition of Smith-magenis syndrome chromosome region, candidate

7 (SMCR7, Accession NP_683684.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMCR7.

[27728] Small muscle protein, x-linked (SMPX, Accession NP_055147.1) is another GAM180 target gene, herein designated TARGET GENE. SMPX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SMPX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMPX BINDING SITE, designated SEQ ID:15935, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27729] Another function of GAM180 is therefore inhibition of Small muscle protein, x-linked (SMPX, Accession NP_055147.1), a gene which is a novel X- chromosomal human gene. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMPX.

[27730] The function of SMPX has been established by previous studies. A wide range of techniques, including differential display, the 2- hybrid system, exon trapping, and recipro-

cal probing, have been applied to isolate human genes for basic functional analysis or as candidates for genetic disorders. In more recent times, large scale sequencing of both the human genome and a growing number of EST libraries has provided tools to improve gene identification. Patzak et al. (1999) studied a partial cDNA clone previously identified by reciprocal probing by Lee et al. (1995). By searching expressed and genomic databases, Patzak et al. (1999) identified 21 ESTs that allowed the assignment of a human extended consensus sequence of 887 bp, suggesting a completely expressed gene termed SMPX. By using the human consensus sequence, the orthologous mouse and rat Smpx genes could be aligned and confirmed by complete sequencing of additional SMPX- related clones obtained by library screening. The human and rodent SMPX genes encode proteins of 88 to 86 and 85 amino acids, respectively. The authors found that the SMPX gene consists of 5 exons and 4 introns, comprising together 52.1 kb. Northern blot analysis revealed that SMPX is preferentially and abundantly expressed in heart and skeletal muscle. By FISH, Patzak et al. (1999) mapped the SMPX gene close to marker DXS7101, 31.9 cM from the short arm telomere of the X chromosome at Xp22.1.

They confirmed this assignment by PCR on monochromosomal and subchromosomal mapping panels and by using the CEPH YAC library. The authors concluded that the expression and mapping data made SMPX a candidate for X-linked cardiac or muscle muscular disorders.

[27731]

[27732] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27733] Patzak, D.; Zhuchenko, O.; Lee, C.- C.; Wehnert, M. : Identification, mapping, and genomic structure of a novel X-chromosomal human gene (SMPX) encoding a small muscular protein. Hum. Genet. 105: 506- 512, 1999. ; and

[27734] Lee, C. C.; Yazdani, A.; Wehnert, M.; Zhao, Z. Y.; Lindsay, E. A.; Bailey, J.; Coolbaugh, M. I.; Couch, L.; Xiong, M.; Chinault, A. C.; Baldini, A.; Caskey, C. T. : Isolation of chromo.

[27735] Further studies establishing the function and utilities of SMPX are found in John Hopkins OMIM database record ID 300226, and in cited publications listed in Table 5, which are hereby incorporated by reference.Sclerosteosis (SOST, Accession NP_079513.1) is another GAM180 target gene, herein designated TARGET GENE. SOST BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by SOST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SOST BINDING SITE, designated SEQ ID:5377, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27736] Another function of GAM180 is therefore inhibition of Sclerosteosis (SOST, Accession NP_079513.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOST.

[27737] SPEC1 (Accession NP_064624.1) is another GAM180 target gene, herein designated TARGET GENE. SPEC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPEC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPEC1 BINDING SITE, designated SEQ ID:8847, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27738] Another function of GAM180 is therefore inhibition of SPEC1 (Accession NP_064624.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPEC1.

[27739] Syntaxin 16 (STX16, Accession NP_003754.1) is another GAM180 target gene, herein designated TARGET GENE. STX16 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by STX16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STX16 BINDING SITE, designated SEQ ID:8099, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27740] Another function of GAM180 is therefore inhibition of Syntaxin 16 (STX16, Accession NP_003754.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STX16.

[27741] Syntaxin 3a (STX3A, Accession NP_004168.1) is another GAM180 target gene, herein designated TARGET GENE. STX3A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STX3A, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STX3A BINDING SITE, designated SEQ ID:15455, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27742] Another function of GAM180 is therefore inhibition of Syntaxin 3a (STX3A, Accession NP_004168.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STX3A.

[27743] Surfeit 5 (SURF5, Accession NP_852468.1) is another GAM180 target gene, herein designated TARGET GENE. SURF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SURF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SURF5 BINDING SITE, designated SEQ ID:4742, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27744] Another function of GAM180 is therefore inhibition of Surfeit 5 (SURF5, Accession NP_852468.1) . Accordingly,

utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURF5.

[27745] Transcription factor 4 (TCF4, Accession NP_003190.1) is another GAM180 target gene, herein designated TARGET GENE. TCF4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TCF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCF4 BINDING SITE, designated SEQ ID:12785, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27746] Another function of GAM180 is therefore inhibition of Transcription factor 4 (TCF4, Accession NP_003190.1), a gene which is a transcriptional activator; interacts with ITF1 (TCF3); and contains basic helix- loop- helix domain. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF4.

[27747] The function of TCF4 has been established by previous studies. The high mobility group (HMG) box is a DNA-binding domain. TCF7 (OMIM Ref. No. 189908), also

called TCF1, and LEF1 (OMIM Ref. No. 153245), also called TCF1- alpha, are human lymphoid transcription factors that contain a virtually identical HMG box. By PCR of human genomic DNA using degenerate oligonucleotides based on the HMG boxes of TCF7 and LEF1, Castrop et al. (1992) identified the TCF7L1 (OMIM Ref. No. 604652) and TCF7L2 genes, which they called TCF3 and TCF4, respectively. TCF7L1 and TCF7L2 were not expressed in cells of the lymphoid lineage. The deduced amino acid sequences of the HMG boxes of TCF7L1, TCF7L2, and TCF7 show striking homology. The authors suggested the existence of a subfamily of TCF7- like HMG box- containing transcription factors.

[27748] Animal model experiments lend further support to the function of TCF4. To study the physiologic role of Tcf4 (which is encoded by the Tcf7l2 gene), Korinek et al. (1998) disrupted Tcf7l2 by homologous recombination. The homozygous null mice died shortly after birth. A single histopathologic abnormality was observed. An apparently normal transition of intestinal endoderm into epithelium occurred at approximately embryonic day (E) 14.5. However, no proliferative compartments were maintained in the prospective crypt regions between the villi.

As a consequence, the neonatal epithelium was composed entirely of differentiated, nondividing villus cells. Korinek et al. (1998) concluded that the genetic program controlled by Tcf7l2 maintains the crypt stem cells of the small intestine. The constitutive activity of Tcf4 in APC-deficient epithelial cells may contribute to their malignant transformation by maintaining stem cell characteristics.

[27749] It is appreciated that the abovementioned animal model for TCF4 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[27750] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[27751] Castrop, J.; van Norren, K.; Clevers, H. : A gene family of HMG- box transcription factors with homology to TCF- 1. Nucleic Acids Res. 20: 611 only, 1992. ; and

[27752] Korinek, V.; Barker, N.; Moerer, P.; van Donselaar, E.; Huls, G.; Peters, P. J.; Clevers, H. : Depletion of epithelial stem-cell compartments in the small intestine of mice lacking Tcf- 4.

[27753] Further studies establishing the function and utilities of TCF4 are found in John Hopkins OMIM database record ID

602228, and in cited publications listed in Table 5, which are hereby incorporated by reference.Tgfb1-induced anti-apoptotic factor 1 (TIAF1, Accession NP_510880.2) is another GAM180 target gene, herein designated TARGET GENE. TIAF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TIAF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TIAF1 BINDING SITE, designated SEQ ID:16174, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27754] Another function of GAM180 is therefore inhibition of Tgfb1-induced anti-apoptotic factor 1 (TIAF1, Accession NP_510880.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIAF1.

[27755] Transmembrane, prostate androgen induced rna (TMEPAI, Accession NP_064567.2) is another GAM180 target gene, herein designated TARGET GENE. TMEPAI BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TMEPAI, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMEPAI BINDING SITE, designated SEQ ID:10288, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27756] Another function of GAM180 is therefore inhibition of Transmembrane, prostate androgen induced rna (TMEPAI, Accession NP_064567.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEPAI.

[27757] Trinucleotide repeat containing 5 (TNRC5, Accession NP_006577.1) is another GAM180 target gene, herein designated TARGET GENE. TNRC5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TNRC5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNRC5 BINDING SITE, designated SEQ ID:1159, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27758] Another function of GAM180 is therefore inhibition of Trinucleotide repeat containing 5 (TNRC5, Accession

NP_006577.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNRC5.

[27759] Topoisomerase (dna) ii alpha 170kda (TOP2A, Accession NP_001058.2) is another GAM180 target gene, herein designated TARGET GENE. TOP2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TOP2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOP2A BINDING SITE, designated SEQ ID:12252, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27760] Another function of GAM180 is therefore inhibition of Topoisomerase (dna) ii alpha 170kda (TOP2A, Accession NP_001058.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOP2A.

[27761] TP53I11 (Accession XP_029347.6) is another GAM180 target gene, herein designated TARGET GENE. TP53I11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by

TP53I11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TP53I11 BINDING SITE, designated SEQ ID:9520, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27762] Another function of GAM180 is therefore inhibition of TP53I11 (Accession XP_029347.6) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53I11.

[27763] TRIAD3 (Accession NP_061884.2) is another GAM180 target gene, herein designated TARGET GENE. TRIAD3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRIAD3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIAD3 BINDING SITE, designated SEQ ID:18793, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27764] Another function of GAM180 is therefore inhibition of TRIAD3 (Accession NP_061884.2) . Accordingly, utilities of

GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIAD3.

[27765] Upstream binding protein 1 (lbp-1a) (UBP1, Accession NP_055332.2) is another GAM180 target gene, herein designated TARGET GENE. UBP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBP1 BINDING SITE, designated SEQ ID:3862, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27766] Another function of GAM180 is therefore inhibition of Upstream binding protein 1 (lbp-1a) (UBP1, Accession NP_055332.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBP1.

[27767] UNC5H2 (Accession NP_734465.1) is another GAM180 target gene, herein designated TARGET GENE. UNC5H2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UNC5H2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of UNC5H2 BINDING SITE, designated SEQ ID:7676, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27768] Another function of GAM180 is therefore inhibition of UNC5H2 (Accession NP_734465.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC5H2.

[27769] VPS39 (Accession XP_031720.2) is another GAM180 target gene, herein designated TARGET GENE. VPS39 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VPS39, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VPS39 BINDING SITE, designated SEQ ID:1316, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27770] Another function of GAM180 is therefore inhibition of VPS39 (Accession XP_031720.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS39.

[27771] WDFY2 (Accession NP_443182.1) is another GAM180 target gene, herein designated TARGET GENE. WDFY2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WDFY2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WDFY2 BINDING SITE, designated SEQ ID:575, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27772] Another function of GAM180 is therefore inhibition of WDFY2 (Accession NP_443182.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDFY2.

[27773] XT3 (Accession NP_071800.1) is another GAM180 target gene, herein designated TARGET GENE. XT3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by XT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of XT3 BINDING SITE, designated SEQ ID:1554, to the nucleotide sequence of GAM180 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:214.

[27774] Another function of GAM180 is therefore inhibition of XT3 (Accession NP_071800.1), a gene which is a Kidney- specific orphan transporter. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XT3.

[27775] The function of XT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.XT3 (Accession NP_064593.1) is another GAM180 target gene, herein designated TARGET GENE. XT3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by XT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of XT3 BINDING SITE, designated SEQ ID:1554, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27776] Another function of GAM180 is therefore inhibition of XT3 (Accession NP_064593.1), a gene which is a Kidney- specific orphan transporter. Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with XT3.

[27777] The function of XT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Zonadhesin (ZAN, Accession NP_775078.1) is another GAM180 target gene, herein designated TARGET GENE. ZAN BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZAN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAN BINDING SITE, designated SEQ ID:17735, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27778] Another function of GAM180 is therefore inhibition of Zonadhesin (ZAN, Accession NP_775078.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAN.

[27779] Zonadhesin (ZAN, Accession NP_775079.1) is another GAM180 target gene, herein designated TARGET GENE. ZAN BINDING SITE is a target binding site found in the 3`

untranslated region of multiple transcripts of mRNA encoded by ZAN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAN BINDING SITE, designated SEQ ID:17735, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27780] Another function of GAM180 is therefore inhibition of Zonadhesin (ZAN, Accession NP_775079.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAN.

[27781] Zonadhesin (ZAN, Accession NP_775080.1) is another GAM180 target gene, herein designated TARGET GENE. ZAN BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZAN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAN BINDING SITE, designated SEQ ID:17735, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27782] Another function of GAM180 is therefore inhibition of

Zonadhesin (ZAN, Accession NP_775080.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAN.

[27783] Zonadhesin (ZAN, Accession NP_775081.1) is another GAM180 target gene, herein designated TARGET GENE. ZAN BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZAN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAN BINDING SITE, designated SEQ ID:17735, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27784] Another function of GAM180 is therefore inhibition of Zonadhesin (ZAN, Accession NP_775081.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAN.

[27785] Zinc finger protein 235 (ZNF235, Accession NP_004225.2) is another GAM180 target gene, herein designated TARGET GENE. ZNF235 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

ZNF235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF235 BINDING SITE, designated SEQ ID:12391, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27786] Another function of GAM180 is therefore inhibition of Zinc finger protein 235 (ZNF235, Accession NP_004225.2) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF235.

[27787] Zinc finger protein 258 (ZNF258, Accession NP_009098.1) is another GAM180 target gene, herein designated TARGET GENE. ZNF258 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ZNF258, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF258 BINDING SITE, designated SEQ ID:8831, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27788] Another function of GAM180 is therefore inhibition of Zinc finger protein 258 (ZNF258, Accession NP_009098.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF258.

[27789] Zinc finger protein 258 (ZNF258, Accession NP_660353.1) is another GAM180 target gene, herein designated TARGET GENE. ZNF258 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ZNF258, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF258 BINDING SITE, designated SEQ ID:8831, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27790] Another function of GAM180 is therefore inhibition of Zinc finger protein 258 (ZNF258, Accession NP_660353.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF258.

[27791] Zinc finger protein 347 (ZNF347, Accession NP_115973.1) is another GAM180 target gene, herein designated TAR-

GET GENE. ZNF347 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF347, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF347 BINDING SITE, designated SEQ ID:7083, to the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, also designated SEQ ID:214.

[27792] Another function of GAM180 is therefore inhibition of Zinc finger protein 347 (ZNF347, Accession NP_115973.1) . Accordingly, utilities of GAM180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF347.

[27793]

[27794] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 181 (GAM181), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[27795] GAM181 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM181 was detected is described hereinabove

with reference to Figs. 8-15.

[27796] GAM181 gene, herein designated GAM GENE, and GAM181 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[27797] GAM181 gene encodes a GAM181 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM181 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM181 precursor RNA is designated SEQ ID:35, and is provided hereinbelow with reference to the sequence listing part.

[27798] GAM181 precursor RNA folds onto itself, forming GAM181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27799] GAM181 precursor RNA folds onto itself, forming GAM181 folded precursor RNA, herein designated GAM FOLDED

PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[27800] Nucleotide sequence of GAM181 precursor RNA, designated SEQ-ID: 35, and a schematic representation of a predicted secondary folding of GAM181 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[27801] An enzyme complex designated DICER COMPLEX, `dices` the GAM181 folded precursor RNA into GAM181 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM181 RNA is designated SEQ ID:395, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby in-

corporated by reference.

[27802] GAM181 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM181 target RNA, herein designated GAM TARGET RNA. GAM181 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[27803] GAM181 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM181 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM181 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM181 RNA may have a different number of target binding sites in untranslated regions of a GAM181 target RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[27804] The complementary binding of GAM181 RNA, herein designated GAM RNA, to target binding sites on GAM181 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM181 target RNA into GAM181 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[27805] It is appreciated that GAM181 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM181 target genes. The mRNA of each one of this plurality of GAM181 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM181 RNA, herein designated GAM RNA, and which when bound by GAM181 RNA causes inhibition of translation of respective one or more GAM181 target proteins.

[27806] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM181 gene, herein designated GAM GENE, on one or more GAM181 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27807] It is appreciated that specific functions and accordingly utilities of GAM181 correlate with, and may be deduced from, the identity of the target genes which GAM181 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[27808]

[27809]

[27810] LOC200197 (Accession XM_114148.1) is a GAM181 target gene, herein designated TARGET GENE. LOC200197 BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200197, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200197 BINDING SITE, designated SEQ ID:17783, to the nucleotide sequence of GAM181 RNA, herein designated GAM RNA, also designated SEQ ID:395.

[27811] A function of GAM181 is therefore inhibition of LOC200197 (Accession XM_114148.1) . Accordingly, utilities of GAM181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200197.

[27812] LOC90906 (Accession XM_034809.1) is another GAM181 target gene, herein designated TARGET GENE. LOC90906 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90906, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90906 BINDING SITE, designated SEQ ID:2635, to the nucleotide sequence of GAM181 RNA, herein designated GAM RNA, also designated SEQ ID:395.

[27813] Another function of GAM181 is therefore inhibition of LOC90906 (Accession XM_034809.1) . Accordingly, utilities of GAM181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90906.

[27814] LOC91137 (Accession NM_138773.1) is another GAM181 target gene, herein designated TARGET GENE. LOC91137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91137 BINDING SITE, designated SEQ ID:17149, to the nucleotide sequence of GAM181 RNA, herein designated GAM RNA, also designated SEQ ID:395.

[27815] Another function of GAM181 is therefore inhibition of LOC91137 (Accession NM_138773.1) . Accordingly, utilities of GAM181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91137.

[27816] NET-5 (Accession NM_006675.2) is another GAM181 target gene, herein designated TARGET GENE. NET-5 BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by NET-5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NET-5 BINDING SITE, designated SEQ ID:464, to the nucleotide sequence of GAM181 RNA, herein designated GAM RNA, also designated SEQ ID:395.

[27817] Another function of GAM181 is therefore inhibition of NET-5 (Accession NM_006675.2) . Accordingly, utilities of GAM181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NET-5.

[27818] SIMRP7 (Accession) is another GAM181 target gene, herein designated TARGET GENE. SIMRP7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIMRP7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIMRP7 BINDING SITE, designated SEQ ID:9314, to the nucleotide sequence of GAM181 RNA, herein designated GAM RNA, also designated SEQ ID:395.

[27819] Another function of GAM181 is therefore inhibition of SIMRP7 (Accession) . Accordingly, utilities of GAM181 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with SIMRP7.

[27820]

[27821] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 182 (GAM182), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[27822] GAM182 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM182 was detected is described hereinabove with reference to Figs. 8-15.

[27823] GAM182 gene, herein designated GAM GENE, and GAM182 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[27824] GAM182 gene encodes a GAM182 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM182 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM182 precursor RNA is designated SEQ ID:144, and is provided hereinbelow with reference to the sequence list-

ing part. Nucleotide sequence SEQ ID:144 is located at position 1427020 relative to chromosome 16.

[27825] GAM182 precursor RNA folds onto itself, forming GAM182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27826] GAM182 precursor RNA folds onto itself, forming GAM182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[27827] Nucleotide sequence of GAM182 precursor RNA, designated SEQ-ID: 144, and a schematic representation of a predicted secondary folding of GAM182 folded precursor

RNA are further described with reference to Table 2, hereby incorporated by reference.

[27828] An enzyme complex designated DICER COMPLEX, `dices` the GAM182 folded precursor RNA into GAM182 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM182 RNA is designated SEQ ID:307, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[27829] GAM182 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM182 target RNA, herein designated GAM TARGET RNA. GAM182 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[27830] GAM182 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM182 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM182 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM182 RNA may have a different number of target binding sites in untranslated regions of a GAM182 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[27831] The complementary binding of GAM182 RNA, herein designated GAM RNA, to target binding sites on GAM182 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM182 target RNA into GAM182 target protein, herein designated GAM TARGET PROTEIN.

GAM target protein is therefore outlined by a broken line.

[27832] It is appreciated that GAM182 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM182 target genes. The mRNA of each one of this plurality of GAM182 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM182 RNA, herein designated GAM RNA, and which when bound by GAM182 RNA causes inhibition of translation of respective one or more GAM182 target proteins.

[27833] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM182 gene, herein designated GAM GENE, on one or more GAM182 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27834] It is appreciated that specific functions and accordingly utilities of GAM182 correlate with, and may be deduced from, the identity of the target genes which GAM182 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[27835]

[27836]

[27837] AF020591 (Accession NM_014480.1) is a GAM182 target gene, herein designated TARGET GENE. AF020591 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AF020591, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AF020591 BINDING SITE, designated SEQ ID:19423, to the nucleotide sequence of GAM182 RNA, herein designated GAM RNA, also designated SEQ ID:307.

[27838] A function of GAM182 is therefore inhibition of AF020591 (Accession NM_014480.1) . Accordingly, utilities of

GAM182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AF020591.

[27839] CASKIN1 (Accession NM_020764.1) is another GAM182 target gene, herein designated TARGET GENE. CASKIN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CASKIN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASKIN1 BINDING SITE, designated SEQ ID:7419, to the nucleotide sequence of GAM182 RNA, herein designated GAM RNA, also designated SEQ ID:307.

[27840] Another function of GAM182 is therefore inhibition of CASKIN1 (Accession NM_020764.1) . Accordingly, utilities of GAM182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASKIN1.

[27841] KIAA0565 (Accession XM_039912.4) is another GAM182 target gene, herein designated TARGET GENE. KIAA0565 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0565, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0565 BINDING SITE, designated SEQ ID:19085, to the nucleotide sequence of GAM182 RNA, herein designated GAM RNA, also designated SEQ ID:307.

[27842] Another function of GAM182 is therefore inhibition of KIAA0565 (Accession XM_039912.4) . Accordingly, utilities of GAM182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0565.

[27843] Lim domain binding 3 (LDB3, Accession XM_084376.6) is another GAM182 target gene, herein designated TARGET GENE. LDB3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LDB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LDB3 BINDING SITE, designated SEQ ID:3284, to the nucleotide sequence of GAM182 RNA, herein designated GAM RNA, also designated SEQ ID:307.

[27844] Another function of GAM182 is therefore inhibition of Lim domain binding 3 (LDB3, Accession XM_084376.6), a gene which could play a role during mating. Accordingly, utili-

ties of GAM182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LDB3.

[27845] The function of LDB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.LOC124470 (Accession) is another GAM182 target gene, herein designated TARGET GENE. LOC124470 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC124470, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC124470 BINDING SITE, designated SEQ ID:12795, to the nucleotide sequence of GAM182 RNA, herein designated GAM RNA, also designated SEQ ID:307.

[27846] Another function of GAM182 is therefore inhibition of LOC124470 (Accession) . Accordingly, utilities of GAM182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124470.

[27847] LOC256207 (Accession) is another GAM182 target gene, herein designated TARGET GENE. LOC256207 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC256207, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256207 BINDING SITE, designated SEQ ID:2860, to the nucleotide sequence of GAM182 RNA, herein designated GAM RNA, also designated SEQ ID:307.

[27848] Another function of GAM182 is therefore inhibition of LOC256207 (Accession) . Accordingly, utilities of GAM182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256207.

[27849] SCYA19 (Accession) is another GAM182 target gene, herein designated TARGET GENE. SCYA19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCYA19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCYA19 BINDING SITE, designated SEQ ID:10974, to the nucleotide sequence of GAM182 RNA, herein designated GAM RNA, also designated SEQ ID:307.

[27850] Another function of GAM182 is therefore inhibition of SCYA19 (Accession) . Accordingly, utilities of GAM182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCYA19.

[27851] Transforming growth factor, alpha (TGFA, Accession NM_003236.1) is another GAM182 target gene, herein designated TARGET GENE. TGFA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGFA BINDING SITE, designated SEQ ID:9112, to the nucleotide sequence of GAM182 RNA, herein designated GAM RNA, also designated SEQ ID:307.

[27852] Another function of GAM182 is therefore inhibition of Transforming growth factor, alpha (TGFA, Accession NM_003236.1), a gene which is able to bind to the egf receptor and to act synergistically with tgf beta to promote anchorage- independent cell proliferation in soft agar. Accordingly, utilities of GAM182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFA.

[27853] The function of TGFA and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.

[27854] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 183 (GAM183), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[27855] GAM183 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM183 was detected is described hereinabove with reference to Figs. 8-15.

[27856] GAM183 gene, herein designated GAM GENE, and GAM183 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[27857] GAM183 gene encodes a GAM183 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM183 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM183 precursor RNA is designated SEQ ID:7, and is provided hereinbelow with reference to the sequence list-

ing part.

[27858] GAM183 precursor RNA folds onto itself, forming GAM183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27859] GAM183 precursor RNA folds onto itself, forming GAM183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[27860] Nucleotide sequence of GAM183 precursor RNA, designated SEQ-ID: 7, and a schematic representation of a predicted secondary folding of GAM183 folded precursor RNA are further described with reference to Table 2, hereby in-

corporated by reference.

[27861] An enzyme complex designated DICER COMPLEX, `dices` the GAM183 folded precursor RNA into GAM183 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM183 RNA is designated SEQ ID:240, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[27862] GAM183 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM183 target RNA, herein designated GAM TARGET RNA. GAM183 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[27863] GAM183 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM183 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM183 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM183 RNA may have a different number of target binding sites in untranslated regions of a GAM183 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[27864] The complementary binding of GAM183 RNA, herein designated GAM RNA, to target binding sites on GAM183 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM183 target RNA into GAM183 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[27865] It is appreciated that GAM183 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM183 target genes. The mRNA of each one of this plurality of GAM183 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM183 RNA, herein designated GAM RNA, and which when bound by GAM183 RNA causes inhibition of translation of respective one or more GAM183 target proteins.

[27866] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM183 gene, herein designated GAM GENE, on one or more GAM183 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27867] It is appreciated that specific functions and accordingly utilities of GAM183 correlate with, and may be deduced from, the identity of the target genes which GAM183 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[27868]

[27869]

[27870] DKFZP434J1813 (Accession) is a GAM183 target gene, herein designated TARGET GENE. DKFZP434J1813 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434J1813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434J1813 BINDING SITE, designated SEQ ID:16705, to the nucleotide sequence of GAM183 RNA, herein designated GAM RNA, also designated SEQ ID:240.

[27871] A function of GAM183 is therefore inhibition of DKFZP434J1813 (Accession) . Accordingly, utilities of GAM183 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with DK-FZP434J1813.

[27872] KIAA1025 (Accession XM_034056.6) is another GAM183 target gene, herein designated TARGET GENE. KIAA1025 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1025, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1025 BINDING SITE, designated SEQ ID:5814, to the nucleotide sequence of GAM183 RNA, herein designated GAM RNA, also designated SEQ ID:240.

[27873] Another function of GAM183 is therefore inhibition of KIAA1025 (Accession XM_034056.6) . Accordingly, utilities of GAM183 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1025.

[27874] MGC22805 (Accession NM_144590.1) is another GAM183 target gene, herein designated TARGET GENE. MGC22805 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC22805, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC22805 BINDING SITE, designated SEQ ID:15928, to the nucleotide sequence of GAM183 RNA, herein designated GAM RNA, also designated SEQ ID:240.

[27875] Another function of GAM183 is therefore inhibition of MGC22805 (Accession NM_144590.1) . Accordingly, utilities of GAM183 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC22805.

[27876] Prostaglandin-endoperoxide synthase 2 (prostaglandin g/h synthase and cyclooxygenase) (PTGS2, Accession NM_000963.1) is another GAM183 target gene, herein designated TARGET GENE. PTGS2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGS2 BINDING SITE, designated SEQ ID:14372, to the nucleotide sequence of GAM183 RNA, herein designated GAM RNA, also designated SEQ ID:240.

[27877] Another function of GAM183 is therefore inhibition of Prostaglandin-endoperoxide synthase 2 (prostaglandin g/

h synthase and cyclooxygenase) (PTGS2, Accession NM_000963.1), a gene which may have a role as a major mediator of inflammation and/or a role for prostanoid signaling in activity- dependent plasticity. and therefore may be associated with Inflammatory diseases such as rheumatoid arthritis. Accordingly, utilities of GAM183 include diagnosis, prevention and treatment of Inflammatory diseases such as rheumatoid arthritis., and of other diseases and clinical conditions associated with PTGS2.

[27878] The function of PTGS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM100.1.

[27879] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 184 (GAM184), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[27880] GAM184 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM184 was detected is described hereinabove with reference to Figs. 8-15.

[27881] GAM184 gene, herein designated GAM GENE, and GAM184 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[27882] GAM184 gene encodes a GAM184 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM184 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM184 precursor RNA is designated SEQ ID:50, and is provided hereinbelow with reference to the sequence listing part.

[27883] GAM184 precursor RNA folds onto itself, forming GAM184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27884] GAM184 precursor RNA folds onto itself, forming GAM184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[27885] Nucleotide sequence of GAM184 precursor RNA, designated SEQ-ID: 50, and a schematic representation of a predicted secondary folding of GAM184 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[27886] An enzyme complex designated DICER COMPLEX, `dices` the GAM184 folded precursor RNA into GAM184 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM184 RNA is designated SEQ ID:284, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[27887] GAM184 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM184 target RNA, herein designated GAM TARGET RNA. GAM184 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[27888] GAM184 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM184 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM184 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM184 RNA may have a different number of target binding sites in untranslated regions of a GAM184 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an

example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[27889] The complementary binding of GAM184 RNA, herein designated GAM RNA, to target binding sites on GAM184 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM184 target RNA into GAM184 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[27890] It is appreciated that GAM184 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM184 target genes. The mRNA of each one of this plurality of GAM184 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM184 RNA, herein designated GAM RNA, and which when bound by GAM184 RNA causes inhibition of translation of respective one or more GAM184 target proteins.

[27891] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM184 gene, herein designated GAM GENE, on one or

more GAM184 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27892] It is appreciated that specific functions and accordingly utilities of GAM184 correlate with, and may be deduced from, the identity of the target genes which GAM184 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[27893]

[27894]

[27895] Transforming growth factor, beta receptor ii (70/80kda) (TGFBR2, Accession NM_003242.3) is a GAM184 target gene, herein designated TARGET GENE. TGFBR2 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFBR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGFBR2 BINDING SITE, designated SEQ ID:9885, to the nucleotide sequence of GAM184 RNA, herein designated GAM RNA, also designated SEQ ID:284.

[27896] A function of GAM184 is therefore inhibition of Transforming growth factor, beta receptor ii (70/80kda) (TGFBR2, Accession NM_003242.3) . Accordingly, utilities of GAM184 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFBR2.

[27897]

[27898] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 185 (GAM185), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[27899] GAM185 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM185 was detected is described hereinabove with reference to Figs. 8-15.

[27900] GAM185 gene, herein designated GAM GENE, and GAM185 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[27901] GAM185 gene encodes a GAM185 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM185 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM185 precursor RNA is designated SEQ ID:78, and is provided hereinbelow with reference to the sequence listing part.

[27902] GAM185 precursor RNA folds onto itself, forming GAM185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27903] GAM185 precursor RNA folds onto itself, forming GAM185

folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[27904] Nucleotide sequence of GAM185 precursor RNA, designated SEQ-ID: 78, and a schematic representation of a predicted secondary folding of GAM185 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[27905] An enzyme complex designated DICER COMPLEX, `dices` the GAM185 folded precursor RNA into GAM185 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM185 RNA is designated SEQ ID:372, and is provided hereinbelow with refer-

ences to the sequence listing part and Table 3, hereby incorporated by reference.

[27906] GAM185 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM185 target RNA, herein designated GAM TARGET RNA. GAM185 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[27907] GAM185 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM185 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM185 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM185 RNA may have a different number of target binding sites in untranslated regions of a GAM185 target

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[27908] The complementary binding of GAM185 RNA, herein designated GAM RNA, to target binding sites on GAM185 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM185 target RNA into GAM185 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[27909] It is appreciated that GAM185 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM185 target genes. The mRNA of each one of this plurality of GAM185 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM185 RNA, herein designated GAM RNA, and which when bound by GAM185 RNA causes inhibition of translation of respective one or more GAM185 target proteins.

[27910] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM185 gene, herein designated GAM GENE, on one or more GAM185 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27911] It is appreciated that specific functions and accordingly utilities of GAM185 correlate with, and may be deduced from, the identity of the target genes which GAM185 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[27912]

[27913]

[27914] Grb2-associated binding protein 2 (GAB2, Accession

NM_080491.1) is a GAM185 target gene, herein designated TARGET GENE. GAB2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GAB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAB2 BINDING SITE, designated SEQ ID:18059, to the nucleotide sequence of GAM185 RNA, herein designated GAM RNA, also designated SEQ ID:372.

[27915] A function of GAM185 is therefore inhibition of Grb2-associated binding protein 2 (GAB2, Accession NM_080491.1), a gene which act as adapters for transmitting various signals. Accordingly, utilities of GAM185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAB2.

[27916] The function of GAB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Growth arrest and dna-damage-inducible, beta (GADD45B, Accession NM_015675.1) is another GAM185 target gene, herein designated TARGET GENE. GADD45B BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by GADD45B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GADD45B BINDING SITE, designated SEQ ID:9982, to the nucleotide sequence of GAM185 RNA, herein designated GAM RNA, also designated SEQ ID:372.

[27917] Another function of GAM185 is therefore inhibition of Growth arrest and dna-damage-inducible, beta (GADD45B, Accession NM_015675.1), a gene which activates MTK1 kinase activity and maybe involved in stress response. Accordingly, utilities of GAM185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GADD45B.

[27918] The function of GADD45B has been established by previous studies. The stress- responsive p38 (see OMIM Ref. No. MAPK14; 600289) and JNK (see OMIM Ref. No. MAPK8; 601158) mitogen- activated protein kinase (MAPK) pathways regulate cell cycle and apoptosis. A human MAP3K, MTK1 (MAP3K4; 602425), mediates activation of both p38 and JNK in response to environmental stresses. By screening a placenta cDNA library using a yeast 2- hybrid method, Takekawa and Saito (1998) isolated cDNAs en-

coding 3 related proteins, GADD45- alpha (GADD45A; 126335), GADD45- beta (GADD45B), and GADD45- gamma (GADD45G; 604949), that bound to an N- terminal domain of MTK1. The deduced GADD45B protein contains 160 amino acids. GADD45A, GADD45B, and GADD45G share 55 to 58% amino acid identity. These proteins activated MTK1 kinase activity, both in vivo and in vitro. All 3 GADD45- like genes were induced by environmental stresses, including methyl methanesulfonate, UV, and gamma irradiation. Expression of the GADD45- like genes induced p38/JNK activation and apoptosis, which could be partially suppressed by coexpression of a dominant inhibitory MTK1 mutant protein. Northern blot analysis detected strong expression of a 1.4- kb GADD45B transcript in heart and liver, with moderate expression in placenta, lung, skeletal muscle, kidney, and pancreas, and little or no expression in brain. Takekawa and Saito (1998) proposed that the GADD45- like proteins mediate activation of the p38/JNK pathway, via MTK1, in response to environmental stresses.

[27919]

[27920] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[27921] De Smaele, E.; Zazzeroni, F.; Papa, S.; Nguyen, D. U.; Jin, R.; Jones, J.; Cong, R.; Franzoso, G. : Induction of gadd45-beta by NF- kappa- B downregulates pro- apoptotic JNK signaling. Nature 414: 308- 313, 2001. ; and

[27922] Takekawa, M.; Saito, H. : A family of stress- inducible GADD45- like proteins mediate activation of the stress-responsive MTK1/MEKK4 MAPKKK. Cell 95: 521- 530, 1998.

[27923] Further studies establishing the function and utilities of GADD45B are found in John Hopkins OMIM database record ID 604948, and in cited publications listed in Table 5, which are hereby incorporated by reference.

[27924] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 186 (GAM186), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[27925] GAM186 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM186 was detected is described hereinabove with reference to Figs. 8-15.

[27926] GAM186 gene, herein designated GAM GENE, and GAM186 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[27927] GAM186 gene encodes a GAM186 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM186 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM186 precursor RNA is designated SEQ ID:57, and is provided hereinbelow with reference to the sequence listing part.

[27928] GAM186 precursor RNA folds onto itself, forming GAM186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27929] GAM186 precursor RNA folds onto itself, forming GAM186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[27930] Nucleotide sequence of GAM186 precursor RNA, designated SEQ-ID: 57, and a schematic representation of a predicted secondary folding of GAM186 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[27931] An enzyme complex designated DICER COMPLEX, `dices` the GAM186 folded precursor RNA into GAM186 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM186 RNA is designated SEQ ID:353, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[27932] GAM186 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM186 target RNA, herein designated GAM TARGET RNA. GAM186 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[27933] GAM186 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM186 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM186 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM186 RNA may have a different number of target binding sites in untranslated regions of a GAM186 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an

example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[27934] The complementary binding of GAM186 RNA, herein designated GAM RNA, to target binding sites on GAM186 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM186 target RNA into GAM186 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[27935] It is appreciated that GAM186 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM186 target genes. The mRNA of each one of this plurality of GAM186 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM186 RNA, herein designated GAM RNA, and which when bound by GAM186 RNA causes inhibition of translation of respective one or more GAM186 target proteins.

[27936] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM186 gene, herein designated GAM GENE, on one or

more GAM186 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27937] It is appreciated that specific functions and accordingly utilities of GAM186 correlate with, and may be deduced from, the identity of the target genes which GAM186 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[27938]

[27939]

[27940] LOC147671 (Accession XM_085844.2) is a GAM186 target gene, herein designated TARGET GENE. LOC147671 BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by LOC147671, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147671 BINDING SITE, designated SEQ ID:2416, to the nucleotide sequence of GAM186 RNA, herein designated GAM RNA, also designated SEQ ID:353.

[27941] A function of GAM186 is therefore inhibition of LOC147671 (Accession XM_085844.2) . Accordingly, utilities of GAM186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147671.

[27942] MGC4093 (Accession NM_030578.1) is another GAM186 target gene, herein designated TARGET GENE. MGC4093 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC4093, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4093 BINDING SITE, designated SEQ ID:15121, to the nucleotide sequence of GAM186 RNA, herein designated GAM RNA, also designated SEQ ID:353.

[27943] Another function of GAM186 is therefore inhibition of

MGC4093 (Accession NM_030578.1) . Accordingly, utilities of GAM186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4093.

[27944] SMAC (Accession NM_138929.1) is another GAM186 target gene, herein designated TARGET GENE. SMAC BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMAC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMAC BINDING SITE, designated SEQ ID:450, to the nucleotide sequence of GAM186 RNA, herein designated GAM RNA, also designated SEQ ID:353.

[27945] Another function of GAM186 is therefore inhibition of SMAC (Accession NM_138929.1), a gene which promotes apoptosis via caspase activation. Accordingly, utilities of GAM186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMAC.

[27946] The function of SMAC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Zuotin related factor 1 (ZRF1, Accession

XM_168590.3) is another GAM186 target gene, herein designated TARGET GENE. ZRF1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZRF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZRF1 BINDING SITE, designated SEQ ID:12343, to the nucleotide sequence of GAM186 RNA, herein designated GAM RNA, also designated SEQ ID:353.

[27947] Another function of GAM186 is therefore inhibition of Zuotin related factor 1 (ZRF1, Accession XM_168590.3) . Accordingly, utilities of GAM186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZRF1.

[27948]

[27949] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 187 (GAM187), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[27950] GAM187 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM187 was detected is described hereinabove with reference to Figs. 8-15.

[27951] GAM187 gene, herein designated GAM GENE, and GAM187 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[27952] GAM187 gene encodes a GAM187 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM187 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM187 precursor RNA is designated SEQ ID:83, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:83 is located at position 48266940 relative to chromosome 17.

[27953] GAM187 precursor RNA folds onto itself, forming GAM187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide

sequence of the second half thereof.

[27954] GAM187 precursor RNA folds onto itself, forming GAM187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[27955] Nucleotide sequence of GAM187 precursor RNA, designated SEQ-ID: 83, and a schematic representation of a predicted secondary folding of GAM187 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[27956] An enzyme complex designated DICER COMPLEX, `dices` the GAM187 folded precursor RNA into GAM187 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy

Group: C) nucleotide sequence of GAM187 RNA is designated SEQ ID:294, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[27957] GAM187 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM187 target RNA, herein designated GAM TARGET RNA. GAM187 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[27958] GAM187 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM187 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM187 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limit-

ing GAM187 RNA may have a different number of target binding sites in untranslated regions of a GAM187 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[27959] The complementary binding of GAM187 RNA, herein designated GAM RNA, to target binding sites on GAM187 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM187 target RNA into GAM187 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[27960] It is appreciated that GAM187 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM187 target genes. The mRNA of each one of this plurality of GAM187 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM187 RNA, herein designated GAM RNA, and which when bound by GAM187 RNA causes inhibition of translation of respective one or more GAM187 target proteins.

[27961] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM187 gene, herein designated GAM GENE, on one or more GAM187 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27962] It is appreciated that specific functions and accordingly utilities of GAM187 correlate with, and may be deduced from, the identity of the target genes which GAM187 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[27963]

[27964]

[27965] Eukaryotic translation initiation factor 4e binding protein 2 (EIF4EBP2, Accession NM_004096.2) is a GAM187 target gene, herein designated TARGET GENE. EIF4EBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF4EBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF4EBP2 BINDING SITE, designated SEQ ID:13732, to the nucleotide sequence of GAM187 RNA, herein designated GAM RNA, also designated SEQ ID:294.

[27966] A function of GAM187 is therefore inhibition of Eukaryotic translation initiation factor 4e binding protein 2 (EIF4EBP2, Accession NM_004096.2), a gene which binds EIF4E and negatively regulates initiation of translation. and therefore may be associated with Cancers. Accordingly, utilities of GAM187 include diagnosis, prevention and treatment of Cancers, and of other diseases and clinical conditions associated with EIF4EBP2.

[27967] The function of EIF4EBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.FLJ20487 (Accession NM_017841.1) is an-

other GAM187 target gene, herein designated TARGET GENE. FLJ20487 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20487, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20487 BINDING SITE, designated SEQ ID:6750, to the nucleotide sequence of GAM187 RNA, herein designated GAM RNA, also designated SEQ ID:294.

[27968] Another function of GAM187 is therefore inhibition of FLJ20487 (Accession NM_017841.1) . Accordingly, utilities of GAM187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20487.

[27969] LOC93259 (Accession XM_050105.2) is another GAM187 target gene, herein designated TARGET GENE. LOC93259 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC93259, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC93259 BINDING SITE, designated SEQ ID:7403, to the nucleotide sequence of GAM187 RNA, herein designated

GAM RNA, also designated SEQ ID:294.

[27970] Another function of GAM187 is therefore inhibition of LOC93259 (Accession XM_050105.2) . Accordingly, utilities of GAM187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93259.

[27971] Prostaglandin f2 receptor negative regulator (PTGFRN, Accession XM_040709.3) is another GAM187 target gene, herein designated TARGET GENE. PTGFRN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGFRN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGFRN BINDING SITE, designated SEQ ID:7229, to the nucleotide sequence of GAM187 RNA, herein designated GAM RNA, also designated SEQ ID:294.

[27972] Another function of GAM187 is therefore inhibition of Prostaglandin f2 receptor negative regulator (PTGFRN, Accession XM_040709.3), a gene which inhibits the binding of prostaglandin f2- alpha (pgf2- alpha) to its specific fp receptor. Accordingly, utilities of GAM187 include diagnosis, prevention and treatment of diseases and clinical con-

ditions associated with PTGFRN.

[27973] The function of PTGFRN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.

[27974] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 188 (GAM188), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[27975] GAM188 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM188 was detected is described hereinabove with reference to Figs. 8-15.

[27976] GAM188 gene, herein designated GAM GENE, and GAM188 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[27977] GAM188 gene encodes a GAM188 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM188 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of

GAM188 precursor RNA is designated SEQ ID:12, and is provided hereinbelow with reference to the sequence listing part.

[27978] GAM188 precursor RNA folds onto itself, forming GAM188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[27979] GAM188 precursor RNA folds onto itself, forming GAM188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[27980] Nucleotide sequence of GAM188 precursor RNA, designated SEQ-ID: 12, and a schematic representation of a

predicted secondary folding of GAM188 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[27981] An enzyme complex designated DICER COMPLEX, `dices` the GAM188 folded precursor RNA into GAM188 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM188 RNA is designated SEQ ID:286, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[27982] GAM188 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM188 target RNA, herein designated GAM TARGET RNA. GAM188 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[27983] GAM188 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM188 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM188 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM188 RNA may have a different number of target binding sites in untranslated regions of a GAM188 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[27984] The complementary binding of GAM188 RNA, herein designated GAM RNA, to target binding sites on GAM188 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM188 target RNA into GAM188 tar-

get protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[27985] It is appreciated that GAM188 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM188 target genes. The mRNA of each one of this plurality of GAM188 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM188 RNA, herein designated GAM RNA, and which when bound by GAM188 RNA causes inhibition of translation of respective one or more GAM188 target proteins.

[27986] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM188 gene, herein designated GAM GENE, on one or more GAM188 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[27987] It is appreciated that specific functions and accordingly utilities of GAM188 correlate with, and may be deduced from, the identity of the target genes which GAM188 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[27988]

[27989]

[27990] DKFZp434M0331 (Accession NM_017600.1) is a GAM188 target gene, herein designated TARGET GENE. DKFZp434M0331 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp434M0331, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434M0331 BINDING SITE, designated SEQ ID:4117, to the nucleotide sequence of GAM188 RNA, herein designated GAM RNA, also designated SEQ ID:286.

[27991] A function of GAM188 is therefore inhibition of DKFZp434M0331 (Accession NM_017600.1) . Accordingly, utilities of GAM188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434M0331.

[27992] Grb2-associated binding protein 3 (GAB3, Accession NM_080612.1) is another GAM188 target gene, herein designated TARGET GENE. GAB3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAB3 BINDING SITE, designated SEQ ID:5720, to the nucleotide sequence of GAM188 RNA, herein designated GAM RNA, also designated SEQ ID:286.

[27993] Another function of GAM188 is therefore inhibition of Grb2-associated binding protein 3 (GAB3, Accession NM_080612.1) . Accordingly, utilities of GAM188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAB3.

[27994] LOC142955 (Accession XM_084389.4) is another GAM188 target gene, herein designated TARGET GENE. LOC142955 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC142955, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC142955 BINDING SITE, designated SEQ ID:12714, to the nucleotide sequence of GAM188 RNA, herein designated GAM RNA, also designated SEQ ID:286.

[27995] Another function of GAM188 is therefore inhibition of LOC142955 (Accession XM_084389.4) . Accordingly, utilities of GAM188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142955.

[27996]

[27997] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 189 (GAM189), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[27998] GAM189 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM189 was detected is described hereinabove with reference to Figs. 8-15.

[27999] GAM189 gene, herein designated GAM GENE, and GAM189 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[28000] GAM189 gene encodes a GAM189 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM189 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM189 precursor RNA is designated SEQ ID:9, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:9 is located at position 95450006 relative to chromosome 4.

[28001] GAM189 precursor RNA folds onto itself, forming GAM189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[28002] GAM189 precursor RNA folds onto itself, forming GAM189 folded precursor RNA, herein designated GAM FOLDED

PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[28003] Nucleotide sequence of GAM189 precursor RNA, designated SEQ-ID: 9, and a schematic representation of a predicted secondary folding of GAM189 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[28004] An enzyme complex designated DICER COMPLEX, `dices` the GAM189 folded precursor RNA into GAM189 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: B) nucleotide sequence of GAM189 RNA is designated SEQ ID:246, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby in-

corporated by reference.

[28005] GAM189 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM189 target RNA, herein designated GAM TARGET RNA. GAM189 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[28006] GAM189 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM189 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM189 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM189 RNA may have a different number of target binding sites in untranslated regions of a GAM189 target RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[28007] The complementary binding of GAM189 RNA, herein designated GAM RNA, to target binding sites on GAM189 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM189 target RNA into GAM189 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[28008] It is appreciated that GAM189 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM189 target genes. The mRNA of each one of this plurality of GAM189 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM189 RNA, herein designated GAM RNA, and which when bound by GAM189 RNA causes inhibition of translation of respective one or more GAM189 target proteins.

[28009] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM189 gene, herein designated GAM GENE, on one or more GAM189 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[28010] It is appreciated that specific functions and accordingly utilities of GAM189 correlate with, and may be deduced from, the identity of the target genes which GAM189 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[28011]

[28012]

[28013] 15E1.2 (Accession XP_290596.1) is a GAM189 target gene, herein designated TARGET GENE. 15E1.2 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by 15E1.2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of 15E1.2 BINDING SITE, designated SEQ ID:12868, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28014] A function of GAM189 is therefore inhibition of 15E1.2 (Accession XP_290596.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 15E1.2.

[28015] Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2) is another GAM189 target gene, herein designated TARGET GENE. A1BG BINDING SITE1 and A1BG BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by A1BG, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A1BG BINDING SITE1 and A1BG BINDING SITE2, designated SEQ ID:18868 and SEQ ID:2534 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:246.

[28016] Another function of GAM189 is therefore inhibition of Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2), a gene which a plasma protein of unknown function. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A1BG.

[28017] The function of A1BG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Aminoadipate-semialdehyde synthase (AASS, Accession NP_005754.2) is another GAM189 target gene, herein designated TARGET GENE. AASS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AASS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AASS BINDING SITE, designated SEQ ID:6339, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28018] Another function of GAM189 is therefore inhibition of Aminoadipate-semialdehyde synthase (AASS, Accession

NP_005754.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AASS.

[28019] ABCA13 (Accession NP_689914.2) is another GAM189 target gene, herein designated TARGET GENE. ABCA13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCA13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCA13 BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28020] Another function of GAM189 is therefore inhibition of ABCA13 (Accession NP_689914.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCA13.

[28021] Atp-binding cassette, sub-family c (cftr/mrp), member 11 (ABCC11, Accession NP_149163.2) is another GAM189 target gene, herein designated TARGET GENE. ABCC11 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded

by ABCC11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCC11 BINDING SITE, designated SEQ ID:7022, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28022] Another function of GAM189 is therefore inhibition of Atp-binding cassette, sub-family c (cftr/mrp), member 11 (ABCC11, Accession NP_149163.2), a gene which acts as a multispecific organic anion pump which can transport nucleotide analogs (by similarity). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC11.

[28023] The function of ABCC11 has been established by previous studies. Tammur et al. (2001) identified ABCC11 and ABCC12 (OMIM Ref. No. 607041) by database analysis using ABC transporter sequences as queries. The deduced 1,382- amino acid ABCC11 protein contains 2 ATP- binding domains and 2 transmembrane regions. It shares 40%, 33%, 32%, and 32% amino acid sequence identity with ABCC5 (OMIM Ref. No. 605251), ABCC4 (OMIM Ref. No. 605250), ABCC2 (OMIM Ref. No. 601107), and ABCC3 (OMIM Ref. No. 604323), respectively. PCR of a 16- tissue

panel revealed expression in all tissues examined except kidney, spleen, and colon. The author determined that a second PCR product identified in lung was a splice variant lacking exon 9. Tammur et al. (2001) mapped the ABCC11 gene to chromosome 16q12.1 by radiation hybrid analysis. They noted that the ABCC11 and ABCC12 genes are contained within a BAC clone mapping to 16q12.1. Tammur et al. (2001) stated that the chromosomal localization, potential function, and expression profiles of the ABCC11 and ABCC12 genes make them promising candidates for paroxysmal kinesigenic choreoathetosis (PKC; 128200) and infantile convulsions with paroxysmal choreoathetosis (ICCA; 602066).

[28024]

[28025] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28026] Tammur, J.; Prades, C.; Arnould, I.; Rzhetsky, A.; Hutchinson, A.; Adachi, M.; Schuetz, J. D.; Swoboda, K. J.; Ptacek, L. J.; Rosier, M.; Dean, M.; Allikmets, R. : Two new genes from the human ATP- binding cassette transporter superfamily, ABCC11 and ABCC12, tandemly duplicated on chromosome 16q12. Gene 273: 89- 96, 2001. ; and

[28027] Bera, T. K.; Lee, S.; Salvatore, G.; Lee, B.; Pastan, I. : MRP8, a new member of ABC transporter superfamily, identified by EST database mining and gene prediction program, is highly ex.

[28028] Further studies establishing the function and utilities of ABCC11 are found in John Hopkins OMIM database record ID 607040, and in cited publications listed in Table 5, which are hereby incorporated by reference.Atp-binding cassette, sub-family d (ald), member 3 (ABCD3, Accession NP_002849.1) is another GAM189 target gene, herein designated TARGET GENE. ABCD3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCD3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCD3 BINDING SITE, designated SEQ ID:14444, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28029] Another function of GAM189 is therefore inhibition of Atp-binding cassette, sub-family d (ald), member 3 (ABCD3, Accession NP_002849.1), a gene which a proba-ble transporter. and therefore is associated with Zellweger

syndrome- 2 (zws- 2). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Zellweger syndrome- 2 (zws- 2)., and of other diseases and clinical conditions associated with ABCD3.

[28030] The function of ABCD3 has been established by previous studies. Peroxisomes are single, membrane- bound, spheroid organelles present in virtually all eukaryotic cells. The polypeptide composition of the peroxisomal membrane is distinct from that of other organelles and comprises 2 quantitatively major (22K and 70K) and several minor peroxisomal membrane proteins. The peroxisome matrix contains more than 40 enzymes which are involved in a variety of metabolic processes including peroxide- based respiration, synthesis of plasmalogen and bile acids, beta- oxidation of very long chain fatty acids, and glyoxylate transamination. Biogenesis of peroxisomes appears to proceed by import of newly synthesized proteins into existing peroxisomes which enlarge and divide. Most matrix enzymes use an SKL (ser- lys- leu) tripeptide at the C- terminus as a targeting sequence, and the import of at least one, acyl- CoA oxidase, is ATP- dependent. Peroxisomal membrane proteins (PMP), as well as the peroxisomal matrix enzymes, are synthesized on free

cytoplasmic polysomes at their mature size. Disorders with defective peroxisome biogenesis include Zellweger syndrome (ZWS1; 214100) and neonatal adrenoleukodystrophy (OMIM Ref. No. 202370). In these disorders, many peroxisomal matrix proteins are mislocated in the cytosol, whereas others, such as PMP70, PMP22 (OMIM Ref. No. 601097), and thiolase precursor, are associated with irregularly shaped vesicles which may be defective peroxisomes or peroxisome precursors. These observations led to the hypothesis that the peroxisome biogenesis defects are due to defective import mechanisms for peroxisomal matrix enzymes. Somatic cell fusion studies indicated the existence of at least 11 complementation groups for ZS and related phenotypes (Moser et al., 1995). PMP70 was mapped to chromosome 1 by analysis of somatic cell hybrid DNAs (Gartner et al., 1992) and regionalized to 1p22- p21 by fluorescence in situ hybridization (1,2:Gartner et al., 1992, 1993). The gene encoding the mouse homolog of PMP70 (Pmp1) was located on chromosome 3 by interspecific backcross analysis.

[28031]

[28032] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[28033] Moser, A. B.; Rasmussen, M.; Naidu, S.; Watkins, P. A.; McGuinness, M.; Hajra, A. K.; Chen, G.; Raymond, G.; Liu, A.; Gordon, D.; Garnaas, K.; Walton, D. S.; Skjedal, O. H.; Guggenheim, M. A.; Jackson, L. G.; Elias, E. R.; Moser, H. W. : Phenotype of patients with peroxisomal disorders subdivided into sixteen complementation groups. J. Pe- diat. 127: 13- 22, 1995. ; and

[28034] Gartner, J.; Kearns, W.; Pearson, P.; Valle, D. : Characteri- zation and localization of the human 70- kD peroxisomal membrane protein (PMP70) gene. (Abstract) Am. J. Hum. Genet. 51 (suppl.

[28035] Further studies establishing the function and utilities of ABCD3 are found in John Hopkins OMIM database record ID 170995, and in cited publications listed in Table 5, which are hereby incorporated by refer- ence.Acyl-coenzyme a dehydrogenase, short/branched chain (ACADSB, Accession NP_001600.1) is another GAM189 target gene, herein designated TARGET GENE. ACADSB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACADSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of ACADSB BINDING SITE, designated SEQ ID:16689, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28036] Another function of GAM189 is therefore inhibition of Acyl-coenzyme a dehydrogenase, short/branched chain (ACADSB, Accession NP_001600.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACADSB.

[28037] Acid phosphatase 5, tartrate resistant (ACP5, Accession NP_001602.1) is another GAM189 target gene, herein designated TARGET GENE. ACP5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACP5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACP5 BINDING SITE, designated SEQ ID:6638, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28038] Another function of GAM189 is therefore inhibition of Acid phosphatase 5, tartrate resistant (ACP5, Accession NP_001602.1) . Accordingly, utilities of GAM189 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with ACP5.

[28039] A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4 (ADAMTS4, Accession NP_005090.1) is another GAM189 target gene, herein designated TARGET GENE. ADAMTS4 BINDING SITE1 and ADAMTS4 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ADAMTS4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAMTS4 BINDING SITE1 and ADAMTS4 BINDING SITE2, designated SEQ ID:1651 and SEQ ID:13757 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28040] Another function of GAM189 is therefore inhibition of A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4 (ADAMTS4, Accession NP_005090.1), a gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAMTS4.

[28041] The function of ADAMTS4 has been established by previous studies. Aggrecan degradation is an important factor in the erosion of articular cartilage in arthritic diseases. This degradation involves proteolysis of the aggrecan core protein near the N terminus, where 2 major cleavage sites have been identified. Matrix metalloproteinases (MMPs) cleave aggrecan between asn341 and phe342. Aggrecanase cleaves aggrecan between glu373 and ala374. Tortorella et al. (1999) purified and partially sequenced bovine aggrecanase- 1. By PCR with primers designed from a highly homologous murine EST, they cloned sequences from the homologous human cDNA. They assembled a full- length open reading frame from this initial human PCR product and from another human EST. The human aggrecanase- 1 (ADAMTS4) open reading frame encodes an 837- amino acid protein with a signal sequence, a propeptide domain, a catalytic domain, a disintegrin- like domain, and a C- terminal domain with a thrombospondin (TSP) type 1 motif. There is a conserved zinc- binding domain and a furin- sensitive sequence. The presence of a probable cysteine switch sequence in aggrecanase- 1 suggested that, like the MMPs, it is synthesized as a zymogen and is cleaved to remove the

propeptide domain and generate the mature active enzyme. A cloned portion of the bovine aggrecanase- 1 cDNA was 94% homologous to the human cDNA. Human aggrecanase- 1 cleaved bovine aggrecan between the glu373- ala374, but not the asn341- phe342, bond. Tortorella et al. (1999) stated that ADAMTS4 mRNA is present in brain, lung, and heart, and at very low levels in placenta and muscle tissues. By RT- PCR, Tortorella et al. (1999) observed upregulation of the aggrecanase- 1 message in stimulated human fetal chondrocytes and in joint tissues from adjuvant arthritic rats. Using a GeneBridge 4 radiation hybrid panel, Ishikawa et al. (1998) mapped the ADAMTS4 gene to chromosome 1. Hurskainen et al. (1999) mapped the human ADAMTS4 gene to chromosome 1 by somatic cell hybrid analysis. They mapped the mouse Adamts4 gene to chromosome 1.

[28042]

[28043] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28044] Tortorella, M. D.; Burn, T. C.; Pratta, M. A.; Abbaszade, I.; Hollis, J. M.; Liu, R.; Rosenfeld, S. A.; Copeland, R. A.; Decicco, C. P.; Wynn, R.; Rockwell, A.; Yang, F.; and 16 oth-

ers : Purification and cloning of aggrecanase- 1: a member of the ADAMTS family of proteins. Science 284: 1664-1666, 1999. ; and

[28045] Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S. : ADAM- TS5, ADAM- TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases: general features and genomic dist.

[28046] Further studies establishing the function and utilities of ADAMTS4 are found in John Hopkins OMIM database record ID 603876, and in cited publications listed in Table 5, which are hereby incorporated by reference.Adenylate cyclase 6 (ADCY6, Accession NP_066193.1) is another GAM189 target gene, herein designated TARGET GENE. ADCY6 BINDING SITE1 and ADCY6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ADCY6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY6 BINDING SITE1 and ADCY6 BINDING SITE2, designated SEQ ID:15161 and SEQ ID:16688 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28047] Another function of GAM189 is therefore inhibition of Adenylate cyclase 6 (ADCY6, Accession NP_066193.1), a gene which this a membrane- bound, ca(2+)- inhibitable adenylyl cyclase (by similarity). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY6.

[28048] The function of ADCY6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.2.Adenylate cyclase 6 (ADCY6, Accession NP_056085.1) is another GAM189 target gene, herein designated TARGET GENE. ADCY6 BINDING SITE1 and ADCY6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ADCY6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY6 BINDING SITE1 and ADCY6 BINDING SITE2, designated SEQ ID:15161 and SEQ ID:19456 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28049] Another function of GAM189 is therefore inhibition of

Adenylate cyclase 6 (ADCY6, Accession NP_056085.1), a gene which this a membrane- bound, ca(2+)- inhibitable adenylyl cyclase (by similarity). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY6.

[28050] The function of ADCY6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.2.Agmatine ureohydrolase (agmatinase) (AGMAT, Accession NP_079034.2) is another GAM189 target gene, herein designated TARGET GENE. AGMAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AGMAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGMAT BINDING SITE, designated SEQ ID:9193, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28051] Another function of GAM189 is therefore inhibition of Agmatine ureohydrolase (agmatinase) (AGMAT, Accession NP_079034.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with AGMAT.

[28052] Aryl hydrocarbon receptor (AHR, Accession NP_001612.1) is another GAM189 target gene, herein designated TARGET GENE. AHR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AHR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AHR BINDING SITE, designated SEQ ID:8217, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28053] Another function of GAM189 is therefore inhibition of Aryl hydrocarbon receptor (AHR, Accession NP_001612.1), a gene which plays a role in modulating carcinogenesis through the induction of xenobiotic- metabolizing enzymes and therefore may be associated with Stomach tumors. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Stomach tumors, and of other diseases and clinical conditions associated with AHR.

[28054] The function of AHR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Absent in melanoma 1 (AIM1, Accession

XP_166300.1) is another GAM189 target gene, herein designated TARGET GENE. AIM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AIM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AIM1 BINDING SITE, designated SEQ ID:16864, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28055] Another function of GAM189 is therefore inhibition of Absent in melanoma 1 (AIM1, Accession XP_166300.1), a gene which is altered in association with tumor suppression in a model of human melanoma and therefore may be associated with Malignant melanoma. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Malignant melanoma, and of other diseases and clinical conditions associated with AIM1.

[28056] The function of AIM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Aldo-keto reductase family 1, member d1 (delta 4-3-ketosteroid-5-beta-reductase) (AKR1D1, Ac-

cession NP_005980.1) is another GAM189 target gene, herein designated TARGET GENE. AKR1D1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AKR1D1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKR1D1 BINDING SITE, designated SEQ ID:8063, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28057] Another function of GAM189 is therefore inhibition of Aldo-keto reductase family 1, member d1 (delta 4-3-ketosteroid-5-beta-reductase) (AKR1D1, Accession NP_005980.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKR1D1.

[28058] Aldehyde dehydrogenase 1 family, member b1 (ALDH1B1, Accession NP_000683.3) is another GAM189 target gene, herein designated TARGET GENE. ALDH1B1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALDH1B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of ALDH1B1 BINDING SITE, designated SEQ ID:2153, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28059] Another function of GAM189 is therefore inhibition of Aldehyde dehydrogenase 1 family, member b1 (ALDH1B1, Accession NP_000683.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH1B1.

[28060] Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1) is another GAM189 target gene, herein designated TARGET GENE. ALOX15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALOX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALOX15 BINDING SITE, designated SEQ ID:19939, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28061] Another function of GAM189 is therefore inhibition of Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1), a gene which converts arachidonic acid to

15s- hydroperoxyeicosatetraenoic acid. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALOX15.

[28062] The function of ALOX15 has been established by previous studies. Yoshimoto et al. (1990) found that the amino acid sequence of human reticulocyte 15- lipoxygenase (Sigal et al., 1988) showed 86% identity with that of porcine leukocyte 12- lipoxygenase (OMIM Ref. No. 152391). Sigal et al. (1988) found 61% sequence similarity between 15-lipoxygenase and 5- lipoxygenase (OMIM Ref. No. 152390). This suggests that in the human 12- lipoxygenase is more closely related evolutionarily to 15- lipoxygenase than to 5- lipoxygenase, even though the comparisons are made between human and porcine enzymes. By PCR analysis of a human- hamster somatic hybrid DNA panel, Funk et al. (1992) demonstrated that genes for 12-lipoxygenase and 15- lipoxygenase are located on human chromosome 17, whereas the most unrelated lipoxygenase (5- lipoxygenase) was mapped to chromosome 10. Kelavkar and Badr (1999) stated that the ALOX15 gene maps to 17p13.3 in close proximity to the tumor- suppressor gene TP53 (OMIM Ref. No. 191170). The ALOX15

gene product is implicated in antiinflammation, membrane remodeling, and cancer development/metastasis. Kelavkar and Badr (1999) described experiments yielding data that supported the hypothesis that loss of the TP53 gene, or gain- of- function activities resulting from the expression of its mutant forms, regulates ALOX15 promoter activity in human and in mouse, albeit in directionally opposite manners. These studies defined a direct link between ALOX15 gene activity and an established tumor-suppressor gene located in close chromosomal proximity. Kelavkar and Badr (1999) referred to this as evidence that 15- lipoxygenase is a mutator gene.

[28063]

[28064] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28065] Kelavkar, U. P.; Badr, K. F. : Effects of mutant p53 expression on human 15- lipoxygenase- promoter activity and murine 12/15- lipoxygenase gene expression: evidence that 15- lipoxygenase is a mutator gene. Proc. Nat. Acad. Sci. 96: 4378- 4383, 1999. ; and

[28066] Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.; Tanabe, T. : Cloning and sequence analysis

of the cDNA for arachidonate 12- lipoxygenase of porcine leukocytes. Proc. Na.

[28067] Further studies establishing the function and utilities of ALOX15 are found in John Hopkins OMIM database record ID 152392, and in cited publications listed in Table 5, which are hereby incorporated by reference.AMID (Accession NP_116186.1) is another GAM189 target gene, herein designated TARGET GENE. AMID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AMID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMID BINDING SITE, designated SEQ ID:5895, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28068] Another function of GAM189 is therefore inhibition of AMID (Accession NP_116186.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMID.

[28069] Ankyrin repeat domain 6 (ANKRD6, Accession NP_055757.1) is another GAM189 target gene, herein designated TARGET GENE. ANKRD6 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by ANKRD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANKRD6 BINDING SITE, designated SEQ ID:1746, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28070] Another function of GAM189 is therefore inhibition of Ankyrin repeat domain 6 (ANKRD6, Accession NP_055757.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKRD6.

[28071] Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) is another GAM189 target gene, herein designated TARGET GENE. AP3S2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AP3S2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP3S2 BINDING SITE, designated SEQ ID:19874, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA,

also designated SEQ ID:246.

[28072] Another function of GAM189 is therefore inhibition of Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3S2.

[28073] Apoptotic protease activating factor (APAF1, Accession NP_001151.1) is another GAM189 target gene, herein designated TARGET GENE. APAF1 BINDING SITE1 and APAF1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APAF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE1 and APAF1 BINDING SITE2, designated SEQ ID:16578 and SEQ ID:19360 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28074] Another function of GAM189 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_001151.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent

activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[28075] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apoptotic protease activating factor (APAF1, Accession NP_037361.1) is another GAM189 target gene, herein designated TARGET GENE. APAF1 BINDING SITE1 and APAF1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APAF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE1 and APAF1 BINDING SITE2, designated SEQ ID:19360 and SEQ ID:16578 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28076] Another function of GAM189 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_037361.1), a gene which functions in the mitochon-

drial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[28077] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.APM1 (Accession NP_004788.1) is another GAM189 target gene, herein designated TARGET GENE. APM1 BINDING SITE1 and APM1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APM1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APM1 BINDING SITE1 and APM1 BINDING SITE2, designated SEQ ID:20035 and SEQ ID:5598 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28078] Another function of GAM189 is therefore inhibition of APM1 (Accession NP_004788.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1.

[28079] Apolipoprotein b mrna editing enzyme, catalytic polypeptide-like 3f (APOBEC3F, Accession NP_660341.2) is another GAM189 target gene, herein designated TARGET GENE. APOBEC3F BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APOBEC3F, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOBEC3F BINDING SITE, designated SEQ ID:5622, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28080] Another function of GAM189 is therefore inhibition of Apolipoprotein b mrna editing enzyme, catalytic polypeptide-like 3f (APOBEC3F, Accession NP_660341.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOBEC3F.

[28081] Apolipoprotein l, 1 (APOL1, Accession NP_663318.1) is another GAM189 target gene, herein designated TARGET GENE. APOL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL1 BINDING SITE, designated SEQ ID:9574, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28082] Another function of GAM189 is therefore inhibition of Apolipoprotein l, 1 (APOL1, Accession NP_663318.1), a gene which may participate in reverse cholesterol transport from peripheral cells to the liver. and therefore may be associated with Schizophrenia. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Schizophrenia, and of other diseases and clinical conditions associated with APOL1.

[28083] The function of APOL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apolipoprotein l, 1 (APOL1, Accession NP_003652.2) is another GAM189 target gene, herein designated TARGET GENE. APOL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates

the complementarity of the nucleotide sequences of APOL1 BINDING SITE, designated SEQ ID:9574, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28084] Another function of GAM189 is therefore inhibition of Apolipoprotein l, 1 (APOL1, Accession NP_003652.2), a gene which may participate in reverse cholesterol transport from peripheral cells to the liver. and therefore may be associated with Schizophrenia. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Schizophrenia, and of other diseases and clinical conditions associated with APOL1.

[28085] The function of APOL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apolipoprotein l, 2 (APOL2, Accession NP_663612.1) is another GAM189 target gene, herein designated TARGET GENE. APOL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

APOL2 BINDING SITE, designated SEQ ID:8064, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28086] Another function of GAM189 is therefore inhibition of Apolipoprotein l, 2 (APOL2, Accession NP_663612.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL2.

[28087] Apolipoprotein l, 2 (APOL2, Accession NP_112092.1) is another GAM189 target gene, herein designated TARGET GENE. APOL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL2 BINDING SITE, designated SEQ ID:8064, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28088] Another function of GAM189 is therefore inhibition of Apolipoprotein l, 2 (APOL2, Accession NP_112092.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with APOL2.

[28089] Amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2, Accession NP_006371.2) is another GAM189 target gene, herein designated TARGET GENE. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APPBP2 BINDING SITE, designated SEQ ID:4095, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28090] Another function of GAM189 is therefore inhibition of Amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2, Accession NP_006371.2), a gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore may be associated with Alzheimer's disease. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alzheimer's disease, and of other diseases and clinical conditions associated with APPBP2.

[28091] The function of APPBP2 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM130.1.APPL (Accession NP_036228.1) is another GAM189 target gene, herein designated TARGET GENE. APPL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APPL BINDING SITE, designated SEQ ID:12068, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28092] Another function of GAM189 is therefore inhibition of APPL (Accession NP_036228.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APPL.

[28093] Aquaporin 2 (collecting duct) (AQP2, Accession NP_000477.1) is another GAM189 target gene, herein designated TARGET GENE. AQP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AQP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP2 BINDING SITE, designated

SEQ ID:18318, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28094] Another function of GAM189 is therefore inhibition of Aquaporin 2 (collecting duct) (AQP2, Accession NP_000477.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP2.

[28095] Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1) is another GAM189 target gene, herein designated TARGET GENE. AQP6 BINDING SITE1 through AQP6 BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by AQP6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE1 through AQP6 BINDING SITE3, designated SEQ ID:3169, SEQ ID:3169 and SEQ ID:7869 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28096] Another function of GAM189 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession

NP_445738.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[28097] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1) is another GAM189 target gene, herein designated TARGET GENE. AQP6 BINDING SITE1 through AQP6 BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by AQP6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE1 through AQP6 BINDING SITE3, designated SEQ ID:8069, SEQ ID:13747 and SEQ ID:6901 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28098] Another function of GAM189 is therefore inhibition of

Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[28099] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) is another GAM189 target gene, herein designated TARGET GENE. ARHGAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP1 BINDING SITE, designated SEQ ID:4096, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28100] Another function of GAM189 is therefore inhibition of Rho gtpase activating protein 1 (ARHGAP1, Accession

NP_004299.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP1.

[28101] ARHGAP11A (Accession NP_055598.1) is another GAM189 target gene, herein designated TARGET GENE. ARHGAP11A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGAP11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP11A BINDING SITE, designated SEQ ID:17742, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28102] Another function of GAM189 is therefore inhibition of ARHGAP11A (Accession NP_055598.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP11A.

[28103] ARK5 (Accession NP_055655.1) is another GAM189 target gene, herein designated TARGET GENE. ARK5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARK5, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARK5 BINDING SITE, designated SEQ ID:17859, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28104] Another function of GAM189 is therefore inhibition of ARK5 (Accession NP_055655.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARK5.

[28105] ARPP-19 (Accession NP_006619.1) is another GAM189 target gene, herein designated TARGET GENE. ARPP-19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARPP-19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARPP-19 BINDING SITE, designated SEQ ID:944, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28106] Another function of GAM189 is therefore inhibition of ARPP-19 (Accession NP_006619.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with ARPP-19.

[28107] Ankyrin repeat and socs box-containing 16 (ASB16, Accession NP_543139.4) is another GAM189 target gene, herein designated TARGET GENE. ASB16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASB16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB16 BINDING SITE, designated SEQ ID:14722, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28108] Another function of GAM189 is therefore inhibition of Ankyrin repeat and socs box-containing 16 (ASB16, Accession NP_543139.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB16.

[28109] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) is another GAM189 target gene, herein designated TARGET GENE. ASB6 BINDING SITE1 and ASB6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by

ASB6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE1 and ASB6 BINDING SITE2, designated SEQ ID:2196 and SEQ ID:10305 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28110] Another function of GAM189 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[28111] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) is another GAM189 target gene, herein designated TARGET GENE. ASB6 BINDING SITE1 and ASB6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ASB6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE1 and ASB6 BINDING SITE2, designated SEQ ID:10305 and SEQ ID:2196 respectively, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[28112] Another function of GAM189 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[28113] ASE-1 (Accession NP_036231.1) is another GAM189 target gene, herein designated TARGET GENE. ASE-1 BINDING SITE1 and ASE-1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ASE-1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASE-1 BINDING SITE1 and ASE-1 BINDING SITE2, designated SEQ ID:1741 and SEQ ID:3101 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28114] Another function of GAM189 is therefore inhibition of ASE-1 (Accession NP_036231.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASE-1.

[28115] ATF7IP2 (Accession NP_079273.1) is another GAM189 target gene, herein designated TARGET GENE. ATF7IP2 BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATF7IP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATF7IP2 BINDING SITE, designated SEQ ID:9602, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28116] Another function of GAM189 is therefore inhibition of ATF7IP2 (Accession NP_079273.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATF7IP2.

[28117] Ataxia telangiectasia mutated (includes complementation groups a, c and d) (ATM, Accession NP_612150.1) is another GAM189 target gene, herein designated TARGET GENE. ATM BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ATM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATM BINDING SITE, designated SEQ ID:1837, to the nucleotide sequence of

GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28118] Another function of GAM189 is therefore inhibition of Ataxia telangiectasia mutated (includes complementation groups a, c and d) (ATM, Accession NP_612150.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATM.

[28119] Atpase, na+/k+ transporting, beta 2 polypeptide (ATP1B2, Accession NP_001669.1) is another GAM189 target gene, herein designated TARGET GENE. ATP1B2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP1B2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP1B2 BINDING SITE, designated SEQ ID:16916, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28120] Another function of GAM189 is therefore inhibition of Atpase, na+/k+ transporting, beta 2 polypeptide (ATP1B2, Accession NP_001669.1), a gene which catalyzes the hydrolysis of ATP coupled with the exchange of Na +/K+

ions across the plasma membrane. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B2.

[28121] The function of ATP1B2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Atpase, (na+)/k+ transporting, beta 4 polypeptide (ATP1B4, Accession NP_036201.1) is another GAM189 target gene, herein designated TARGET GENE. ATP1B4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP1B4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP1B4 BINDING SITE, designated SEQ ID:13042, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28122] Another function of GAM189 is therefore inhibition of Atpase, (na+)/k+ transporting, beta 4 polypeptide (ATP1B4, Accession NP_036201.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B4.

[28123] Atpase, h+ transporting, lysosomal 38kda, v0 subunit d

isoform 2 (ATP6V0D2, Accession NP_689778.1) is another GAM189 target gene, herein designated TARGET GENE. ATP6V0D2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP6V0D2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP6V0D2 BINDING SITE, designated SEQ ID:15039, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28124] Another function of GAM189 is therefore inhibition of Atpase, h+ transporting, lysosomal 38kda, v0 subunit d isoform 2 (ATP6V0D2, Accession NP_689778.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V0D2.

[28125] ATP6V1A (Accession NP_001681.2) is another GAM189 target gene, herein designated TARGET GENE. ATP6V1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP6V1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of ATP6V1A BINDING SITE, designated SEQ ID:18868, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28126] Another function of GAM189 is therefore inhibition of ATP6V1A (Accession NP_001681.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V1A.

[28127] Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) is another GAM189 target gene, herein designated TARGET GENE. ATP7A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:4112, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28128] Another function of GAM189 is therefore inhibition of Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) . Accordingly,

utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A.

[28129] Atpase, class i, type 8b, member 2 (ATP8B2, Accession XP_290875.1) is another GAM189 target gene, herein designated TARGET GENE. ATP8B2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP8B2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP8B2 BINDING SITE, designated SEQ ID:8634, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28130] Another function of GAM189 is therefore inhibition of Atpase, class i, type 8b, member 2 (ATP8B2, Accession XP_290875.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8B2.

[28131] Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) is another GAM189 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:11802, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28132] Another function of GAM189 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[28133] Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) is another GAM189 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:11802, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28134] Another function of GAM189 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[28135] Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 4 (B4GALT4, Accession NP_003769.1) is another GAM189 target gene, herein designated TARGET GENE. B4GALT4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B4GALT4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B4GALT4 BINDING SITE, designated SEQ ID:11028, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28136] Another function of GAM189 is therefore inhibition of Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 4 (B4GALT4, Accession NP_003769.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT4.

[28137] Xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase i) (B4GALT7, Accession NP_009186.1) is another GAM189 target gene, herein designated TARGET GENE. B4GALT7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B4GALT7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B4GALT7 BINDING SITE, designated SEQ ID:18475, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28138] Another function of GAM189 is therefore inhibition of Xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase i) (B4GALT7, Accession NP_009186.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT7.

[28139] BA108L7.2 (Accession NP_112233.2) is another GAM189 target gene, herein designated TARGET GENE. BA108L7.2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BA108L7.2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BA108L7.2 BINDING SITE, designated SEQ ID:10888, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28140] Another function of GAM189 is therefore inhibition of BA108L7.2 (Accession NP_112233.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BA108L7.2.

[28141] Beta-site app-cleaving enzyme 2 (BACE2, Accession NP_036237.2) is another GAM189 target gene, herein designated TARGET GENE. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE2 BINDING SITE, designated SEQ ID:11052, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28142] Another function of GAM189 is therefore inhibition of Beta-site app-cleaving enzyme 2 (BACE2, Accession

NP_036237.2), a gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore may be associated with Alzheimer's disease and down syndrome. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alzheimer's disease and down syndrome, and of other diseases and clinical conditions associated with BACE2.

[28143] The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Beta-site app-cleaving enzyme 2 (BACE2, Accession NP_620476.1) is another GAM189 target gene, herein designated TARGET GENE. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE2 BINDING SITE, designated SEQ ID:11052, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28144] Another function of GAM189 is therefore inhibition of Beta-site app-cleaving enzyme 2 (BACE2, Accession

NP_620476.1), a gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore may be associated with Alzheimer's disease and down syndrome. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alzheimer's disease and down syndrome, and of other diseases and clinical conditions associated with BACE2.

[28145] The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Beta-site app-cleaving enzyme 2 (BACE2, Accession NP_620477.1) is another GAM189 target gene, herein designated TARGET GENE. BACE2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE2 BINDING SITE, designated SEQ ID:11052, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28146] Another function of GAM189 is therefore inhibition of Beta-site app-cleaving enzyme 2 (BACE2, Accession

NP_620477.1), a gene which cleaves intracellularly the b-secretase site of amyloid precursor protein and therefore may be associated with Alzheimer's disease and down syndrome. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alzheimer's disease and down syndrome, and of other diseases and clinical conditions associated with BACE2.

[28147] The function of BACE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Bcl2-associated athanogene 5 (BAG5, Accession NP_004864.1) is another GAM189 target gene, herein designated TARGET GENE. BAG5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BAG5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAG5 BINDING SITE, designated SEQ ID:5695, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28148] Another function of GAM189 is therefore inhibition of Bcl2-associated athanogene 5 (BAG5, Accession

NP_004864.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAG5.

[28149] BART1 (Accession NP_036238.1) is another GAM189 target gene, herein designated TARGET GENE. BART1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BART1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BART1 BINDING SITE, designated SEQ ID:16830, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28150] Another function of GAM189 is therefore inhibition of BART1 (Accession NP_036238.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BART1.

[28151] Bromodomain adjacent to zinc finger domain, 2a (BAZ2A, Accession NP_038477.1) is another GAM189 target gene, herein designated TARGET GENE. BAZ2A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BAZ2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAZ2A BINDING SITE, designated SEQ ID:8852, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28152] Another function of GAM189 is therefore inhibition of Bromodomain adjacent to zinc finger domain, 2a (BAZ2A, Accession NP_038477.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAZ2A.

[28153] BCAP31 (Accession NP_005736.2) is another GAM189 target gene, herein designated TARGET GENE. BCAP31 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCAP31, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCAP31 BINDING SITE, designated SEQ ID:4861, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28154] Another function of GAM189 is therefore inhibition of BCAP31 (Accession NP_005736.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with BCAP31.

[28155] B-cell cll/lymphoma 10 (BCL10, Accession NP_003912.1) is another GAM189 target gene, herein designated TARGET GENE. BCL10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCL10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCL10 BINDING SITE, designated SEQ ID:19576, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28156] Another function of GAM189 is therefore inhibition of B-cell cll/lymphoma 10 (BCL10, Accession NP_003912.1), a gene which is a positive regulator of lymphocyte proliferation, NF- kappaB activator. and therefore may be associated with Malt lymphoma, follicular lymphoma. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Malt lymphoma, follicular lymphoma, and of other diseases and clinical conditions associated with BCL10.

[28157] The function of BCL10 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.B double prime 1, subunit of rna polymerase iii transcription initiation factor iiib (BDP1, Accession NP_060899.1) is another GAM189 target gene, herein designated TARGET GENE. BDP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BDP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BDP1 BINDING SITE, designated SEQ ID:19556, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28158] Another function of GAM189 is therefore inhibition of B double prime 1, subunit of rna polymerase iii transcription initiation factor iiib (BDP1, Accession NP_060899.1), a gene which activates RNA polymerase III transcription. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDP1.

[28159] The function of BDP1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM146.1.BENE (Accession NP_005425.1) is another GAM189 target gene, herein designated TARGET GENE. BENE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BENE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BENE BINDING SITE, designated SEQ ID:6009, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28160] Another function of GAM189 is therefore inhibition of BENE (Accession NP_005425.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BENE.

[28161] BHD (Accession NP_659434.2) is another GAM189 target gene, herein designated TARGET GENE. BHD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BHD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BHD BINDING SITE, designated SEQ ID:9036, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28162] Another function of GAM189 is therefore inhibition of BHD (Accession NP_659434.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BHD.

[28163] BMF (Accession NP_277038.1) is another GAM189 target gene, herein designated TARGET GENE. BMF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BMF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BMF BINDING SITE, designated SEQ ID:759, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28164] Another function of GAM189 is therefore inhibition of BMF (Accession NP_277038.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMF.

[28165] BNIP-S (Accession NP_612122.1) is another GAM189 target gene, herein designated TARGET GENE. BNIP-S BINDING SITE is a target binding site found in the 3` untrans-

lated region of multiple transcripts of mRNA encoded by BNIP-S, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BNIP-S BINDING SITE, designated SEQ ID:5845, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28166] Another function of GAM189 is therefore inhibition of BNIP-S (Accession NP_612122.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BNIP-S.

[28167] BRIP1 (Accession NP_114432.1) is another GAM189 target gene, herein designated TARGET GENE. BRIP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BRIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BRIP1 BINDING SITE, designated SEQ ID:13904, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28168] Another function of GAM189 is therefore inhibition of BRIP1 (Accession NP_114432.1) . Accordingly, utilities of

GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRIP1.

[28169] Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession NP_008979.2) is another GAM189 target gene, herein designated TARGET GENE. BTN3A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTN3A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTN3A1 BINDING SITE, designated SEQ ID:2067, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28170] Another function of GAM189 is therefore inhibition of Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession NP_008979.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN3A1.

[28171] BXDC1 (Accession XP_166303.1) is another GAM189 target gene, herein designated TARGET GENE. BXDC1 BINDING SITE1 and BXDC1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by BXDC1, corresponding to target binding sites such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BXDC1 BINDING SITE1 and BXDC1 BINDING SITE2, designated SEQ ID:4549 and SEQ ID:12129 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28172] Another function of GAM189 is therefore inhibition of BXDC1 (Accession XP_166303.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BXDC1.

[28173] Chromosome 11 open reading frame 17 (C11orf17, Accession NP_065693.2) is another GAM189 target gene, herein designated TARGET GENE. C11orf17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C11orf17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C11orf17 BINDING SITE, designated SEQ ID:11525, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28174] Another function of GAM189 is therefore inhibition of Chromosome 11 open reading frame 17 (C11orf17, Ac-

cession NP_065693.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf17.

[28175] Chromosome 13 open reading frame 1 (C13orf1, Accession NP_065189.1) is another GAM189 target gene, herein designated TARGET GENE. C13orf1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C13orf1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C13orf1 BINDING SITE, designated SEQ ID:5746, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28176] Another function of GAM189 is therefore inhibition of Chromosome 13 open reading frame 1 (C13orf1, Accession NP_065189.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C13orf1.

[28177] Chromosome 14 open reading frame 1 (C14orf1, Accession NP_009107.1) is another GAM189 target gene, herein designated TARGET GENE. C14orf1 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by C14orf1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf1 BINDING SITE, designated SEQ ID:12744, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28178] Another function of GAM189 is therefore inhibition of Chromosome 14 open reading frame 1 (C14orf1, Accession NP_009107.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf1.

[28179] C14orf113 (Accession NP_060100.1) is another GAM189 target gene, herein designated TARGET GENE. C14orf113 BINDING SITE1 and C14orf113 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C14orf113, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf113 BINDING SITE1 and C14orf113 BINDING SITE2, designated SEQ ID:18863 and SEQ ID:5052 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:246.

[28180] Another function of GAM189 is therefore inhibition of C14orf113 (Accession NP_060100.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf113.

[28181] C14orf143 (Accession NP_660274.1) is another GAM189 target gene, herein designated TARGET GENE. C14orf143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf143 BINDING SITE, designated SEQ ID:17955, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28182] Another function of GAM189 is therefore inhibition of C14orf143 (Accession NP_660274.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf143.

[28183] C14orf92 (Accession NP_055643.1) is another GAM189 target gene, herein designated TARGET GENE. C14orf92

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf92, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf92 BINDING SITE, designated SEQ ID:14861, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28184] Another function of GAM189 is therefore inhibition of C14orf92 (Accession NP_055643.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf92.

[28185] Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) is another GAM189 target gene, herein designated TARGET GENE. C1orf24 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C1orf24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:19538, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[28186] Another function of GAM189 is therefore inhibition of Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24.

[28187] C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) is another GAM189 target gene, herein designated TARGET GENE. C1QTNF6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1QTNF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1QTNF6 BINDING SITE, designated SEQ ID:14882, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28188] Another function of GAM189 is therefore inhibition of C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QTNF6.

[28189] Chromosome 20 open reading frame 147 (C20orf147, Ac-

cession NP_689880.1) is another GAM189 target gene, herein designated TARGET GENE. C20orf147 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf147, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf147 BINDING SITE, designated SEQ ID:16257, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28190] Another function of GAM189 is therefore inhibition of Chromosome 20 open reading frame 147 (C20orf147, Accession NP_689880.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf147.

[28191] Chromosome 21 open reading frame 67 (C21orf67, Accession NP_478068.1) is another GAM189 target gene, herein designated TARGET GENE. C21orf67 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C21orf67, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C21orf67

BINDING SITE, designated SEQ ID:6569, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28192] Another function of GAM189 is therefore inhibition of Chromosome 21 open reading frame 67 (C21orf67, Accession NP_478068.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf67.

[28193] Chromosome 22 open reading frame 19 (C22orf19, Accession NP_003669.2) is another GAM189 target gene, herein designated TARGET GENE. C22orf19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C22orf19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C22orf19 BINDING SITE, designated SEQ ID:18897, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28194] Another function of GAM189 is therefore inhibition of Chromosome 22 open reading frame 19 (C22orf19, Accession NP_003669.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with C22orf19.

[28195] C4orf9 (Accession XP_035572.1) is another GAM189 target gene, herein designated TARGET GENE. C4orf9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C4orf9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C4orf9 BINDING SITE, designated SEQ ID:15574, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28196] Another function of GAM189 is therefore inhibition of C4orf9 (Accession XP_035572.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C4orf9.

[28197] Chromosome 6 open reading frame 33 (C6orf33, Accession NP_588608.1) is another GAM189 target gene, herein designated TARGET GENE. C6orf33 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf33, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf33 BIND-

ING SITE, designated SEQ ID:6896, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28198] Another function of GAM189 is therefore inhibition of Chromosome 6 open reading frame 33 (C6orf33, Accession NP_588608.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf33.

[28199] C6orf5 (Accession NP_056339.2) is another GAM189 target gene, herein designated TARGET GENE. C6orf5 BINDING SITE1 and C6orf5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C6orf5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf5 BINDING SITE1 and C6orf5 BINDING SITE2, designated SEQ ID:10099 and SEQ ID:12805 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28200] Another function of GAM189 is therefore inhibition of C6orf5 (Accession NP_056339.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with C6orf5.

[28201] C6orf57 (Accession NP_660310.1) is another GAM189 target gene, herein designated TARGET GENE. C6orf57 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf57, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf57 BINDING SITE, designated SEQ ID:2114, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28202] Another function of GAM189 is therefore inhibition of C6orf57 (Accession NP_660310.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf57.

[28203] Complement component 7 (C7, Accession NP_000578.1) is another GAM189 target gene, herein designated TARGET GENE. C7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of C7 BINDING SITE, designated SEQ ID:17778, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28204] Another function of GAM189 is therefore inhibition of Complement component 7 (C7, Accession NP_000578.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C7.

[28205] Chromosome 9 open reading frame 5 (C9orf5, Accession NP_114401.1) is another GAM189 target gene, herein designated TARGET GENE. C9orf5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C9orf5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C9orf5 BINDING SITE, designated SEQ ID:14258, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28206] Another function of GAM189 is therefore inhibition of Chromosome 9 open reading frame 5 (C9orf5, Accession NP_114401.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with C9orf5.

[28207] Chromosome 9 open reading frame 9 (C9orf9, Accession NP_061829.2) is another GAM189 target gene, herein designated TARGET GENE. C9orf9 BINDING SITE1 and C9orf9 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C9orf9, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C9orf9 BINDING SITE1 and C9orf9 BINDING SITE2, designated SEQ ID:11520 and SEQ ID:5477 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28208] Another function of GAM189 is therefore inhibition of Chromosome 9 open reading frame 9 (C9orf9, Accession NP_061829.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf9.

[28209] CAB2 (Accession NP_219487.2) is another GAM189 target gene, herein designated TARGET GENE. CAB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAB2 BINDING SITE, designated SEQ ID:9181, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28210] Another function of GAM189 is therefore inhibition of CAB2 (Accession NP_219487.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAB2.

[28211] Calcium binding protein 4 (CABP4, Accession NP_660201.1) is another GAM189 target gene, herein designated TARGET GENE. CABP4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CABP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CABP4 BINDING SITE, designated SEQ ID:7624, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28212] Another function of GAM189 is therefore inhibition of Calcium binding protein 4 (CABP4, Accession NP_660201.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with CABP4.

[28213] Calneuron 1 (CALN1, Accession NP_113656.1) is another GAM189 target gene, herein designated TARGET GENE. CALN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CALN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CALN1 BINDING SITE, designated SEQ ID:17850, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28214] Another function of GAM189 is therefore inhibition of Calneuron 1 (CALN1, Accession NP_113656.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALN1.

[28215] Calcium modulating ligand (CAMLG, Accession NP_001736.1) is another GAM189 target gene, herein designated TARGET GENE. CAMLG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAMLG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of CAMLG BINDING SITE, designated SEQ ID:18944, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28216] Another function of GAM189 is therefore inhibition of Calcium modulating ligand (CAMLG, Accession NP_001736.1), a gene which is likely involved in the mobilization of calcium as a result of the tcr/cd3 complex interaction. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMLG.

[28217] The function of CAMLG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Calpain 6 (CAPN6, Accession NP_055104.2) is another GAM189 target gene, herein designated TARGET GENE. CAPN6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAPN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAPN6 BINDING SITE, designated SEQ ID:2208, to the nucleotide sequence of GAM189 RNA,

herein designated GAM RNA, also designated SEQ ID:246.

[28218] Another function of GAM189 is therefore inhibition of Calpain 6 (CAPN6, Accession NP_055104.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPN6.

[28219] CAPRI (Accession NP_008920.3) is another GAM189 target gene, herein designated TARGET GENE. CAPRI BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAPRI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAPRI BINDING SITE, designated SEQ ID:4271, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28220] Another function of GAM189 is therefore inhibition of CAPRI (Accession NP_008920.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPRI.

[28221] Caspase recruitment domain family, member 6 (CARD6, Accession NP_115976.2) is another GAM189 target gene, herein designated TARGET GENE. CARD6 BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by CARD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CARD6 BINDING SITE, designated SEQ ID:9036, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28222] Another function of GAM189 is therefore inhibition of Caspase recruitment domain family, member 6 (CARD6, Accession NP_115976.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD6.

[28223] Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_001215.1) is another GAM189 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE, designated

SEQ ID:16398, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28224] Another function of GAM189 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_001215.1), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[28225] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116765.1) is another GAM189 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of CASP2 BINDING SITE, designated SEQ ID:16398, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28226] Another function of GAM189 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116765.1), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[28227] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116764.1) is another GAM189 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE, designated SEQ ID:16398, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28228] Another function of GAM189 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116764.1), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[28229] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116766.1) is another GAM189 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE, designated SEQ ID:16398, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28230] Another function of GAM189 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116766.1), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[28231] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203520.1) is another GAM189 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28232] Another function of GAM189 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203520.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[28233] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203519.1) is another GAM189 target gene, herein designated TARGET GENE.

CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28234] Another function of GAM189 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203519.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[28235] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_001219.2) is another GAM189 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28236] Another function of GAM189 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_001219.2), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[28237] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203521.1) is another GAM189 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28238] Another function of GAM189 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203521.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM189 include diagnosis, prevention and

treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[28239] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.CASPR4 (Accession NP_620481.1) is another GAM189 target gene, herein designated TARGET GENE. CASPR4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASPR4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASPR4 BINDING SITE, designated SEQ ID:13634, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28240] Another function of GAM189 is therefore inhibition of CASPR4 (Accession NP_620481.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASPR4.

[28241] Core-binding factor, runt domain, alpha subunit 2;

translocated to, 2 (CBFA2T2, Accession NP_787060.1) is another GAM189 target gene, herein designated TARGET GENE. CBFA2T2 BINDING SITE1 and CBFA2T2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CBFA2T2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CBFA2T2 BINDING SITE1 and CBFA2T2 BINDING SITE2, designated SEQ ID:8572 and SEQ ID:8572 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28242] Another function of GAM189 is therefore inhibition of Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_787060.1), a gene which is a putative transcription factor. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T2.

[28243] The function of CBFA2T2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM55.1.Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_787060.1) is another GAM189 target gene, herein designated TARGET GENE. CBFA2T2 BINDING SITE1 and CBFA2T2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CBFA2T2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CBFA2T2 BINDING SITE1 and CBFA2T2 BINDING SITE2, designated SEQ ID:8242 and SEQ ID:9543 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28244] Another function of GAM189 is therefore inhibition of Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_787060.1), a gene which is a putative transcription factor. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T2.

[28245] The function of CBFA2T2 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM55.1.Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) is another GAM189 target gene, herein designated TARGET GENE. CCL22 BINDING SITE1 and CCL22 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CCL22, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL22 BINDING SITE1 and CCL22 BINDING SITE2, designated SEQ ID:15049 and SEQ ID:1679 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28246] Another function of GAM189 is therefore inhibition of Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL22.

[28247] Cyclin f (CCNF, Accession NP_001752.1) is another GAM189 target gene, herein designated TARGET GENE. CCNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCNF, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCNF BINDING SITE, designated SEQ ID:17624, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28248] Another function of GAM189 is therefore inhibition of Cyclin f (CCNF, Accession NP_001752.1), a gene which likely to be involved in the control of the cell cycle during s phase and g2. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNF.

[28249] The function of CCNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Ccr4 carbon catabolite repression 4-like (s. cerevisiae) (CCRN4L, Accession NP_036250.2) is another GAM189 target gene, herein designated TARGET GENE. CCRN4L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCRN4L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCRN4L BINDING SITE, designated SEQ

ID:4698, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28250] Another function of GAM189 is therefore inhibition of Ccr4 carbon catabolite repression 4-like (s. cerevisiae) (CCRN4L, Accession NP_036250.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCRN4L.

[28251] Cd209 antigen (CD209, Accession NP_066978.1) is another GAM189 target gene, herein designated TARGET GENE. CD209 BINDING SITE1 and CD209 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CD209, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD209 BINDING SITE1 and CD209 BINDING SITE2, designated SEQ ID:17051 and SEQ ID:4298 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28252] Another function of GAM189 is therefore inhibition of Cd209 antigen (CD209, Accession NP_066978.1), a gene which may play an important role in the CD4- indepen-

dent association of HIV with cells. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD209.

[28253] The function of CD209 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Cd24 antigen (small cell lung carcinoma cluster 4 antigen) (CD24, Accession NP_037362.1) is another GAM189 target gene, herein designated TARGET GENE. CD24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD24 BINDING SITE, designated SEQ ID:19572, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28254] Another function of GAM189 is therefore inhibition of Cd24 antigen (small cell lung carcinoma cluster 4 antigen) (CD24, Accession NP_037362.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD24.

[28255] Cd5 antigen (p56-62) (CD5, Accession NP_055022.1) is

another GAM189 target gene, herein designated TARGET GENE. CD5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CD5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD5 BINDING SITE, designated SEQ ID:1049, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28256] Another function of GAM189 is therefore inhibition of Cd5 antigen (p56-62) (CD5, Accession NP_055022.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD5.

[28257] Cd84 antigen (leukocyte antigen) (CD84, Accession NP_003865.1) is another GAM189 target gene, herein designated TARGET GENE. CD84 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD84, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD84 BINDING SITE, designated SEQ ID:514, to the nucleotide sequence of GAM189 RNA,

herein designated GAM RNA, also designated SEQ ID:246.

[28258] Another function of GAM189 is therefore inhibition of Cd84 antigen (leukocyte antigen) (CD84, Accession NP_003865.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD84.

[28259] Cdc14 cell division cycle 14 homolog b (s. cerevisiae) (CDC14B, Accession NP_201589.1) is another GAM189 target gene, herein designated TARGET GENE. CDC14B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDC14B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC14B BINDING SITE, designated SEQ ID:17127, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28260] Another function of GAM189 is therefore inhibition of Cdc14 cell division cycle 14 homolog b (s. cerevisiae) (CDC14B, Accession NP_201589.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

CDC14B.

[28261] Cell division cycle 2-like 2 (CDC2L2, Accession NP_296370.1) is another GAM189 target gene, herein designated TARGET GENE. CDC2L2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CDC2L2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC2L2 BINDING SITE, designated SEQ ID:15084, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28262] Another function of GAM189 is therefore inhibition of Cell division cycle 2-like 2 (CDC2L2, Accession NP_296370.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC2L2.

[28263] Cdc6 cell division cycle 6 homolog (s. cerevisiae) (CDC6, Accession NP_001245.1) is another GAM189 target gene, herein designated TARGET GENE. CDC6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDC6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC6 BINDING SITE, designated SEQ ID:9211, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28264] Another function of GAM189 is therefore inhibition of Cdc6 cell division cycle 6 homolog (s. cerevisiae) (CDC6, Accession NP_001245.1), a gene which is a component of the origin recognition complex (orc) that binds origins of replication. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC6.

[28265] The function of CDC6 has been established by previous studies. In yeasts, Cdc6 (Saccharomyces cerevisiae) and Cdc18 (Schizosaccharomyces pombe) associate with the origin recognition complex (ORC) proteins to render cells competent for DNA replication. Thus, Cdc6 has a critical regulatory role in the initiation of DNA replication in yeast. Williams et al. (1997) isolated cDNAs encoding Xenopus and human homologs of yeast CDC6. They designated the human and Xenopus proteins p62(cdc6). Independently, in a yeast 2- hybrid assay using PCNA (OMIM Ref. No. 176740) as bait, Saha et al. (1998) isolated cDNAs encod-

ing the human CDC6/Cdc18 homolog. These authors reported that the predicted 560- amino acid human protein shares approximately 33% sequence identity with the 2 yeast proteins. On Western blots of HeLa cell extracts, human CDC6/cdc18 migrates as a 66- kD protein. Although Northern blots indicated that CDC6/Cdc18 mRNA levels peak at the onset of S phase and diminish at the onset of mitosis in HeLa cells, the authors found that total CDC6/Cdc18 protein level is unchanged throughout the cell cycle. Immunofluorescent analysis of epitope- tagged protein revealed that human CDC6/Cdc18 is nuclear in G1- and cytoplasmic in S- phase cells, suggesting that DNA replication may be regulated by either the translocation of this protein between the nucleus and cytoplasm or by selective degradation of the protein in the nucleus. Immunoprecipitation studies showed that human CDC6/Cdc18 associates in vivo with cyclin A (OMIM Ref. No. 123835), CDK2 (OMIM Ref. No. 116953), and ORC1 (OMIM Ref. No. 601902). The association of cyclin- CDK2 with CDC6/Cdc18 was specifically inhibited by a factor present in mitotic cell extracts. Saha et al. (1998) suggested that if the interaction between CDC6/Cdc18 with the S phase- promoting factor cyclin- CDK2 is essential

for the initiation of DNA replication, the mitotic inhibitor of this interaction could prevent a premature interaction until the appropriate time in G1.

[28266]

[28267] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28268] Williams, R. S.; Shohet, R. V.; Stillman, B. : A human protein related to yeast Cdc6p. Proc. Nat. Acad. Sci. 94: 142-147, 1997. ; and

[28269] Saha, P.; Chen, J.; Thome, K. C.; Lawlis, S. J.; Hou, Z.- H.; Hendricks, M.; Parvin, J. D.; Dutta, A. : Human CDC6/Cdc18 associates with Orc1 and cyclin- cdk and is selectively eliminated.

[28270] Further studies establishing the function and utilities of CDC6 are found in John Hopkins OMIM database record ID 602627, and in cited publications listed in Table 5, which are hereby incorporated by reference.CDCP1 (Accession NP_073753.3) is another GAM189 target gene, herein designated TARGET GENE. CDCP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDCP1, corresponding to a target binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDCP1 BINDING SITE, designated SEQ ID:12091, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28271] Another function of GAM189 is therefore inhibition of CDCP1 (Accession NP_073753.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDCP1.

[28272] Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) is another GAM189 target gene, herein designated TARGET GENE. CDH1 BINDING SITE1 and CDH1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CDH1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH1 BINDING SITE1 and CDH1 BINDING SITE2, designated SEQ ID:12580 and SEQ ID:5514 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28273] Another function of GAM189 is therefore inhibition of Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Acces-

sion NP_004351.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH1.

[28274] Cadherin 17, li cadherin (liver-intestine) (CDH17, Accession NP_004054.2) is another GAM189 target gene, herein designated TARGET GENE. CDH17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDH17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH17 BINDING SITE, designated SEQ ID:13851, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28275] Another function of GAM189 is therefore inhibition of Cadherin 17, li cadherin (liver-intestine) (CDH17, Accession NP_004054.2), a gene which may have a role in the morphological organization of liver and intestine and involved in intestinal peptide transport. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH17.

[28276] The function of CDH17 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM161.1.CDK11 (Accession XP_166324.1) is another GAM189 target gene, herein designated TARGET GENE. CDK11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDK11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDK11 BINDING SITE, designated SEQ ID:8162, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28277] Another function of GAM189 is therefore inhibition of CDK11 (Accession XP_166324.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDK11.

[28278] CDKAL1 (Accession NP_060244.1) is another GAM189 target gene, herein designated TARGET GENE. CDKAL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDKAL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDKAL1 BINDING SITE, designated SEQ ID:1255, to the nucleotide

sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28279] Another function of GAM189 is therefore inhibition of CDKAL1 (Accession NP_060244.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKAL1.

[28280] Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) is another GAM189 target gene, herein designated TARGET GENE. CEACAM8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CEACAM8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CEACAM8 BINDING SITE, designated SEQ ID:17969, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28281] Another function of GAM189 is therefore inhibition of Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEACAM8.

[28282] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) is another GAM189 target gene, herein designated TARGET GENE. CECR1 BINDING SITE1 and CECR1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CECR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE1 and CECR1 BINDING SITE2, designated SEQ ID:4574 and SEQ ID:9037 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28283] Another function of GAM189 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[28284] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) is another GAM189 target gene, herein designated TARGET GENE. CECR1 BINDING SITE1 and CECR1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts

of mRNA encoded by CECR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE1 and CECR1 BINDING SITE2, designated SEQ ID:9037 and SEQ ID:4574 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28285] Another function of GAM189 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[28286] Centromere protein h (CENPH, Accession NP_075060.1) is another GAM189 target gene, herein designated TARGET GENE. CENPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CENPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENPH BINDING SITE, designated SEQ ID:19549, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ

ID:246.

[28287] Another function of GAM189 is therefore inhibition of Centromere protein h (CENPH, Accession NP_075060.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENPH.

[28288] Centromere protein j (CENPJ, Accession NP_060921.2) is another GAM189 target gene, herein designated TARGET GENE. CENPJ BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CENPJ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENPJ BINDING SITE, designated SEQ ID:13565, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28289] Another function of GAM189 is therefore inhibition of Centromere protein j (CENPJ, Accession NP_060921.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENPJ.

[28290] CGI-150 (Accession NP_057164.1) is another GAM189 target gene, herein designated TARGET GENE. CGI-150

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CGI-150, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-150 BINDING SITE, designated SEQ ID:2191, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28291] Another function of GAM189 is therefore inhibition of CGI-150 (Accession NP_057164.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-150.

[28292] CGI-18 (Accession NP_057031.1) is another GAM189 target gene, herein designated TARGET GENE. CGI-18 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CGI-18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-18 BINDING SITE, designated SEQ ID:18313, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28293] Another function of GAM189 is therefore inhibition of CGI-18 (Accession NP_057031.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-18.

[28294] CGI-43 (Accession NP_056437.1) is another GAM189 target gene, herein designated TARGET GENE. CGI-43 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CGI-43, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-43 BINDING SITE, designated SEQ ID:14860, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28295] Another function of GAM189 is therefore inhibition of CGI-43 (Accession NP_056437.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-43.

[28296] Chromosome condensation 1-like (CHC1L, Accession NP_001259.1) is another GAM189 target gene, herein designated TARGET GENE. CHC1L BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CHC1L, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHC1L BINDING SITE, designated SEQ ID:15582, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28297] Another function of GAM189 is therefore inhibition of Chromosome condensation 1-like (CHC1L, Accession NP_001259.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHC1L.

[28298] Chromatin accessibility complex 1 (CHRAC1, Accession NP_059140.1) is another GAM189 target gene, herein designated TARGET GENE. CHRAC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHRAC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHRAC1 BINDING SITE, designated SEQ ID:9475, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28299] Another function of GAM189 is therefore inhibition of

Chromatin accessibility complex 1 (CHRAC1, Accession NP_059140.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRAC1.

[28300] Carbohydrate (chondroitin) synthase 1 (CHSY1, Accession NP_055733.2) is another GAM189 target gene, herein designated TARGET GENE. CHSY1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHSY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHSY1 BINDING SITE, designated SEQ ID:11924, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28301] Another function of GAM189 is therefore inhibition of Carbohydrate (chondroitin) synthase 1 (CHSY1, Accession NP_055733.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHSY1.

[28302] Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2) is another GAM189 target gene, herein designated TARGET GENE. CIAS1 BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by CIAS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIAS1 BINDING SITE, designated SEQ ID:13461, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28303] Another function of GAM189 is therefore inhibition of Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2), a gene which may mediate protein- protein interactions; contains a leucine rich repeat and therefore may be associated with Familial cold autoinflammatory syndrome, muckle- wells syndrome. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Familial cold autoinflammatory syndrome, muckle- wells syndrome, and of other diseases and clinical conditions associated with CIAS1.

[28304] The function of CIAS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM90.1.CIP29 (Accession NP_115740.3) is another GAM189 target gene, herein designated TARGET GENE.

CIP29 BINDING SITE1 and CIP29 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CIP29, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIP29 BINDING SITE1 and CIP29 BINDING SITE2, designated SEQ ID:3509 and SEQ ID:20120 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28305] Another function of GAM189 is therefore inhibition of CIP29 (Accession NP_115740.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIP29.

[28306] Claudin 19 (CLDN19, Accession NP_683763.1) is another GAM189 target gene, herein designated TARGET GENE. CLDN19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLDN19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLDN19 BINDING SITE, designated SEQ ID:5914, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28307] Another function of GAM189 is therefore inhibition of Claudin 19 (CLDN19, Accession NP_683763.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLDN19.

[28308] C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2) is another GAM189 target gene, herein designated TARGET GENE. CLECSF12 BINDING SITE1 and CLECSF12 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CLECSF12, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLECSF12 BINDING SITE1 and CLECSF12 BINDING SITE2, designated SEQ ID:16192 and SEQ ID:15296 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28309] Another function of GAM189 is therefore inhibition of C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2), a gene which is a pattern- recognition receptor . Accordingly, utilities of GAM189 include diag-

nosis, prevention and treatment of diseases and clinical conditions associated with CLECSF12.

[28310] The function of CLECSF12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Chloride intracellular channel 5 (CLIC5, Accession NP_058625.1) is another GAM189 target gene, herein designated TARGET GENE. CLIC5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CLIC5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLIC5 BINDING SITE, designated SEQ ID:19116, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28311] Another function of GAM189 is therefore inhibition of Chloride intracellular channel 5 (CLIC5, Accession NP_058625.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLIC5.

[28312] Ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) (CLN8, Accession NP_061764.2)

is another GAM189 target gene, herein designated TARGET GENE. CLN8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLN8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLN8 BINDING SITE, designated SEQ ID:515, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28313] Another function of GAM189 is therefore inhibition of Ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) (CLN8, Accession NP_061764.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLN8.

[28314] Chloride channel, nucleotide-sensitive, 1a (CLNS1A, Accession NP_001284.1) is another GAM189 target gene, herein designated TARGET GENE. CLNS1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLNS1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLNS1A BINDING

SITE, designated SEQ ID:18823, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28315] Another function of GAM189 is therefore inhibition of Chloride channel, nucleotide-sensitive, 1a (CLNS1A, Accession NP_001284.1), a gene which may participate in cellular volume control . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLNS1A.

[28316] The function of CLNS1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Cell matrix adhesion regulator (CMAR, Accession NP_005191.2) is another GAM189 target gene, herein designated TARGET GENE. CMAR BINDING SITE1 and CMAR BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CMAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CMAR BINDING SITE1 and CMAR BINDING SITE2, designated SEQ ID:5053 and SEQ ID:18767 respectively, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[28317] Another function of GAM189 is therefore inhibition of Cell matrix adhesion regulator (CMAR, Accession NP_005191.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CMAR.

[28318] Calponin 2 (CNN2, Accession NP_004359.1) is another GAM189 target gene, herein designated TARGET GENE. CNN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNN2 BINDING SITE, designated SEQ ID:9959, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28319] Another function of GAM189 is therefore inhibition of Calponin 2 (CNN2, Accession NP_004359.1), a gene which may be involved in the structural organization and/or anchorage of actin filaments. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNN2.

[28320] The function of CNN2 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.2',3'-cyclic nucleotide 3' phosphodiesterase (CNP, Accession NP_149124.1) is another GAM189 target gene, herein designated TARGET GENE. CNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNP BINDING SITE, designated SEQ ID:606, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28321] Another function of GAM189 is therefore inhibition of 2',3'-cyclic nucleotide 3' phosphodiesterase (CNP, Accession NP_149124.1), a gene which can link tubulin to membranes and may regulate cytoplasmic microtubule distribution. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNP.

[28322] The function of CNP has been established by previous studies. Cyclic nucleotide phosphodiesterase is a useful marker of myelin. CNPase is a membrane- bound enzyme

found at high concentrations in central nervous system myelin and in the outer segments of photoreceptors in the retina (Vogel and Thompson, 1988). Two proteins with CNP activity are known to exist in brain and lymphoid tissues. They appear to be the products of distinct but related mRNA species. Kurihara et al. (1990) showed that the 2 gene products can arise by translation of 2 mRNAs alternatively spliced from a single transcript. In bovine and human brain, there appears to be a single species of mRNA (Vogel and Thompson, 1988), and the bovine brain and retinal forms of the enzyme appear to be identical in sequence Bifulco et al. (2002) demonstrated that CNP is firmly associated with tubulin (OMIM Ref. No. 602529) from brain tissue and thyroid cells. They showed that CNP acts as a microtubule- associated protein in promoting microtubule assembly. This activity was found to reside in the C terminus of the enzyme. The authors concluded that CNP is a membrane- bound microtubule- associated protein that can link tubulin to membranes and may regulate cytoplasmic microtubule distribution

[28323]

[28324] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[28325] Vogel, U. S.; Thompson, R. J. : Molecular structure, localization, and possible functions of the myelin- associated enzyme 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterase. J. Neurochem. 50: 1667- 1677, 1988. ; and

[28326] Bifulco, M.; Laezza, C.; Stingo, S.; Wolff, J. : 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterase: a membrane- bound, microtubule- associated protein and membrane anchor for tub.

[28327] Further studies establishing the function and utilities of CNP are found in John Hopkins OMIM database record ID 123830, and in cited publications listed in Table 5, which are hereby incorporated by reference.Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) is another GAM189 target gene, herein designated TARGET GENE. COLEC12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COLEC12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COLEC12 BINDING SITE, designated SEQ ID:11525, to the nucleotide se-

quence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28328] Another function of GAM189 is therefore inhibition of Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC12.

[28329] Coronin, actin binding protein, 1c (CORO1C, Accession NP_055140.1) is another GAM189 target gene, herein designated TARGET GENE. CORO1C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CORO1C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CORO1C BINDING SITE, designated SEQ ID:13595, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28330] Another function of GAM189 is therefore inhibition of Coronin, actin binding protein, 1c (CORO1C, Accession NP_055140.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CORO1C.

[28331] Cox15 homolog, cytochrome c oxidase assembly protein (yeast) (COX15, Accession NP_510870.1) is another GAM189 target gene, herein designated TARGET GENE. COX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COX15 BINDING SITE, designated SEQ ID:7552, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28332] Another function of GAM189 is therefore inhibition of Cox15 homolog, cytochrome c oxidase assembly protein (yeast) (COX15, Accession NP_510870.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COX15.

[28333] Carboxypeptidase a4 (CPA4, Accession NP_057436.1) is another GAM189 target gene, herein designated TARGET GENE. CPA4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of CPA4 BINDING SITE, designated SEQ ID:8942, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28334] Another function of GAM189 is therefore inhibition of Carboxypeptidase a4 (CPA4, Accession NP_057436.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPA4.

[28335] CPR8 (Accession NP_065790.1) is another GAM189 target gene, herein designated TARGET GENE. CPR8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CPR8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPR8 BINDING SITE, designated SEQ ID:13999, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28336] Another function of GAM189 is therefore inhibition of CPR8 (Accession NP_065790.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPR8.

[28337] Carbamoyl-phosphate synthetase 1, mitochondrial (CPS1, Accession NP_001866.2) is another GAM189 target gene, herein designated TARGET GENE. CPS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPS1 BINDING SITE, designated SEQ ID:14493, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28338] Another function of GAM189 is therefore inhibition of Carbamoyl-phosphate synthetase 1, mitochondrial (CPS1, Accession NP_001866.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPS1.

[28339] Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) is another GAM189 target gene, herein designated TARGET GENE. CPSF2 BINDING SITE1 and CPSF2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CPSF2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPSF2 BINDING SITE1 and CPSF2 BINDING SITE2, designated SEQ ID:1877 and SEQ ID:591 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28340] Another function of GAM189 is therefore inhibition of Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPSF2.

[28341] Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000642.2) is another GAM189 target gene, herein designated TARGET GENE. CR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CR1 BINDING SITE, designated SEQ ID:17292, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28342] Another function of GAM189 is therefore inhibition of

Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000642.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CR1.

[28343] Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000564.1) is another GAM189 target gene, herein designated TARGET GENE. CR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CR1 BINDING SITE, designated SEQ ID:17292, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28344] Another function of GAM189 is therefore inhibition of Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000564.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CR1.

[28345] Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) is another GAM189 target gene, herein designated TARGET GENE. CRLF3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRLF3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRLF3 BINDING SITE, designated SEQ ID:7105, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28346] Another function of GAM189 is therefore inhibition of Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRLF3.

[28347] Cofactor required for sp1 transcriptional activation, subunit 6, 77kda (CRSP6, Accession NP_004259.3) is another GAM189 target gene, herein designated TARGET GENE. CRSP6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRSP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of CRSP6 BINDING SITE, designated SEQ ID:7661, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28348] Another function of GAM189 is therefore inhibition of Co-factor required for sp1 transcriptional activation, subunit 6, 77kda (CRSP6, Accession NP_004259.3), a gene which is required for Sp1 mediated transcriptional activation with TAF(II)s. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRSP6.

[28349] The function of CRSP6 has been established by previous studies. Using a HeLa cell line, Ito et al. (1999) cloned TRAP80, the gene encoding the 80- kD subunit of the TRAP complex. (For background information on thyroid hormone receptor- associated proteins (TRAPs), see 300182). The TRAP80 cDNA encodes a 717- amino acid protein that has no obvious motifs other than a short leucine zipper in the middle of the sequence. The TRAP80 cDNA appears to be equivalent to the p78 component of the mouse Mediator (Jiang et al., 1998). Northern blot analysis of multiple human tissues showed that the TRAP80 gene is ubiquitously expressed as an approximately 3.0- kb transcript Gene transcription requires fac-

tors that recognize transcriptional enhancer sites in DNA. These factors work with coactivators to direct transcriptional initiation by the RNA polymerase II apparatus (see OMIM Ref. No. POLR2A, 180660). Transcriptional activation by enhancer- binding factors such as SP1 (OMIM Ref. No. 189906) requires interaction with the TFIID complex (see OMIM Ref. No. TAF2A, 313650). To identify other potential SP1 cofactors, Ryu et al. (1999) developed an in vitro transcription assay consisting of TFIIA (GTF2A1; 600520), RNA polII, and the basal transcription factors GTF2B (OMIM Ref. No. 189963), GTF2E (OMIM Ref. No. 189962), GTF2F (OMIM Ref. No. 189968), and GTF2H (OMIM Ref. No. 189972), supplemented with TFIID or TBP (OMIM Ref. No. 600075). By sequential chromatography, they excluded PC4 (OMIM Ref. No. 600503) as an SP1 cofactor and identified a multisubunit cofactor, CRSP (cofactor required for SP1 activation), which, along with TFIID, is required for efficient activation by SP1. CRSP behaves as a single complex of approximately 700 kD. Ryu et al. (1999) tentatively identified 9 polypeptides as CRSP subunits (see OMIM Ref. No. also PPARBP, 604311). Using microsequence peptide analysis, they cloned a CRSP cDNA encoding a 77- kD protein, CRSP6, which they termed

CRSP77

[28350]

[28351] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28352] Ito, M.; Yuan, C.- X.; Malik, S.; Gu, W.; Fondell, J. D.; Yamamura, S.; Fu, Z.- Y.; Zhang, X.; Qin, J.; Roeder, R. G. : Identity between TRAP and SMCC complexes indicates novel pathways for the function of nuclear receptors and diverse mammalian activators. Molec. Cell 3: 361- 370, 1999. ; and

[28353] Ryu, S.; Zhou, S.; Ladurner, A. G.; Tjian, R. : The transcriptional cofactor complex CRSP is required for activity of the enhancer- binding protein Sp1. Nature 397: 446- 450, 1999.

[28354] Further studies establishing the function and utilities of CRSP6 are found in John Hopkins OMIM database record ID 603810, and in cited publications listed in Table 5, which are hereby incorporated by reference.Cartilage associated protein (CRTAP, Accession NP_006362.1) is another GAM189 target gene, herein designated TARGET GENE. CRTAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRTAP,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRTAP BINDING SITE, designated SEQ ID:7107, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28355] Another function of GAM189 is therefore inhibition of Cartilage associated protein (CRTAP, Accession NP_006362.1), a gene which is a novel developmentally regulated chick embryo protein. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRTAP.

[28356] The function of CRTAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.CSE-C (Accession NP_061851.1) is another GAM189 target gene, herein designated TARGET GENE. CSE-C BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CSE-C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSE-C BINDING SITE, designated

SEQ ID:2336, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28357] Another function of GAM189 is therefore inhibition of CSE-C (Accession NP_061851.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE-C.

[28358] Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_803185.1) is another GAM189 target gene, herein designated TARGET GENE. CSE1L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CSE1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSE1L BINDING SITE, designated SEQ ID:6312, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28359] Another function of GAM189 is therefore inhibition of Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_803185.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE1L.

[28360] Casein kinase 2, alpha prime polypeptide (CSNK2A2, Ac-

cession NP_001887.1) is another GAM189 target gene, herein designated TARGET GENE. CSNK2A2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CSNK2A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSNK2A2 BINDING SITE, designated SEQ ID:15382, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28361] Another function of GAM189 is therefore inhibition of Casein kinase 2, alpha prime polypeptide (CSNK2A2, Accession NP_001887.1), a gene which catalyzes the phosphorylation of serine or threonine residues in proteins. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK2A2.

[28362] The function of CSNK2A2 has been established by previous studies. Phosphorylation of the human p53 protein (OMIM Ref. No. 191170) at ser392 is responsive to ultraviolet (UV) but not gamma irradiation. Keller et al. (2001) identified and purified a mammalian UV- activated protein kinase complex that phosphorylates ser392 in vitro. This

kinase complex contains CK2 and the chromatin transcriptional elongation factor FACT, a heterodimer of SPT16 (OMIM Ref. No. 605012) and SSRP1 (OMIM Ref. No. 604328). In vitro studies showed that FACT alters the specificity of CK2 in the complex such that it selectively phosphorylates p53 over other substrates, including casein. In addition, phosphorylation by the kinase complex was found to enhance p53 activity. These results provided a potential mechanism for p53 activation by UV irradiation Doray et al. (2002) demonstrated that the Golgi- localized, gamma- ear- containing adenosine diphosphate ribosylation factor- binding proteins (GGA1, 606004 and GGA3, 606006) and the coat protein adaptor protein- 1 (AP- 1) complex (see OMIM Ref. No. AP1G2, 603534) colocalize in clathrin- coated buds of the trans- Golgi networks of mouse L cells and human HeLa cells. Binding studies revealed a direct interaction between the hinge domains of the GGAs and the gamma- ear domain of AP-1. Further, AP- 1 contained bound casein kinase- 2 that phosphorylated GGA1 and GGA3, thereby causing autoinhibition. Doray et al. (2002) demonstrated that this autoinhibition could induce the directed transfer of mannose 6- phosphate receptors (see OMIM Ref. No. 154540) from

the GGAs to AP- 1. Mannose 6- phosphate receptors that were defective in binding to GGAs were poorly incorporated into adaptor protein complex containing clathrin coated vesicles. Thus, Doray et al. (2002) concluded that GGAs and the AP- 1 complex interact to package mannose 6- phosphate receptors into AP- 1- containing coated vesicles

[28363] Animal model experiments lend further support to the function of CSNK2A2. To determine the functional and developmental role of protein kinase casein kinase II, Xu et al. (1999) used homologous recombination to disrupt the gene encoding Csnk2a2 in transgenic mice. They found that Csnk2a2 is preferentially expressed in late stages of spermatogenesis, and male mice in which Csnk2a2 has been disrupted are infertile, with oligospermia and globozoospermia ('round- headed spermatozoa'). This was the first demonstration of the unique role for a Ck2 isoform in development. The primary spermatogenic defect in the Csnk2a2 - /- testis is a specific abnormality of anterior head shaping of elongating spermatids; this is the first defined gene that regulates sperm head morphogenesis. As the germ cells differentiate, they are capable of undergoing chromatin condensation, although many

abnormal cells are deleted through apoptosis or Sertoli cell phagocytosis. The few that survived to populate the epididymis exhibited head abnormalities similar to those described in human globozoospermia; thus, Csnk2a2 may be a candidate gene for inherited abnormalities of sperm morphogenesis

[28364] It is appreciated that the abovementioned animal model for CSNK2A2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[28365] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28366] Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S. : Cooperation of GGAs and AP- 1 in packaging MPRs at the trans- Golgi network. Science 297: 1700- 1703, 2002. ; and

[28367] Xu, X.; Toselli, P. A.; Russell, L. D.; Seldin, D. C. : Globo-zoospermia in mice lacking the casein kinase II alpha-prime catalytic subunit. Nature Genet. 23: 118- 121, 1999.

[28368] Further studies establishing the function and utilities of CSNK2A2 are found in John Hopkins OMIM database

record ID 115442, and in cited publications listed in Table 5, which are hereby incorporated by reference.CTEN (Accession NP_116254.3) is another GAM189 target gene, herein designated TARGET GENE. CTEN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTEN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTEN BINDING SITE, designated SEQ ID:14746, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28369] Another function of GAM189 is therefore inhibition of CTEN (Accession NP_116254.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTEN.

[28370] Cardiotrophin 1 (CTF1, Accession NP_001321.1) is another GAM189 target gene, herein designated TARGET GENE. CTF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of CTF1 BINDING SITE, designated SEQ ID:13287, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28371] Another function of GAM189 is therefore inhibition of Cardiotrophin 1 (CTF1, Accession NP_001321.1), a gene which may play a role in cardiac hypertrophy. and therefore may be associated with Cardiac hypertrophy. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Cardiac hypertrophy, and of other diseases and clinical conditions associated with CTF1.

[28372] The function of CTF1 has been established by previous studies. Heart failure is a leading cause of mortality worldwide. A hallmark of the disease is dilated cardiac hypertrophy, which is accompanied by a reactivation of genes expressed in fetal heart development. Reasoning that fetal or embryonic growth factors may mediate the onset of cardiac hypertrophy, Pennica et al. (1995) coupled expression cloning with an embryonic stem cell-based model of cardiogenesis to isolate a 21.5- kD protein, cardiotrophin 1, that potently induces cardiac myocyte hypertrophy in vitro. Amino acid similarity data indicated that CT1 is a member of the family of cytokines that includes leukemia inhibitory factor (LIF; 159540), cil-

iary neurotrophic factor (CNTF; 118945), oncostatin M (OSM; 165095), interleukin 6 (IL6; 147620), and interleukin 11 (IL11; 147681). Several members of this family that are known to signal through the transmembrane protein gp130 (OMIM Ref. No. 162820) stimulate cardiac myocyte hypertrophy, like cardiotrophin 1, suggesting that the gp130 signaling pathway may play a role in cardiac hypertrophy. The 1.4- kb CT1 mRNA is present in the heart and several other mouse tissues Amyotrophic lateral sclerosis (ALS; 105400) is mainly a sporadic neurodegenerative disorder characterized by loss of cortical and spinal motoneurons. Some familial ALS (FALS) cases have been linked to dominant mutations in the gene encoding Cu/Zn superoxide dismutase (SOD1; 147450). Transgenic mice overexpressing a mutated form of human SOD1 with a gly93- to- ala substitution (147450.0008) develop progressive muscle wasting and paralysis as a result of spinal motoneuron loss and die at 5 to 6 months. Bordet et al. (2001) investigated the effects of neurotrophic factor gene delivery in this FALS model. Intramuscular injection of an adenoviral vector encoding CTF1 in SOD1(G93A) newborn mice delayed the onset of motor impairment as assessed in the rotarod test. By CTF1 treatment, axonal degenera-

tion was slowed, skeletal muscle atrophy was largely reduced, and the time- course of motor impairment was significantly decreased

[28373]

[28374] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28375] Pennica, D.; King, K. L.; Shaw, K. J.; Luis, E.; Rullamas, J.; Luoh, S.- M.; Darbonne, W. C.; Knutzon, D. S.; Yen, R.; Chien, K. R.; Baker, J. B.; Wood, W. I. : Expression cloning of cardiotrophin 1, a cytokine that induces cardiac myocyte hypertrophy. Proc. Nat. Acad. Sci. 92: 1142- 1146, 1995. ; and

[28376] Bordet, T.; Lesbordes, J.- C.; Rouhani, S.; Castelnau-Ptakhine, L.; Schmalbruch, H.; Haase, G.; Kahn, A. : Protective effects of cardiotrophin- 1 adenoviral gene transfer on neuromuscular.

[28377] Further studies establishing the function and utilities of CTF1 are found in John Hopkins OMIM database record ID 600435, and in cited publications listed in Table 5, which are hereby incorporated by reference.Cathepsin s (CTSS, Accession NP_004070.3) is another GAM189 target gene, herein designated TARGET GENE. CTSS BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by CTSS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSS BINDING SITE, designated SEQ ID:4517, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28378] Another function of GAM189 is therefore inhibition of Cathepsin s (CTSS, Accession NP_004070.3), a gene which is a lysosomal cysteine (thiol) protease that cleaves elastin. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSS.

[28379] The function of CTSS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Chemokine (c-x-c motif) ligand 16 (CXCL16, Accession NP_071342.1) is another GAM189 target gene, herein designated TARGET GENE. CXCL16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CXCL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CXCL16 BINDING SITE, designated SEQ ID:17688, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28380] Another function of GAM189 is therefore inhibition of Chemokine (c-x-c motif) ligand 16 (CXCL16, Accession NP_071342.1), a gene which induces calcium mobilization. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCL16.

[28381] The function of CXCL16 has been established by previous studies. Using a 2- step EST database search in which putative transcripts were scanned for the occurrence of functional patterns, Matloubian et al. (2000) identified a cDNA encoding a CXC chemokine that they termed CXCL16. The predicted 273- amino acid CXCL16 protein, which is 49% identical to the 246- amino acid mouse sequence, contains a non- glu/leu/arg (ELR) motif- containing CXC chemokine domain, a mucin- like spacer region, a transmembrane domain, and a cytoplasmic tail with a potential tyrosine phosphorylation and SH2 protein- binding site. CXCL16 was the first transmembrane CXC

chemokine identified; CX3CL1 (SCYD1; 601880), which also has a mucin- like spacer region, was the only other known transmembrane chemokine. Northern blot analysis of mouse and human tissues detected a 2.2- kb CXCL16 transcript in spleen, lymph nodes, Peyer patches, lung, kidney, small intestine, and thymus, with weak expression in heart and liver and no expression in brain and bone marrow. Flow cytometry and Western blot analysis demonstrated expression of an approximately 60- kD glycosylated cell- surface protein as well as a cell supernatant 35- kD soluble protein. Flow cytometry of cells from mouse tissues indicated that CXCL16 is found on CD11C (ITGAX; 151510)- positive splenic and lymph node dendritic cells; this expression was increased after injection with lipopolysaccharide. Immunohistochemical analysis showed that CXCL16 is expressed in T- cell areas of the splenic white pulp, lymph nodes, the thymus medulla, and, interestingly, in the splenic red pulp. No staining was observed in B- cell areas. After injection of inflammatory mediators, expression was enhanced in T- cell zones and, more prominently, in splenic red pulp. Chemotaxis assays found that CXCL16 induced a strong chemotactic response in activated CD8 T cells. In addition, CXCL16 in-

duced calcium mobilization. Expression cloning of mouse Cxcl16 identified a protein with 71% amino acid identity to human BONZO (OMIM Ref. No. 605163), which Matloubian et al. (2000) renamed CXCR6. Human and mouse cells expressing CXCR6 showed a strong chemotactic response to CXCL16 but not to other chemokines. The authors concluded that CXCL16 and CXCR6 probably function in interactions between dendritic cells and T cells and in regulating T- cell migration in the splenic red pulp.

Macrophages endocytose oxidized low density lipoprotein (OxLDL) by a receptor- mediated mechanism. By expression cloning from a phorbol ester- stimulated THP- 1 cell library, Shimaoka et al. (2000) isolated a cDNA encoding SRPSOX (scavenger receptor that binds phophatidylserine and oxidized lipoprotein). The deduced 254- amino acid type I transmembrane protein is identical to the CXCL16 protein reported by Matloubian et al. (2000) except that SRPSOX differs by 2 residues and lacks the N- terminal 19 amino acids. Cells expressing SRPSOX bound to phophatidylserine- coated plates; this binding could be inhibited by OxLDL. Scatchard analysis confirmed that SRPSOX is a specific receptor for OxLDL but not LDL or acetyl- LDL. Fluorescence microscopy demonstrated

OxLDL uptake in SRPSOX- expressing cells. Immunoblot analysis showed that SRPSOX is expressed as a 30- kD protein in human and mouse macrophages. Northern blot analysis revealed differentiation- inducible expression of 1.8- and 2.5- kb transcripts in macrophages.

[28382]

[28383] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28384] Matloubian, M.; David, A.; Engel, S.; Ryan, J. E.; Cyster, J. G. : A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzo. Nature Immun. 1: 298- 304, 2000. ; and

[28385] Shimaoka, T.; Kume, N.; Minami, M.; Hayashida, K.; Kataoka, H.; Kita, T.; Yonehara, S. : Molecular cloning of a novel scavenger receptor for oxidized low density lipoprotein, SR- PSOX.

[28386] Further studies establishing the function and utilities of CXCL16 are found in John Hopkins OMIM database record ID 605398, and in cited publications listed in Table 5, which are hereby incorporated by reference.CYCS (Accession NP_061820.1) is another GAM189 target gene, herein designated TARGET GENE. CYCS BINDING SITE1

through CYCS BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by CYCS, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYCS BINDING SITE1 through CYCS BINDING SITE3, designated SEQ ID:9339, SEQ ID:18991 and SEQ ID:18868 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28387] Another function of GAM189 is therefore inhibition of CYCS (Accession NP_061820.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYCS.

[28388] Cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2, Accession NP_001331.1) is another GAM189 target gene, herein designated TARGET GENE. CYLC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYLC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYLC2 BINDING SITE, designated SEQ ID:15540, to the nucleotide

sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28389] Another function of GAM189 is therefore inhibition of Cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2, Accession NP_001331.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYLC2.

[28390] Cytochrome p450, subfamily i (aromatic compound-inducible), polypeptide 2 (CYP1A2, Accession NP_000752.1) is another GAM189 target gene, herein designated TARGET GENE. CYP1A2 BINDING SITE1 through CYP1A2 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by CYP1A2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP1A2 BINDING SITE1 through CYP1A2 BINDING SITE3, designated SEQ ID:6637, SEQ ID:13576 and SEQ ID:18279 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28391] Another function of GAM189 is therefore inhibition of Cytochrome p450, subfamily i (aromatic compound-inducible), polypeptide 2 (CYP1A2, Accession

NP_000752.1), a gene which intervenes in an NADPH- dependent electron transport pathway. and therefore may be associated with Porphyria cutanea tarda. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Porphyria cutanea tarda, and of other diseases and clinical conditions associated with CYP1A2.

[28392] The function of CYP1A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1) is another GAM189 target gene, herein designated TARGET GENE. CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CYP2B6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2, designated SEQ ID:2194 and SEQ ID:10618 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28393] Another function of GAM189 is therefore inhibition of Cy-

tochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1), a gene which oxidizes a variety of structurally unrelated compounds, including steroids, fatty acids, and xenobiotics. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP2B6.

[28394] The function of CYP2B6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily ivf, polypeptide 3 (leukotriene b4 omega hydroxylase) (CYP4F3, Accession NP_000887.1) is another GAM189 target gene, herein designated TARGET GENE. CYP4F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP4F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP4F3 BINDING SITE, designated SEQ ID:9158, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28395] Another function of GAM189 is therefore inhibition of Cy-

tochrome p450, subfamily ivf, polypeptide 3 (leukotriene b4 omega hydroxylase) (CYP4F3, Accession NP_000887.1), a gene which converts leukotriene B4 into the less active 20- hydroxy- leukotriene B4. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP4F3.

[28396] The function of CYP4F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.1.CYP51A1 (Accession NP_000777.1) is another GAM189 target gene, herein designated TARGET GENE. CYP51A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP51A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP51A1 BINDING SITE, designated SEQ ID:2152, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28397] Another function of GAM189 is therefore inhibition of CYP51A1 (Accession NP_000777.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with CYP51A1.

[28398] Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1) is another GAM189 target gene, herein designated TARGET GENE. CYP8B1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP8B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP8B1 BINDING SITE, designated SEQ ID:5978, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28399] Another function of GAM189 is therefore inhibition of Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1), a gene which functions in bile acid biosynthesis. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP8B1.

[28400] The function of CYP8B1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM47.1.Debranching enzyme homolog 1 (s. cerevisiae) (DBR1, Accession NP_057300.1) is another GAM189 target gene, herein designated TARGET GENE. DBR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DBR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DBR1 BINDING SITE, designated SEQ ID:7961, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28401] Another function of GAM189 is therefore inhibition of Debranching enzyme homolog 1 (s. cerevisiae) (DBR1, Accession NP_057300.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBR1.

[28402] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) is another GAM189 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:16590, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28403] Another function of GAM189 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[28404] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835364.1) is another GAM189 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:16590, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28405] Another function of GAM189 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin)

(DCX, Accession NP_835364.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[28406] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) is another GAM189 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:16590, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28407] Another function of GAM189 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[28408] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) is another GAM189 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated re-

gion of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:16590, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28409] Another function of GAM189 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[28410] Desmin (DES, Accession NP_001918.2) is another GAM189 target gene, herein designated TARGET GENE. DES BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DES BINDING SITE, designated SEQ ID:14498, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28411] Another function of GAM189 is therefore inhibition of

Desmin (DES, Accession NP_001918.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DES.

[28412] Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1) is another GAM189 target gene, herein designated TARGET GENE. DFFB BINDING SITE1 and DFFB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DFFB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DFFB BINDING SITE1 and DFFB BINDING SITE2, designated SEQ ID:9091 and SEQ ID:2019 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28413] Another function of GAM189 is therefore inhibition of Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1), a gene which induces DNA fragmentation and chromatin condensation during apoptosis. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with DFFB.

[28414] The function of DFFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Dihydrofolate reductase (DHFR, Accession NP_000782.1) is another GAM189 target gene, herein designated TARGET GENE. DHFR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHFR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DHFR BINDING SITE, designated SEQ ID:8052, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28415] Another function of GAM189 is therefore inhibition of Dihydrofolate reductase (DHFR, Accession NP_000782.1), a gene which converts dihydrofolate into tetrahydrofolate. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DHFR.

[28416] The function of DHFR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM64.1.Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1) is another GAM189 target gene, herein designated TARGET GENE. DIAPH2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DIAPH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DIAPH2 BINDING SITE, designated SEQ ID:14492, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28417] Another function of GAM189 is therefore inhibition of Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1), a gene which may affect in oogenesis and therefore may be associated with Premature ovarian failure . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Premature ovarian failure ., and of other diseases and clinical conditions associated with DIAPH2.

[28418] The function of DIAPH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Disrupted in schizophrenia 1 (DISC1, Acces-

sion NP_061132.1) is another GAM189 target gene, herein designated TARGET GENE. DISC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DISC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DISC1 BINDING SITE, designated SEQ ID:1298, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28419] Another function of GAM189 is therefore inhibition of Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1), a gene which has globular N- terminal domain(s) and a helical C- terminal domain. and therefore may be associated with Schizophrenia . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Schizophrenia ., and of other diseases and clinical conditions associated with DISC1.

[28420] The function of DISC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.DKFZP434B1727 (Accession NP_115519.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZP434B1727 BINDING SITE is a target bind-

ing site found in the 3` untranslated region of mRNA encoded by DKFZP434B1727, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434B1727 BINDING SITE, designated SEQ ID:4014, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28421] Another function of GAM189 is therefore inhibition of DKFZP434B1727 (Accession NP_115519.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434B1727.

[28422] DKFZp434C0923 (Accession NP_060068.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp434C0923 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434C0923, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434C0923 BINDING SITE, designated SEQ ID:8235, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:246.

[28423] Another function of GAM189 is therefore inhibition of DKFZp434C0923 (Accession NP_060068.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434C0923.

[28424] DKFZP434C212 (Accession XP_044196.3) is another GAM189 target gene, herein designated TARGET GENE. DKFZP434C212 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434C212, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434C212 BINDING SITE, designated SEQ ID:8661, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28425] Another function of GAM189 is therefore inhibition of DKFZP434C212 (Accession XP_044196.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C212.

[28426] DKFZP434D146 (Accession NP_056410.2) is another

GAM189 target gene, herein designated TARGET GENE. DKFZP434D146 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434D146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434D146 BINDING SITE, designated SEQ ID:2209, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28427] Another function of GAM189 is therefore inhibition of DKFZP434D146 (Accession NP_056410.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434D146.

[28428] DKFZp434E2220 (Accession NP_060082.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp434E2220 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp434E2220, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434E2220 BINDING SITE,

designated SEQ ID:11326, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28429] Another function of GAM189 is therefore inhibition of DKFZp434E2220 (Accession NP_060082.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E2220.

[28430] DKFZP434F0318 (Accession NP_110444.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZP434F0318 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F0318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434F0318 BINDING SITE, designated SEQ ID:16771, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28431] Another function of GAM189 is therefore inhibition of DKFZP434F0318 (Accession NP_110444.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZP434F0318.

[28432] DKFZp434F1719 (Accession NP_115624.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp434F1719 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434F1719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434F1719 BINDING SITE, designated SEQ ID:3951, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28433] Another function of GAM189 is therefore inhibition of DKFZp434F1719 (Accession NP_115624.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434F1719.

[28434] DKFZp434K1210 (Accession NP_060076.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp434K1210 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434K1210, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434K1210 BINDING SITE, designated SEQ ID:4195, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28435] Another function of GAM189 is therefore inhibition of DKFZp434K1210 (Accession NP_060076.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434K1210.

[28436] DKFZp547H025 (Accession NP_064546.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp547H025 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547H025, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547H025 BINDING SITE, designated SEQ ID:14246, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28437] Another function of GAM189 is therefore inhibition of DKFZp547H025 (Accession NP_064546.1) . Accordingly, util-

ities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547H025.

[28438] DKFZp547P234 (Accession NP_694590.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp547P234 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547P234, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547P234 BINDING SITE, designated SEQ ID:11057, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28439] Another function of GAM189 is therefore inhibition of DKFZp547P234 (Accession NP_694590.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547P234.

[28440] DKFZP564G092 (Accession NP_056416.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZP564G092 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

DKFZP564G092, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564G092 BINDING SITE, designated SEQ ID:2662, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28441] Another function of GAM189 is therefore inhibition of DKFZP564G092 (Accession NP_056416.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564G092.

[28442] DKFZP564I122 (Accession XP_032397.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZP564I122 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564I122, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564I122 BINDING SITE, designated SEQ ID:16590, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28443] Another function of GAM189 is therefore inhibition of DKFZP564I122 (Accession XP_032397.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564I122.

[28444] DKFZP564K0322 (Accession NP_114429.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZP564K0322 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564K0322, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564K0322 BINDING SITE, designated SEQ ID:17964, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28445] Another function of GAM189 is therefore inhibition of DKFZP564K0322 (Accession NP_114429.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564K0322.

[28446] DKFZp564K142 (Accession NP_115497.2) is another GAM189 target gene, herein designated TARGET GENE.

DKFZp564K142 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp564K142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp564K142 BINDING SITE, designated SEQ ID:2663, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28447] Another function of GAM189 is therefore inhibition of DKFZp564K142 (Accession NP_115497.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp564K142.

[28448] DKFZP564O0523 (Accession NP_115496.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZP564O0523 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O0523, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564O0523 BINDING SITE, designated SEQ ID:3686, to the nucleotide sequence of

GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28449] Another function of GAM189 is therefore inhibition of DKFZP564O0523 (Accession NP_115496.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564O0523.

[28450] DKFZP566D1346 (Accession NP_110443.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZP566D1346 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP566D1346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566D1346 BINDING SITE, designated SEQ ID:10539, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28451] Another function of GAM189 is therefore inhibition of DKFZP566D1346 (Accession NP_110443.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566D1346.

[28452] DKFZP566I1024 (Accession NP_056226.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZP566I1024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP566I1024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566I1024 BINDING SITE, designated SEQ ID:12353, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28453] Another function of GAM189 is therefore inhibition of DKFZP566I1024 (Accession NP_056226.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566I1024.

[28454] DKFZp586C0721 (Accession XP_098416.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp586C0721 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp586C0721, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of DKFZp586C0721 BINDING SITE, designated SEQ ID:12173, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28455] Another function of GAM189 is therefore inhibition of DKFZp586C0721 (Accession XP_098416.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp586C0721.

[28456] DKFZP586D0919 (Accession NP_056248.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZP586D0919 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586D0919, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586D0919 BINDING SITE, designated SEQ ID:11134, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28457] Another function of GAM189 is therefore inhibition of DKFZP586D0919 (Accession NP_056248.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZP586D0919.

[28458] DKFZp667B1218 (Accession NP_808881.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp667B1218 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp667B1218, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667B1218 BINDING SITE, designated SEQ ID:15574, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28459] Another function of GAM189 is therefore inhibition of DKFZp667B1218 (Accession NP_808881.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp667B1218.

[28460] DKFZp667E0512 (Accession XP_117353.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp667E0512 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp667E0512, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667E0512 BINDING SITE, designated SEQ ID:8492, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28461] Another function of GAM189 is therefore inhibition of DKFZp667E0512 (Accession XP_117353.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp667E0512.

[28462] DKFZp761B107 (Accession NP_775734.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp761B107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761B107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B107 BINDING SITE, designated SEQ ID:13571, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28463] Another function of GAM189 is therefore inhibition of DK-

FZp761B107 (Accession NP_775734.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B107.

[28464] DKFZp761B128 (Accession NP_689650.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp761B128 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761B128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B128 BINDING SITE, designated SEQ ID:17969, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28465] Another function of GAM189 is therefore inhibition of DKFZp761B128 (Accession NP_689650.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B128.

[28466] DKFZp761G2113 (Accession XP_046017.3) is another GAM189 target gene, herein designated TARGET GENE. DKFZp761G2113 BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by DKFZp761G2113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761G2113 BINDING SITE, designated SEQ ID:7769, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28467] Another function of GAM189 is therefore inhibition of DKFZp761G2113 (Accession XP_046017.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761G2113.

[28468] DKFZp761H039 (Accession NP_061181.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp761H039 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761H039, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761H039 BINDING SITE, designated SEQ ID:15190, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:246.

[28469] Another function of GAM189 is therefore inhibition of DKFZp761H039 (Accession NP_061181.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761H039.

[28470] DKFZp761J139 (Accession NP_115656.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp761J139 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761J139, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761J139 BINDING SITE, designated SEQ ID:5768, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28471] Another function of GAM189 is therefore inhibition of DKFZp761J139 (Accession NP_115656.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761J139.

[28472] DKFZp761K1423 (Accession NP_060892.1) is another

GAM189 target gene, herein designated TARGET GENE. DKFZp761K1423 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761K1423, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761K1423 BINDING SITE, designated SEQ ID:1317, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28473] Another function of GAM189 is therefore inhibition of DKFZp761K1423 (Accession NP_060892.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761K1423.

[28474] DKFZp761N1114 (Accession XP_086327.6) is another GAM189 target gene, herein designated TARGET GENE. DKFZp761N1114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761N1114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761N1114 BINDING SITE,

designated SEQ ID:13529, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28475] Another function of GAM189 is therefore inhibition of DKFZp761N1114 (Accession XP_086327.6) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761N1114.

[28476] DKFZp761O0113 (Accession NP_060879.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp761O0113 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761O0113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761O0113 BINDING SITE, designated SEQ ID:7699, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28477] Another function of GAM189 is therefore inhibition of DKFZp761O0113 (Accession NP_060879.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZp761O0113.

[28478] DKFZp761P1121 (Accession NP_690870.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp761P1121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761P1121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761P1121 BINDING SITE, designated SEQ ID:9147, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28479] Another function of GAM189 is therefore inhibition of DKFZp761P1121 (Accession NP_690870.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761P1121.

[28480] DKFZp762C2414 (Accession NP_848637.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp762C2414 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762C2414, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762C2414 BINDING SITE, designated SEQ ID:4056, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28481] Another function of GAM189 is therefore inhibition of DKFZp762C2414 (Accession NP_848637.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762C2414.

[28482] DKFZp762I137 (Accession NP_689624.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp762I137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762I137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762I137 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28483] Another function of GAM189 is therefore inhibition of DKFZp762I137 (Accession NP_689624.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762I137.

[28484] DKFZp762I194 (Accession NP_689597.1) is another GAM189 target gene, herein designated TARGET GENE. DKFZp762I194 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762I194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762I194 BINDING SITE, designated SEQ ID:6884, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28485] Another function of GAM189 is therefore inhibition of DKFZp762I194 (Accession NP_689597.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762I194.

[28486] DKFZp762L0311 (Accession NP_061189.2) is another GAM189 target gene, herein designated TARGET GENE. DKFZp762L0311 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

DKFZp762L0311, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762L0311 BINDING SITE, designated SEQ ID:9194, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28487] Another function of GAM189 is therefore inhibition of DKFZp762L0311 (Accession NP_061189.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762L0311.

[28488] Dickkopf homolog 3 (xenopus laevis) (DKK3, Accession NP_037385.1) is another GAM189 target gene, herein designated TARGET GENE. DKK3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DKK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKK3 BINDING SITE, designated SEQ ID:20069, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28489] Another function of GAM189 is therefore inhibition of Dickkopf homolog 3 (xenopus laevis) (DKK3, Accession NP_037385.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKK3.

[28490] Dickkopf homolog 3 (xenopus laevis) (DKK3, Accession NP_056965.2) is another GAM189 target gene, herein designated TARGET GENE. DKK3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DKK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKK3 BINDING SITE, designated SEQ ID:20069, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28491] Another function of GAM189 is therefore inhibition of Dickkopf homolog 3 (xenopus laevis) (DKK3, Accession NP_056965.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKK3.

[28492] Dynein, axonemal, heavy polypeptide 11 (DNAH11, Accession NP_003768.1) is another GAM189 target gene,

herein designated TARGET GENE. DNAH11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DNAH11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DNAH11 BINDING SITE, designated SEQ ID:1214, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28493] Another function of GAM189 is therefore inhibition of Dynein, axonemal, heavy polypeptide 11 (DNAH11, Accession NP_003768.1), a gene which may function as a motor protein. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAH11.

[28494] The function of DNAH11 has been established by previous studies. Inversus viscerum (iv/iv) mice exhibit randomized left- right patterning; half of iv/iv homozygotes develop situs inversus (Okada et al., 1999; Supp et al., 1999). To examine how flow affects left- right patterning, Nonaka et al. (2002) developed a system in which mouse embryos are cultured under an artificial fluid flow. This artificial flow was able to direct the situs of mutant mouse em-

bryos with immotile cilia. Nonaka et al. (2002) concluded that their results provided the first evidence for the role of mechanical fluid flow in left- right patterning.

[28495] Animal model experiments lend further support to the function of DNAH11. Inversus viscerum (iv/iv) mice exhibit randomized left- right patterning; half of iv/iv homozygotes develop situs inversus (Okada et al., 1999; Supp et al., 1999). To examine how flow affects left- right patterning, Nonaka et al. (2002) developed a system in which mouse embryos are cultured under an artificial fluid flow. This artificial flow was able to direct the situs of mutant mouse embryos with immotile cilia. Nonaka et al. (2002) concluded that their results provided the first evidence for the role of mechanical fluid flow in left- right patterning.

[28496] It is appreciated that the abovementioned animal model for DNAH11 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[28497] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28498] McGrath, J.; Horwich, A. L.; Brueckner, M. : Duplication/deficiency mapping of situs inversus viscerum (iv), a gene

that determines left- right asymmetry in the mouse. Genomics 14: 643- 648, 1992. ; and

[28499] Nonaka, S.; Shiratori, H.; Saijoh, Y.; Hamada, H. : Determination of left- right patterning of the mouse embryo by artificial nodal flow. Nature 418: 96- 99, 2002.

[28500] Further studies establishing the function and utilities of DNAH11 are found in John Hopkins OMIM database record ID 603339, and in cited publications listed in Table 5, which are hereby incorporated by reference.Dnaj (hsp40) homolog, subfamily b, member 5 (DNAJB5, Accession NP_036398.2) is another GAM189 target gene, herein designated TARGET GENE. DNAJB5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DNAJB5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DNAJB5 BINDING SITE, designated SEQ ID:5815, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28501] Another function of GAM189 is therefore inhibition of Dnaj (hsp40) homolog, subfamily b, member 5 (DNAJB5, Accession NP_036398.2) . Accordingly, utilities of

GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAJB5.

[28502] DRIM (Accession NP_055318.1) is another GAM189 target gene, herein designated TARGET GENE. DRIM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DRIM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DRIM BINDING SITE, designated SEQ ID:6633, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28503] Another function of GAM189 is therefore inhibition of DRIM (Accession NP_055318.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRIM.

[28504] Dentatorubral-pallidoluysian atrophy (atrophin-1) (DRPLA, Accession NP_001931.1) is another GAM189 target gene, herein designated TARGET GENE. DRPLA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DRPLA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of DRPLA BINDING SITE, designated SEQ ID:9796, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28505] Another function of GAM189 is therefore inhibition of Dentatorubral-pallidoluysian atrophy (atrophin-1) (DRPLA, Accession NP_001931.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRPLA.

[28506] Desmocollin 3 (DSC3, Accession NP_001932.1) is another GAM189 target gene, herein designated TARGET GENE. DSC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE, designated SEQ ID:7559, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28507] Another function of GAM189 is therefore inhibition of Desmocollin 3 (DSC3, Accession NP_001932.1), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of GAM189 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with DSC3.

[28508] The function of DSC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Desmocollin 3 (DSC3, Accession NP_077741.1) is another GAM189 target gene, herein designated TARGET GENE. DSC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE, designated SEQ ID:7559, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28509] Another function of GAM189 is therefore inhibition of Desmocollin 3 (DSC3, Accession NP_077741.1), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC3.

[28510] The function of DSC3 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Down syndrome critical region gene 6 (DSCR6, Accession NP_061835.1) is another GAM189 target gene, herein designated TARGET GENE. DSCR6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSCR6 BINDING SITE, designated SEQ ID:14954, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28511] Another function of GAM189 is therefore inhibition of Down syndrome critical region gene 6 (DSCR6, Accession NP_061835.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSCR6.

[28512] Dual specificity phosphatase 19 (DUSP19, Accession NP_543152.1) is another GAM189 target gene, herein designated TARGET GENE. DUSP19 BINDING SITE1 and DUSP19 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DUSP19, corre-

sponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP19 BINDING SITE1 and DUSP19 BINDING SITE2, designated SEQ ID:5768 and SEQ ID:15367 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28513] Another function of GAM189 is therefore inhibition of Dual specificity phosphatase 19 (DUSP19, Accession NP_543152.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP19.

[28514] Endometrial bleeding associated factor (left-right determination, factor a; transforming growth factor beta superfamily) (EBAF, Accession NP_003231.2) is another GAM189 target gene, herein designated TARGET GENE. EBAF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EBAF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EBAF BINDING SITE, designated SEQ ID:18275, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[28515] Another function of GAM189 is therefore inhibition of Endometrial bleeding associated factor (left-right determination, factor a; transforming growth factor beta superfamily) (EBAF, Accession NP_003231.2), a gene which LEFT- RIGHT AXIS MALFORMATIONS and therefore is associated with Left- right axis malformations. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Left- right axis malformations, and of other diseases and clinical conditions associated with EBAF.

[28516] The function of EBAF has been established by previous studies. Because of the possibility that Lefty mutations may be associated with human L- R axis malformations, Kosaki et al. (1999) characterized 2 human homologs, LEFTY A and LEFTY B (OMIM Ref. No. 603037). PCR screening of a PAC genomic library identified a clone that contained both LEFTY A and LEFTY B genes. Restriction mapping showed that the genes are separated by approximately 50 kb and are oriented in tandem. The 2 genes were localized by FISH to 1q42, a region syntenic to the location to which the mouse Lefty genes have been mapped at 1H5 (Meno et al., 1997). Both LEFTY A and LEFTY B contain 4 exons which are spliced at identical po-

sitions, and both genes encode proteins with 366 amino acids. LEFTY A was found to be identical to EBAF, the cDNA previously identified by Kothapalli et al. (1997). The deduced amino acid sequences of LEFTY A and LEFTY B are more similar to each other than to Lefty- 1 or Lefty- 2 of the mouse. Analysis of 126 human cases of L- R axis malformation showed 1 nonsense and 1 missense mutation in the LEFTY A gene. Both mutations lay in the cysteine- knot region of the LEFTY A protein, and the phenotype of affected individuals was very similar to that typically seen in Lefty- 1 - /- mice with L- R axis malformations. Because of the possibility that Lefty mutations may be associated with human L- R axis malformations, Kosaki et al. (1999) characterized 2 human homologs, LEFTY A and LEFTY B (OMIM Ref. No. 603037). PCR screening of a PAC genomic library identified a clone that contained both LEFTY A and LEFTY B genes. Restriction mapping showed that the genes are separated by approximately 50 kb and are oriented in tandem. The 2 genes were localized by FISH to 1q42, a region syntenic to the location to which the mouse Lefty genes have been mapped at 1H5 (Meno et al., 1997). Both LEFTY A and LEFTY B contain 4 exons which are spliced at identical positions, and both genes

encode proteins with 366 amino acids. LEFTY A was found to be identical to EBAF, the cDNA previously identified by Kothapalli et al. (1997). The deduced amino acid sequences of LEFTY A and LEFTY B are more similar to each other than to Lefty- 1 or Lefty- 2 of the mouse. Analysis of 126 human cases of L- R axis malformation showed 1 nonsense and 1 missense mutation in the LEFTY A gene. Both mutations lay in the cysteine- knot region of the LEFTY A protein, and the phenotype of affected individuals was very similar to that typically seen in Lefty- 1 - /- mice with L- R axis malformations.

[28517] Animal model experiments lend further support to the function of EBAF. Lefty- 1, lefty- 2, and nodal (OMIM Ref. No. 601265) are expressed on the left side of developing mouse embryos and are implicated in L- R determination. Meno et al. (1998) examined the role of lefty- 1 by analyzing mutant mice lacking this gene. The lefty- 1- deficient mice showed a variety of L- R positional defects in visceral organs. The most common feature of lefty- 1 - /- mice was thoracic left isomerism (rather than right isomerism). The lack of lefty- 1 resulted in bilateral expression of nodal, lefty- 2, and Pitx2 (OMIM Ref. No. 601542), a homeo box gene normally expressed on the left side.

These observations suggested that the role of lefty- 1 is to restrict the expression of lefty- 2 and nodal to the left side, and that lefty- 2 or nodal encode a signal for 'left-ness.'

[28518] It is appreciated that the abovementioned animal model for EBAF is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[28519] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28520] Kosaki, K.; Bassi, M. T.; Kosaki, R.; Lewin, M.; Belmont, J.; Schauer, G.; Casey, B. : Characterization and mutation analysis of human LEFTY A and LEFTY B, homologues of murine genes implicated in left- right axis development. Am. J. Hum. Genet. 64: 712- 721, 1999. ; and

[28521] Meno, C.; Shimono, A.; Saijoh, Y.; Yashiro, K.; Mochida, K.; Ohishi, S.; Noji, S.; Kondoh, H.; Hamada, H. : Lefty- 1 is required for left- right determination as a regulator of lefty- 2 an.

[28522] Further studies establishing the function and utilities of EBAF are found in John Hopkins OMIM database record ID 601877, and in cited publications listed in Table 5, which

are hereby incorporated by reference.Endothelial differentiation, sphingolipid g-protein-coupled receptor, 8 (EDG8, Accession NP_110387.1) is another GAM189 target gene, herein designated TARGET GENE. EDG8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EDG8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDG8 BINDING SITE, designated SEQ ID:12263, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28523] Another function of GAM189 is therefore inhibition of Endothelial differentiation, sphingolipid g-protein-coupled receptor, 8 (EDG8, Accession NP_110387.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDG8.

[28524] EEF2K (Accession NP_037434.1) is another GAM189 target gene, herein designated TARGET GENE. EEF2K BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EEF2K, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EEF2K BINDING SITE, designated SEQ ID:2595, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28525] Another function of GAM189 is therefore inhibition of EEF2K (Accession NP_037434.1), a gene which phosphorylates serine or threonine on the eukaryotic elongation factor- 2 and therefore may be associated with Systemic lupus erythematosus and cancer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Systemic lupus erythematosus and cancer, and of other diseases and clinical conditions associated with EEF2K.

[28526] The function of EEF2K has been established by previous studies. Using degenerate PCR primers based on worm and rabbit peptide sequences for Eef2k, followed by 5- prime and 3- prime RACE and RT- PCR on a glioma cell line, Ryazanov et al. (1997) obtained cDNAs encoding rodent and human EEF2K. The deduced 725- amino acid human protein is 90% identical to the rodent proteins. EEF2K lacks homology to other serine/threonine kinases or to other calmodulin- dependent kinases, apart from a glycine- rich loop that is part of the ATP- binding site. All

EEF2K sequences contain a highly- conserved 200- residue catalytic domain. There is also a conserved C- terminal coiled- coil region. SDS- PAGE and functional analysis showed expression of a 100- kD protein whose activity was strictly calmodulin- dependent. Northern blot analysis revealed ubiquitous expression of a major 3.1- kb transcript and minor 6.1- and 2.5- kb transcripts. Expression was particularly abundant in heart and skeletal muscle, suggesting that EEF2 phosphorylation may be particularly important in muscle. Arora et al. (2002) found that a majority of patients with systemic lupus erythematosus (SLE; 152700) have high titer anti- EEF2K antibodies capable of immunoprecipitating functional enzyme.

[28527]

[28528] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28529] Ryazanov, A. G.; Ward, M. D.; Mendola, C. E.; Pavur, K. S.; Dorovkov, M. V.; Wiedmann, M.; Erdjument- Bromage, H.; Tempst, P.; Parmer, T. G.; Prostko, C. R.; Germino, F. J.; Hait, W. N. : Identification of a new class of protein kinases represented by eukaryotic elongation factor- 2 ki-

nase. Proc. Nat. Acad. Sci. 94: 4884- 4889, 1997. ; and

[28530] Arora, S.; Yang, J.- M.; Craft, J.; Hait, W. : Detection of anti- elongation factor 2 kinase (calmodulin- dependent protein kinase III) antibodies in patients with systemic lupus erythemato.

[28531] Further studies establishing the function and utilities of EEF2K are found in John Hopkins OMIM database record ID 606968, and in cited publications listed in Table 5, which are hereby incorporated by reference.Eh-domain containing 1 (EHD1, Accession NP_006786.2) is another GAM189 target gene, herein designated TARGET GENE. EHD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EHD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EHD1 BINDING SITE, designated SEQ ID:7065, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28532] Another function of GAM189 is therefore inhibition of Eh-domain containing 1 (EHD1, Accession NP_006786.2), a gene which may be involved in ligand- initiated endocytosis. Accordingly, utilities of GAM189 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with EHD1.

[28533] The function of EHD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.Eh-domain containing 2 (EHD2, Accession NP_055416.2) is another GAM189 target gene, herein designated TARGET GENE. EHD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EHD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EHD2 BINDING SITE, designated SEQ ID:4837, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28534] Another function of GAM189 is therefore inhibition of Eh-domain containing 2 (EHD2, Accession NP_055416.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHD2.

[28535] Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kda (EIF2S3, Accession NP_001406.1) is another GAM189 target gene, herein designated TARGET

GENE. EIF2S3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF2S3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF2S3 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28536] Another function of GAM189 is therefore inhibition of Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kda (EIF2S3, Accession NP_001406.1), a gene which functions in the early steps of protein synthesis. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2S3.

[28537] The function of EIF2S3 has been established by previous studies. Translation initiation factor eIF- 2 is a heterotrimeric GTP- binding protein involved in the recruitment of methionyl- tRNA(i) to the 40 S ribosomal subunit. Gasper et al. (1994) cloned a human cDNA encoding the largest subunit of eIF- 2, EIF2G. The EIF2G cDNA encodes a 472- amino acid protein with a molecular mass of 51.8 kD and contains 3 consensus GTP- binding elements. Hu-

man EIF2G is highly related to the yeast homolog, GCD11, exhibiting 71% sequence identity and an additional 13% similarity. Genes controlling the functions of spermatogenesis, Spy, and expression of the male- specific minor transplantation antigen H- Y, Hya (OMIM Ref. No. 426000), map to a region of the short arm of the mouse Y chromosome, delta- Sxr(b), that lies between the zinc finger genes Zfy1 and Zfy2 (OMIM Ref. No. 490000) and is deleted in Sxr(b) mutant mice. These Sxr(b) mice arose from an original sex- reversed mutation, Sxr(a), that carries a duplication of most of the Y chromosome short arm translocated to the telomeric end of the pseudoautosomal region of the Y chromosome. Several genes were mapped to that interval of the mouse Y chromosome and each was found to have a homolog on the X chromosome. Four of them, Zfy1 and Zfy2 (OMIM Ref. No. 490000), Ube1y (OMIM Ref. No. 489000), and Dffry (OMIM Ref. No. 400005), are expressed specifically in the testis and their X homologs (Zfx, 314980; Ube1x, 314370; Dffrx, 300072) are not transcribed from the inactive X chromosome. A further 2, Smyc (OMIM Ref. No. 426000) and Uty (OMIM Ref. No. 400009), are ubiquitously expressed and their X homologs (Smcx, 314690; Utx, 300128) escape X inacti-

vation. Ehrmann et al. (1998) identified another gene from this region of the mouse Y chromosome. It was found to encode the highly conserved eukaryotic translation initiation factor eIF- 2- gamma. In the mouse this gene was found to be ubiquitously expressed, to have an X chromosome homolog that maps close to Dmd (OMIM Ref. No. 300377), and to escape X inactivation. The coding regions of the X and Y genes show 86% nucleotide identity and encode the putative products with 98% amino acid identity. Ehrmann et al. (1998) found that the human homolog is located on Xp21 and also escapes X inactivation. No evidence of a Y copy of this gene was found in humans, however. In both humans and mice, Ehrmann et al. (1998) identified autosomal retroposons of EIF2G in both humans and mice and an additional retroposon on the X chromosome in some mouse strains. Ark blot analysis of eutherian and metatherian genomic DNA indicated that X- Y homologs are present in all species tested except in simian primates and kangaroo and that retroposons are common to a wide range of mammals. ('Zoo blots' are Southern blots of genomic DNA from multiple species without regard to gender; 'ark blots' are Southern blots used to compare male and female from multiple species.)

[28538]

[28539] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28540] Ehrmann, I. E.; Ellis, P. S.; Mazeyrat, S.; Duthie, S.; Brock- dorff, N.; Mattei, M. G.; Gavin, M. A.; Affara, N. A.; Brown, G. M.; Simpson, E.; Mitchell, M. J.; Scott, D. M. : Character- ization of genes encoding translation initiation factor eIF- 2- gamma in mouse and human: sex chromosome local- ization, escape from X- inactivation and evolution. Hum. Molec. Genet. 7: 1725- 1737, 1998. ; and

[28541] Gasper, N. J.; Kinzy, T. G.; Scherer, B. J.; Humbelin, M.; Hershey, J. W. B.; Merrick, W. C. : Translation initiation factor eIF- 2: cloning and expression of the human cDNA encoding the.

[28542] Further studies establishing the function and utilities of EIF2S3 are found in John Hopkins OMIM database record ID 300161, and in cited publications listed in Table 5, which are hereby incorporated by reference.Eukaryotic translation initiation factor 5a2 (EIF5A2, Accession NP_065123.1) is another GAM189 target gene, herein designated TARGET GENE. EIF5A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by EIF5A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF5A2 BINDING SITE, designated SEQ ID:8340, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28543] Another function of GAM189 is therefore inhibition of Eukaryotic translation initiation factor 5a2 (EIF5A2, Accession NP_065123.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF5A2.

[28544] ELP3 (Accession NP_060561.3) is another GAM189 target gene, herein designated TARGET GENE. ELP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ELP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ELP3 BINDING SITE, designated SEQ ID:14236, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28545] Another function of GAM189 is therefore inhibition of ELP3 (Accession NP_060561.3) . Accordingly, utilities of

GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELP3.

[28546] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690884.1) is another GAM189 target gene, herein designated TARGET GENE. EMR2 BINDING SITE1 and EMR2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by EMR2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE1 and EMR2 BINDING SITE2, designated SEQ ID:13462 and SEQ ID:17743 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28547] Another function of GAM189 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690884.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[28548] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690884.1) is

another GAM189 target gene, herein designated TARGET GENE. EMR2 BINDING SITE1 and EMR2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by EMR2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE1 and EMR2 BINDING SITE2, designated SEQ ID:17743 and SEQ ID:13462 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28549] Another function of GAM189 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690884.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[28550] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690885.1) is another GAM189 target gene, herein designated TARGET GENE. EMR2 BINDING SITE1 and EMR2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by EMR2, correspond-

ing to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE1 and EMR2 BINDING SITE2, designated SEQ ID:17743 and SEQ ID:13462 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28551] Another function of GAM189 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690885.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[28552] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690880.1) is another GAM189 target gene, herein designated TARGET GENE. EMR2 BINDING SITE1 and EMR2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by EMR2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE1 and EMR2 BINDING SITE2, designated SEQ

ID:13462 and SEQ ID:17743 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28553] Another function of GAM189 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690880.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[28554] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690883.1) is another GAM189 target gene, herein designated TARGET GENE. EMR2 BINDING SITE1 and EMR2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by EMR2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE1 and EMR2 BINDING SITE2, designated SEQ ID:17743 and SEQ ID:17743 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28555] Another function of GAM189 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690883.1) . Accordingly, utilities of GAM189 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with EMR2.

[28556] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690885.1) is another GAM189 target gene, herein designated TARGET GENE. EMR2 BINDING SITE1 and EMR2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by EMR2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE1 and EMR2 BINDING SITE2, designated SEQ ID:13462 and SEQ ID:13462 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28557] Another function of GAM189 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690885.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[28558] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_038475.2) is

another GAM189 target gene, herein designated TARGET GENE. EMR2 BINDING SITE1 and EMR2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by EMR2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE1 and EMR2 BINDING SITE2, designated SEQ ID:17743 and SEQ ID:13462 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28559] Another function of GAM189 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_038475.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[28560] Endonuclease g-like 1 (ENDOGL1, Accession NP_005098.1) is another GAM189 target gene, herein designated TARGET GENE. ENDOGL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ENDOGL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ENDOGL1 BINDING SITE, designated SEQ ID:5031, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28561] Another function of GAM189 is therefore inhibition of Endonuclease g-like 1 (ENDOGL1, Accession NP_005098.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENDOGL1.

[28562] Epha8 (EPHA8, Accession NP_065387.1) is another GAM189 target gene, herein designated TARGET GENE. EPHA8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EPHA8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EPHA8 BINDING SITE, designated SEQ ID:1229, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28563] Another function of GAM189 is therefore inhibition of Epha8 (EPHA8, Accession NP_065387.1), a gene which Eph- related receptor tyrosine kinase A8. Accordingly,

utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPHA8.

[28564] The function of EPHA8 has been established by previous studies. See EPH (EPHA1; 179610) for background on Eph receptors and their ligands, the ephrins. Chan and Watt (1991) identified human and rat DNAs encoding 2 novel members of the EPH subclass of putative receptor protein- tyrosine kinases. Rat cDNA clones encoding EEK (EPH- and ELK- related kinase) were isolated from a brain cDNA library probed with DNA encoding the kinase region of the insulin receptor- related receptor (INSRR; 147671). The EEK protein was predicted to contain all the amino acid residues conserved in the catalytic domains of protein- tyrosine kinases and was most similar to 2 putative receptor protein- tyrosine kinases of the EPH subclass, ELK (EPHB1; 600600) and EPH, showing 69 and 57% identity, respectively. Human genomic DNAs, encoding part of EEK as well as another putative protein tyrosine kinase most similar to ELK (90%) and symbolized ERK (EPHB2; 600997) for ELK- related kinase, were isolated and partially characterized. The novel identity of these 2 EPH-family genes was further supported by Southern blot anal-

ysis and localization to human chromosome 1. In Northern blot analysis of rat RNA, DNAs encoding rat EEK and human ERK hybridized to transcripts most abundant in brain and lung, respectively. These 2 new members of the EPH subclass of receptor protein- tyrosine kinases, EEK and ERK, may therefore have tissue- specific functions distinct from those of the other EPH family members.

[28565] Animal model experiments lend further support to the function of EPHA8. Park et al. (1997) generated mice homozygous for a mutation that disrupts the gene encoding EPHA8, a member of the Eph family of tyrosine proteinase receptors. EphA8 - /- mice developed to term, were fertile, and did not display obvious anatomical or physiologic defects.

[28566] It is appreciated that the abovementioned animal model for EPHA8 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[28567] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28568] Chan, J.; Watt, V. M. : Eek and erk, new members of the eph subclass of receptor protein- tyrosine kinases. Onco-

gene 6: 1057- 1061, 1991. ; and

[28569] Park, S.; Frisen, J.; Barbacid, M. : Aberrant axonal projections in mice lacking EphA8 (Eek) tyrosine protein kinase receptors. EMBO J. 16: 3106- 3114, 1997.

[28570] Further studies establishing the function and utilities of EPHA8 are found in John Hopkins OMIM database record ID 176945, and in cited publications listed in Table 5, which are hereby incorporated by reference.Epiregulin (EREG, Accession NP_001423.1) is another GAM189 target gene, herein designated TARGET GENE. EREG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EREG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EREG BINDING SITE, designated SEQ ID:17956, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28571] Another function of GAM189 is therefore inhibition of Epiregulin (EREG, Accession NP_001423.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EREG.

[28572] Ellis van creveld syndrome (EVC, Accession NP_714928.1) is another GAM189 target gene, herein designated TARGET GENE. EVC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EVC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:18115, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28573] Another function of GAM189 is therefore inhibition of Ellis van creveld syndrome (EVC, Accession NP_714928.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC.

[28574] Ellis van creveld syndrome (EVC, Accession NP_055371.1) is another GAM189 target gene, herein designated TARGET GENE. EVC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EVC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:18115, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28575] Another function of GAM189 is therefore inhibition of Ellis van creveld syndrome (EVC, Accession NP_055371.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC.

[28576] Ecotropic viral integration site 5 (EVI5, Accession NP_005656.2) is another GAM189 target gene, herein designated TARGET GENE. EVI5 BINDING SITE1 and EVI5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by EVI5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVI5 BINDING SITE1 and EVI5 BINDING SITE2, designated SEQ ID:7219 and SEQ ID:11607 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28577] Another function of GAM189 is therefore inhibition of Ecotropic viral integration site 5 (EVI5, Accession

NP_005656.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVI5.

[28578] Enhancer of zeste homolog 1 (drosophila) (EZH1, Accession NP_001982.2) is another GAM189 target gene, herein designated TARGET GENE. EZH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EZH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EZH1 BINDING SITE, designated SEQ ID:14083, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28579] Another function of GAM189 is therefore inhibition of Enhancer of zeste homolog 1 (drosophila) (EZH1, Accession NP_001982.2), a gene which may act in transcriptional regulation and heterochromatin maintenance. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EZH1.

[28580] The function of EZH1 has been established by previous studies. Transcription mapping efforts within chromo-

some 17q21 identified a human homolog of the Drosophila gene 'enhancer of zeste' E(z). In Drosophila, the gene acts as a negative regulator of segment identity genes of the Antennapedia and Bithorax complexes. Abel et al. (1996) reported the full- length protein coding sequence of the human homolog, EZH1, and compared the respective protein sequences in human and Drosophila. EZH1 encodes a protein of 747 amino acids that displays 55% amino acid identity overall (70% similarity) with the Drosophila protein. The strong sequence conservation suggested potential roles for EZH1 in human development as a transcriptional regulator and as a component of protein complexes that stably maintain heterochromatin. EZH1 is expressed as 2 major transcripts in all adult and fetal human tissues surveyed; comparison of cloned cDNAs suggested that alternative splicing may account for at least part of the transcript size differences. Analysis of an EZH1 cDNA revealed an unusual splicing event involving EZH1 and a tandemly linked gene GPR2 (OMIM Ref. No. 600240) and suggested a potential mechanism for modifying the EZH1 protein in the conserved C- terminal domain. The GPR2 gene maps to 17q21.1- q21.3 in the vicinity of the BRCA1 gene (OMIM Ref. No. 113705). See

also EZH2 (OMIM Ref. No. 601573). By FISH, Laible et al. (1999) mapped the mouse Ezh1 gene to chromosome 11.

[28581]

[28582] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28583] Abel, K. J.; Brody, L. C.; Valdes, J. M.; Erdos, M. R.; McKinley, D. R.; Castilla, L. H.; Merajver, S. D.; Couch, F. J.; Friedman, L. S.; Ostermeyer, E. A.; Lynch, E. D.; King, M.-C.; Welcsh, P. L.; Osborne- Lawrence, S.; Spillman, M.; Bowcock, A. M.; Collins, F. S.; Weber, B. L. : Characterization of EZH1, a human homolog of Drosophila enhancer of zeste near BRCA1. Genomics 37: 161- 171, 1996. ; and

[28584] Laible, G.; Haynes, A. R.; Lebersorger, A.; O'Carroll, D.; Mattei, M.- G.; Denny, P.; Brown, S. D. M.; Jenuwein, T. : The murine polycomb- group genes Ezh1 and Ezh2 map close to Hox gene.

[28585] Further studies establishing the function and utilities of EZH1 are found in John Hopkins OMIM database record ID 601674, and in cited publications listed in Table 5, which are hereby incorporated by reference.F11R (Accession NP_653087.1) is another GAM189 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:2664, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28586] Another function of GAM189 is therefore inhibition of F11R (Accession NP_653087.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[28587] F11R (Accession NP_653085.1) is another GAM189 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:2664, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28588] Another function of GAM189 is therefore inhibition of

F11R (Accession NP_653085.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[28589] F11R (Accession NP_653086.1) is another GAM189 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:2664, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28590] Another function of GAM189 is therefore inhibition of F11R (Accession NP_653086.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[28591] F11R (Accession NP_058642.1) is another GAM189 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:2664, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28592] Another function of GAM189 is therefore inhibition of F11R (Accession NP_058642.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[28593] Coagulation factor ii (thrombin) receptor-like 3 (F2RL3, Accession NP_003941.1) is another GAM189 target gene, herein designated TARGET GENE. F2RL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F2RL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F2RL3 BINDING SITE, designated SEQ ID:4234, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28594] Another function of GAM189 is therefore inhibition of Coagulation factor ii (thrombin) receptor-like 3 (F2RL3, Accession NP_003941.1), a gene which Protease- activated receptor 4; G protein- coupled receptor that increases

phosphoinositide hydrolysis. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2RL3.

[28595] The function of F2RL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1) is another GAM189 target gene, herein designated TARGET GENE. F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F3 BINDING SITE, designated SEQ ID:18492, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28596] Another function of GAM189 is therefore inhibition of Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1), a gene which functions in normal hemostasis. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F3.

[28597] The function of F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Coagulation factor v (proaccelerin, labile factor) (F5, Accession NP_000121.1) is another GAM189 target gene, herein designated TARGET GENE. F5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by F5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F5 BINDING SITE, designated SEQ ID:7269, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28598] Another function of GAM189 is therefore inhibition of Coagulation factor v (proaccelerin, labile factor) (F5, Accession NP_000121.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F5.

[28599] Fatty acid binding protein 2, intestinal (FABP2, Accession NP_000125.1) is another GAM189 target gene, herein designated TARGET GENE. FABP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by FABP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FABP2 BINDING SITE, designated SEQ ID:2195, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28600] Another function of GAM189 is therefore inhibition of Fatty acid binding protein 2, intestinal (FABP2, Accession NP_000125.1), a gene which may have a role in dietary fat uptake or processing. and therefore may be associated with Cardiovascular disease and type 2 diabetes. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Cardiovascular disease and type 2 diabetes., and of other diseases and clinical conditions associated with FABP2.

[28601] The function of FABP2 has been established by previous studies. To test the hypothesis that the A54T FABP2 polymorphism is associated with impaired lipid metabolism and cardiovascular disease, Carlsson et al. (2000) compared clinical characteristics and a parental history of cardiovascular disease between 213 sib pairs discordant for the polymorphism. Sibs with an excess of the thr54 allele had higher triglyceride and cholesterol concentrations

than sibs with the ala54 allele. Parents of offspring with the thr/thr and thr/ala genotypes reported an increased prevalence of stroke compared to parents of offspring with the ala/ala genotype. The authors confirmed the association of the FABP2 thr54 allele with increased concentrations of cholesterol and triglycerides in genotype- discordant sib pairs. They also presented novel evidence that genetic variation in the FABP2 gene may increase susceptibility to stroke. To assess whether increased intestinal triglyceride input leads to elevated fasting and postprandial triglycerides in type 2 diabetes (NIDDM), Georgopoulos et al. (2000) studied the ala54- to- thr polymorphism of FABP2, which is associated with increased intestinal input of triglyceride. Of the 287 diabetic patients screened, 108 (37.6%) were heterozygous and 31 (10.8%) were homozygous for the thr54 allele. Mean fasting plasma triglyceride levels in patients with the wild- type (OMIM Ref. No. n = 80), those heterozygous for the thr54 allele (OMIM Ref. No. n = 57), and those homozygous for it (OMIM Ref. No. n = 18) were 2.0 +/- 0.09, 2.7 +/- 0.20, and 3.8 +/- 0.43 mmol/L, respectively. A linear relationship of mean fasting plasma triglyceride levels between the 3 groups was found. After fat ingestion, the postpran-

dial area under the curve of plasma triglyceride and chylomicrons was higher in the thr54/thr54 (n = 6) than in the wild- type (n = 9). The authors concluded that their results support the hypothesis that, in type 2 diabetes, increased intestinal input of triglyceride can lead to elevated fasting and postprandial plasma triglycerides. triglyceride.

[28602]

[28603] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28604] Carlsson, M.; Orho- Melander, M.; Hedenbro, J.; Almgren, P.; Groop, L. C. : The T54 allele of the intestinal fatty acid-binding protein 2 is associated with a parental history of stroke. J. Clin. Endocr. Metab. 85: 2801- 2804, 2000. ; and

[28605] Georgopoulos, A.; Aras, O.; Tsai, M. Y. : Codon- 54 polymorphism of the fatty acid- binding protein 2 gene is associated with elevation of fasting and postprandial triglyceride in type 2.

[28606] Further studies establishing the function and utilities of FABP2 are found in John Hopkins OMIM database record ID 134640, and in cited publications listed in Table 5, which are hereby incorporated by reference.Fanconi ane-

mia, complementation group e (FANCE, Accession NP_068741.1) is another GAM189 target gene, herein designated TARGET GENE. FANCE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCE BINDING SITE, designated SEQ ID:5597, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28607] Another function of GAM189 is therefore inhibition of Fanconi anemia, complementation group e (FANCE, Accession NP_068741.1), a gene which is a possible regulator of lymphocyte and platelet function. and therefore is associated with Fanconi anemia, complementation group e. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Fanconi anemia, complementation group e., and of other diseases and clinical conditions associated with FANCE.

[28608] The function of FANCE has been established by previous studies. A number sign (#) is used with this entry because Fanconi anemia is caused by mutation in 1 of the Fanconi anemia complementation group genes: FANCA (OMIM Ref.

No. 607139), FANCB (OMIM Ref. No. 227660), FANCC (OMIM Ref. No. 227645), FANCD1 (OMIM Ref. No. 605724), FANCD2 (OMIM Ref. No. 227646), FANCE (OMIM Ref. No. 600901), FANCF (OMIM Ref. No. 603467), FANCG (OMIM Ref. No. 602956). The previously designated FANCH complementation group (Joenje et al., 1997) was found by Joenje et al. (2000) to be the same as FANCA. Joenje et al. (1995) presented evidence for a fifth subtype of Fanconi anemia, designated group E. Buchwald (1995) stated that 6 of 31 patients (12.7%) could be classified as group E. The FACE group is defined as being different from groups A (OMIM Ref. No. 227650), B (OMIM Ref. No. 227660), C (OMIM Ref. No. 227645), and D (OMIM Ref. No. 227646) and may itself be heterogeneous.

[28609]

[28610] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28611] Joenje, H.; Lo Ten Foe, J. R.; Oostra, A. B.; van Berkel, C. G. M.; Rooimans, M. A.; Schroeder- Kurth, T.; Wegner, R.- D.; Gille, J. J. P.; Buchwald, M.; Arwert, F. : Classification of Fanconi anemia patients by complementation analysis: evidence for a fifth genetic subtype. Blood 86: 2156- 2160,

1995. ; and

[28612] Buchwald, M. : Complementation groups: one or more per gene? Nature Genet. 11: 228- 230, 1995.

[28613] Further studies establishing the function and utilities of FANCE are found in John Hopkins OMIM database record ID 600901, and in cited publications listed in Table 5, which are hereby incorporated by reference.Fanconi anemia, complementation group f (FANCF, Accession NP_073562.1) is another GAM189 target gene, herein designated TARGET GENE. FANCF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCF BINDING SITE, designated SEQ ID:5816, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28614] Another function of GAM189 is therefore inhibition of Fanconi anemia, complementation group f (FANCF, Accession NP_073562.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCF.

[28615] FAT3 (Accession XP_061871.5) is another GAM189 target

gene, herein designated TARGET GENE. FAT3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FAT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FAT3 BINDING SITE, designated SEQ ID:8236, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28616] Another function of GAM189 is therefore inhibition of FAT3 (Accession XP_061871.5) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAT3.

[28617] FBXW8 (Accession NP_036306.1) is another GAM189 target gene, herein designated TARGET GENE. FBXW8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXW8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXW8 BINDING SITE, designated SEQ ID:11845, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ

ID:246.

[28618] Another function of GAM189 is therefore inhibition of FBXW8 (Accession NP_036306.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW8.

[28619] FBXW8 (Accession NP_699179.2) is another GAM189 target gene, herein designated TARGET GENE. FBXW8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXW8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXW8 BINDING SITE, designated SEQ ID:11845, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28620] Another function of GAM189 is therefore inhibition of FBXW8 (Accession NP_699179.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW8.

[28621] Fc fragment of iga, receptor for (FCAR, Accession NP_579813.1) is another GAM189 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through

FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:17643, SEQ ID:10448 and SEQ ID:10448 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28622] Another function of GAM189 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579813.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[28623] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Ac-

cession NP_579811.1) is another GAM189 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:10448, SEQ ID:10448 and SEQ ID:10448 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28624] Another function of GAM189 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579811.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[28625] The function of FCAR and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Accession NP_579807.1) is another GAM189 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:10448, SEQ ID:3819 and SEQ ID:10448 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28626] Another function of GAM189 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579807.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[28627] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Accession NP_579814.1) is another GAM189 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:17643, SEQ ID:497 and SEQ ID:11291 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28628] Another function of GAM189 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579814.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of

Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[28629] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) is another GAM189 target gene, herein designated TARGET GENE. FER1L4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FER1L4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FER1L4 BINDING SITE, designated SEQ ID:11291, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28630] Another function of GAM189 is therefore inhibition of Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER1L4.

[28631] Fasciculation and elongation protein zeta 1 (zygin i) (FEZ1, Accession NP_072043.1) is another GAM189 target gene,

herein designated TARGET GENE. FEZ1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FEZ1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FEZ1 BINDING SITE, designated SEQ ID:5204, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28632] Another function of GAM189 is therefore inhibition of Fasciculation and elongation protein zeta 1 (zygin i) (FEZ1, Accession NP_072043.1), a gene which Zygin 1; may have a role in axonal outgrowth; has similarity to C. elegans UNC- 76. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEZ1.

[28633] The function of FEZ1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Fibroblast growth factor 5 (FGF5, Accession NP_004455.1) is another GAM189 target gene, herein designated TARGET GENE. FGF5 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by FGF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE, designated SEQ ID:14382, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28634] Another function of GAM189 is therefore inhibition of Fibroblast growth factor 5 (FGF5, Accession NP_004455.1), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5.

[28635] The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.1.Fibroblast growth factor 5 (FGF5, Accession NP_149134.1) is another GAM189 target gene, herein designated TARGET GENE. FGF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of FGF5 BINDING SITE, designated SEQ ID:14382, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28636] Another function of GAM189 is therefore inhibition of Fibroblast growth factor 5 (FGF5, Accession NP_149134.1), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5.

[28637] The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.1.Four and a half lim domains 2 (FHL2, Accession NP_001441.2) is another GAM189 target gene, herein designated TARGET GENE. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FHL2 BINDING SITE, designated SEQ ID:16589, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ

ID:246.

[28638] Another function of GAM189 is therefore inhibition of Four and a half lim domains 2 (FHL2, Accession NP_001441.2), a gene which Contains four LIM domains and an additional zinc finger. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHL2.

[28639] The function of FHL2 has been established by previous studies. LIM proteins contain a highly conserved double zinc finger motif called the LIM domain. By searching sequence databases with a partial human SLIM1 (FHL1; 300163) cDNA, Morgan and Madgwick (1996) identified partial SLIM3 cDNAs. Genini et al. (1997) used subtractive cloning to isolate a gene that is downregulated during transformation of normal myoblasts to rhabdomyosarcoma cells. The gene, termed DRAL for 'down- regulated in rhabdomyosarcoma LIM protein,' encodes a 279- amino acid polypeptide with an observed mass of 32 kD. The protein sequence contains 4 complete LIM domains and the second half of a fifth LIM domain. DRAL appears to be a member of the LIM- only class of proteins, which consist primarily of LIM domains and little else. Southern blotting revealed a single- copy gene that is conserved among

vertebrates. Northern blotting revealed that the DRAL gene is expressed at highest levels in heart and ovary, and at lower levels in skeletal muscle, prostate, testis, small intestine, and colon. Results of Northern blotting of tumor cell lines suggested to Genini et al. (1997) that this gene may be downregulated during transformation of a variety of cell types. Genini et al. (1997) used in situ hybridization to map the human FHL2 gene to 2q12- q14. By fluorescence in situ hybridization, Chan et al. (1998) mapped the FHL2 gene to 2q12- q13. Using the yeast 2- hybrid system, Tanahashi and Tabira (2000) screened for proteins interacting with an Alzheimer disease gene, presenilin- 2 (OMIM Ref. No. 600759), and cloned DRAL. DRAL interacted with a hydrophilic loop region (amino acids 269- 298) in the endoproteolytic N- terminal fragment of PS2, but not that of PS1 (OMIM Ref. No. 104311), although residues 269 to 298 of PS2 and the corresponding PS1 sequence differ by only 3 amino acids. Each of 9 PS2 point mutations within a region from residues 275 to 296 abolished the binding. The in vitro interaction was confirmed by affinity column assay and the physiologic interactions between endogenous PS2 and DRAL by coimmunoprecipitation from human lung fibroblast MRC5 cells. The au-

thors suggested that DRAL functions as a link between PS2 and an intracellular signaling pathway.

[28640]

[28641] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28642] Genini, M.; Schwalbe, P.; Scholl, F. A.; Remppis, A.; Mattei, M.- G.; Schafer, B. W. : Subtractive cloning and characterization of DRAL, a novel LIM- domain protein down- regulated in rhabdomyosarcoma. DNA Cell Biol. 16: 433- 442, 1997. ; and

[28643] Tanahashi, H.; Tabira, T. : Alzheimer's disease- associated presenilin 2 interacts with DRAL, an LIM- domain protein. Hum. Molec. Genet. 9: 2281- 2289, 2000.

[28644] Further studies establishing the function and utilities of FHL2 are found in John Hopkins OMIM database record ID 602633, and in cited publications listed in Table 5, which are hereby incorporated by reference.FISH (Accession NP_055446.1) is another GAM189 target gene, herein designated TARGET GENE. FISH BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FISH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FISH BINDING SITE, designated SEQ ID:13261, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28645] Another function of GAM189 is therefore inhibition of FISH (Accession NP_055446.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FISH.

[28646] Fk506 binding protein 9, 63 kda (FKBP9, Accession NP_009201.1) is another GAM189 target gene, herein designated TARGET GENE. FKBP9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FKBP9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FKBP9 BINDING SITE, designated SEQ ID:7851, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28647] Another function of GAM189 is therefore inhibition of Fk506 binding protein 9, 63 kda (FKBP9, Accession NP_009201.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with FKBP9.

[28648] FLJ00001 (Accession XP_088525.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ00001 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ00001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ00001 BINDING SITE, designated SEQ ID:14844, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28649] Another function of GAM189 is therefore inhibition of FLJ00001 (Accession XP_088525.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00001.

[28650] FLJ00060 (Accession XP_028154.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ00060 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ00060, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ00060 BINDING SITE, designated SEQ ID:11528, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28651] Another function of GAM189 is therefore inhibition of FLJ00060 (Accession XP_028154.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00060.

[28652] FLJ10101 (Accession NP_078994.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ10101 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10101 BINDING SITE, designated SEQ ID:9189, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28653] Another function of GAM189 is therefore inhibition of FLJ10101 (Accession NP_078994.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10101.

[28654] FLJ10232 (Accession NP_060503.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ10232 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10232, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10232 BINDING SITE, designated SEQ ID:19236, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28655] Another function of GAM189 is therefore inhibition of FLJ10232 (Accession NP_060503.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10232.

[28656] FLJ10298 (Accession NP_060520.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ10298 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10298, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10298 BINDING SITE, designated SEQ ID:2615, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28657] Another function of GAM189 is therefore inhibition of FLJ10298 (Accession NP_060520.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10298.

[28658] FLJ10346 (Accession NP_060535.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ10346 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10346 BINDING SITE, designated SEQ ID:19219, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28659] Another function of GAM189 is therefore inhibition of FLJ10346 (Accession NP_060535.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10346.

[28660] FLJ10520 (Accession NP_060594.2) is another GAM189

target gene, herein designated TARGET GENE. FLJ10520 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10520, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10520 BINDING SITE, designated SEQ ID:4272, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28661] Another function of GAM189 is therefore inhibition of FLJ10520 (Accession NP_060594.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10520.

[28662] FLJ10535 (Accession NP_060599.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ10535 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10535, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10535 BINDING SITE, designated SEQ ID:9543, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[28663] Another function of GAM189 is therefore inhibition of FLJ10535 (Accession NP_060599.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10535.

[28664] FLJ10560 (Accession NP_060608.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ10560 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10560, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10560 BINDING SITE, designated SEQ ID:15591, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28665] Another function of GAM189 is therefore inhibition of FLJ10560 (Accession NP_060608.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10560.

[28666] FLJ10713 (Accession NP_060659.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ10713

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10713, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10713 BINDING SITE, designated SEQ ID:7909, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28667] Another function of GAM189 is therefore inhibition of FLJ10713 (Accession NP_060659.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10713.

[28668] FLJ10846 (Accession NP_060711.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ10846 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10846, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10846 BINDING SITE, designated SEQ ID:11528, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28669] Another function of GAM189 is therefore inhibition of FLJ10846 (Accession NP_060711.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10846.

[28670] FLJ10847 (Accession NP_060712.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ10847 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10847, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10847 BINDING SITE, designated SEQ ID:19357, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28671] Another function of GAM189 is therefore inhibition of FLJ10847 (Accession NP_060712.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10847.

[28672] FLJ10922 (Accession NP_060743.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ10922 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ10922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10922 BINDING SITE, designated SEQ ID:18818, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28673] Another function of GAM189 is therefore inhibition of FLJ10922 (Accession NP_060743.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10922.

[28674] FLJ11323 (Accession NP_060860.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ11323 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ11323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11323 BINDING SITE, designated SEQ ID:2044, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28675] Another function of GAM189 is therefore inhibition of

FLJ11323 (Accession NP_060860.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11323.

[28676] FLJ11467 (Accession NP_079239.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ11467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11467 BINDING SITE, designated SEQ ID:834, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28677] Another function of GAM189 is therefore inhibition of FLJ11467 (Accession NP_079239.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11467.

[28678] FLJ11710 (Accession NP_079122.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ11710 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11710, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11710 BINDING SITE, designated SEQ ID:9688, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28679] Another function of GAM189 is therefore inhibition of FLJ11710 (Accession NP_079122.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11710.

[28680] FLJ11715 (Accession NP_078840.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ11715 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11715, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11715 BINDING SITE, designated SEQ ID:3305, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28681] Another function of GAM189 is therefore inhibition of FLJ11715 (Accession NP_078840.1) . Accordingly, utilities

of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11715.

[28682] FLJ11800 (Accession NP_079250.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ11800 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11800, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11800 BINDING SITE, designated SEQ ID:10847, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28683] Another function of GAM189 is therefore inhibition of FLJ11800 (Accession NP_079250.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11800.

[28684] FLJ12076 (Accession NP_079463.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ12076 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12076, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12076 BINDING SITE, designated SEQ ID:8886, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28685] Another function of GAM189 is therefore inhibition of FLJ12076 (Accession NP_079463.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12076.

[28686] FLJ12363 (Accession NP_115543.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ12363 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12363, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12363 BINDING SITE, designated SEQ ID:17722, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28687] Another function of GAM189 is therefore inhibition of FLJ12363 (Accession NP_115543.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12363.

[28688] FLJ12572 (Accession NP_075056.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ12572 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ12572, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12572 BINDING SITE, designated SEQ ID:17515, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28689] Another function of GAM189 is therefore inhibition of FLJ12572 (Accession NP_075056.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12572.

[28690] FLJ12586 (Accession NP_078896.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ12586 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ12586, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ12586 BINDING SITE, designated SEQ ID:10410, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28691] Another function of GAM189 is therefore inhibition of FLJ12586 (Accession NP_078896.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12586.

[28692] FLJ12649 (Accession XP_291344.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ12649 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12649, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12649 BINDING SITE, designated SEQ ID:3686, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28693] Another function of GAM189 is therefore inhibition of FLJ12649 (Accession XP_291344.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ12649.

[28694] FLJ12687 (Accession NP_079193.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ12687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12687 BINDING SITE, designated SEQ ID:3324, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28695] Another function of GAM189 is therefore inhibition of FLJ12687 (Accession NP_079193.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12687.

[28696] FLJ12747 (Accession XP_290972.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ12747 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12747, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ12747 BINDING SITE, designated SEQ ID:10683, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28697] Another function of GAM189 is therefore inhibition of FLJ12747 (Accession XP_290972.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12747.

[28698] FLJ12787 (Accession NP_115551.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ12787 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12787, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12787 BINDING SITE, designated SEQ ID:14839, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28699] Another function of GAM189 is therefore inhibition of FLJ12787 (Accession NP_115551.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12787.

[28700] FLJ12800 (Accession NP_075054.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ12800 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12800, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12800 BINDING SITE, designated SEQ ID:4261, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28701] Another function of GAM189 is therefore inhibition of FLJ12800 (Accession NP_075054.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12800.

[28702] FLJ12888 (Accession NP_079221.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ12888 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12888, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12888 BINDING SITE, designated SEQ ID:17723, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28703] Another function of GAM189 is therefore inhibition of FLJ12888 (Accession NP_079221.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12888.

[28704] FLJ12903 (Accession NP_073590.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ12903 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12903, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12903 BINDING SITE, designated SEQ ID:10224, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28705] Another function of GAM189 is therefore inhibition of FLJ12903 (Accession NP_073590.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12903.

[28706] FLJ12960 (Accession NP_078914.1) is another GAM189

target gene, herein designated TARGET GENE. FLJ12960 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12960, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12960 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28707] Another function of GAM189 is therefore inhibition of FLJ12960 (Accession NP_078914.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12960.

[28708] FLJ12973 (Accession NP_079184.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ12973 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12973, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12973 BINDING SITE, designated SEQ ID:5230, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[28709] Another function of GAM189 is therefore inhibition of FLJ12973 (Accession NP_079184.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12973.

[28710] FLJ12975 (Accession NP_079085.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ12975 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12975 BINDING SITE, designated SEQ ID:2409, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28711] Another function of GAM189 is therefore inhibition of FLJ12975 (Accession NP_079085.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12975.

[28712] FLJ12986 (Accession XP_290685.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ12986

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12986, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12986 BINDING SITE, designated SEQ ID:6037, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28713] Another function of GAM189 is therefore inhibition of FLJ12986 (Accession XP_290685.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12986.

[28714] FLJ13072 (Accession XP_117117.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ13072 BINDING SITE1 and FLJ13072 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ13072, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13072 BINDING SITE1 and FLJ13072 BINDING SITE2, designated SEQ ID:13729 and SEQ ID:2223 respectively, to the nucleotide sequence of

GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28715] Another function of GAM189 is therefore inhibition of FLJ13072 (Accession XP_117117.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13072.

[28716] FLJ13114 (Accession NP_078817.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ13114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13114 BINDING SITE, designated SEQ ID:11919, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28717] Another function of GAM189 is therefore inhibition of FLJ13114 (Accession NP_078817.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13114.

[28718] FLJ13197 (Accession NP_078890.1) is another GAM189

target gene, herein designated TARGET GENE. FLJ13197 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13197, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13197 BINDING SITE, designated SEQ ID:8231, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28719] Another function of GAM189 is therefore inhibition of FLJ13197 (Accession NP_078890.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13197.

[28720] FLJ13352 (Accession NP_078868.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ13352 BINDING SITE1 and FLJ13352 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ13352, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13352 BINDING SITE1 and FLJ13352 BINDING SITE2, designated SEQ ID:13318 and

SEQ ID:10493 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28721] Another function of GAM189 is therefore inhibition of FLJ13352 (Accession NP_078868.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13352.

[28722] FLJ13456 (Accession XP_038291.5) is another GAM189 target gene, herein designated TARGET GENE. FLJ13456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13456 BINDING SITE, designated SEQ ID:8163, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28723] Another function of GAM189 is therefore inhibition of FLJ13456 (Accession XP_038291.5) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13456.

[28724] FLJ13910 (Accession NP_073617.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ13910 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13910, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13910 BINDING SITE, designated SEQ ID:7691, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28725] Another function of GAM189 is therefore inhibition of FLJ13910 (Accession NP_073617.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13910.

[28726] FLJ13984 (Accession NP_079046.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ13984 BINDING SITE1 and FLJ13984 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ13984, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13984 BINDING SITE1 and

FLJ13984 BINDING SITE2, designated SEQ ID:10809 and SEQ ID:4819 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28727] Another function of GAM189 is therefore inhibition of FLJ13984 (Accession NP_079046.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13984.

[28728] FLJ14100 (Accession NP_079301.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ14100 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14100, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14100 BINDING SITE, designated SEQ ID:12143, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28729] Another function of GAM189 is therefore inhibition of FLJ14100 (Accession NP_079301.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ14100.

[28730] FLJ14260 (Accession NP_079303.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ14260 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14260, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14260 BINDING SITE, designated SEQ ID:921, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28731] Another function of GAM189 is therefore inhibition of FLJ14260 (Accession NP_079303.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14260.

[28732] FLJ14351 (Accession NP_079008.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ14351 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14351, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ14351 BINDING SITE, designated SEQ ID:8586, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28733] Another function of GAM189 is therefore inhibition of FLJ14351 (Accession NP_079008.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14351.

[28734] FLJ14442 (Accession NP_116174.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ14442 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14442 BINDING SITE, designated SEQ ID:16259, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28735] Another function of GAM189 is therefore inhibition of FLJ14442 (Accession NP_116174.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14442.

[28736] FLJ14803 (Accession NP_116231.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ14803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14803 BINDING SITE, designated SEQ ID:939, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28737] Another function of GAM189 is therefore inhibition of FLJ14803 (Accession NP_116231.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14803.

[28738] FLJ14957 (Accession NP_116255.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ14957 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14957, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14957 BINDING SITE, designated SEQ ID:13527, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28739] Another function of GAM189 is therefore inhibition of FLJ14957 (Accession NP_116255.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14957.

[28740] FLJ20045 (Accession NP_060108.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20045 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20045 BINDING SITE, designated SEQ ID:12557, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28741] Another function of GAM189 is therefore inhibition of FLJ20045 (Accession NP_060108.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20045.

[28742] FLJ20070 (Accession NP_060122.1) is another GAM189

target gene, herein designated TARGET GENE. FLJ20070 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20070, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20070 BINDING SITE, designated SEQ ID:7530, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28743] Another function of GAM189 is therefore inhibition of FLJ20070 (Accession NP_060122.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20070.

[28744] FLJ20079 (Accession NP_060126.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20079 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20079, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20079 BINDING SITE, designated SEQ ID:14265, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[28745] Another function of GAM189 is therefore inhibition of FLJ20079 (Accession NP_060126.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20079.

[28746] FLJ20095 (Accession NP_060136.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20095 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20095, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20095 BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28747] Another function of GAM189 is therefore inhibition of FLJ20095 (Accession NP_060136.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20095.

[28748] FLJ20136 (Accession NP_060154.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20136

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20136 BINDING SITE, designated SEQ ID:4536, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28749] Another function of GAM189 is therefore inhibition of FLJ20136 (Accession NP_060154.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20136.

[28750] FLJ20147 (Accession NP_060157.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20147 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20147, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20147 BINDING SITE, designated SEQ ID:2624, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28751] Another function of GAM189 is therefore inhibition of FLJ20147 (Accession NP_060157.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20147.

[28752] FLJ20245 (Accession NP_060193.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20245 BINDING SITE1 and FLJ20245 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ20245, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20245 BINDING SITE1 and FLJ20245 BINDING SITE2, designated SEQ ID:5275 and SEQ ID:8581 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28753] Another function of GAM189 is therefore inhibition of FLJ20245 (Accession NP_060193.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20245.

[28754] FLJ20257 (Accession NP_062552.1) is another GAM189

target gene, herein designated TARGET GENE. FLJ20257 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20257, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20257 BINDING SITE, designated SEQ ID:7206, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28755] Another function of GAM189 is therefore inhibition of FLJ20257 (Accession NP_062552.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20257.

[28756] FLJ20344 (Accession NP_060246.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20344 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20344, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20344 BINDING SITE, designated SEQ ID:4079, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[28757] Another function of GAM189 is therefore inhibition of FLJ20344 (Accession NP_060246.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20344.

[28758] FLJ20359 (Accession NP_060251.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20359 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20359, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20359 BINDING SITE, designated SEQ ID:11024, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28759] Another function of GAM189 is therefore inhibition of FLJ20359 (Accession NP_060251.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20359.

[28760] FLJ20375 (Accession NP_060264.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ20375

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20375, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20375 BINDING SITE, designated SEQ ID:9357, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28761] Another function of GAM189 is therefore inhibition of FLJ20375 (Accession NP_060264.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20375.

[28762] FLJ20511 (Accession NP_060323.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20511 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20511, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20511 BINDING SITE, designated SEQ ID:17759, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28763] Another function of GAM189 is therefore inhibition of FLJ20511 (Accession NP_060323.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20511.

[28764] FLJ20527 (Accession NP_060333.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20527 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20527, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20527 BINDING SITE, designated SEQ ID:17075, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28765] Another function of GAM189 is therefore inhibition of FLJ20527 (Accession NP_060333.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20527.

[28766] FLJ20671 (Accession NP_060394.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20671 BINDING SITE1 and FLJ20671 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by FLJ20671, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20671 BINDING SITE1 and FLJ20671 BINDING SITE2, designated SEQ ID:16491 and SEQ ID:13041 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28767] Another function of GAM189 is therefore inhibition of FLJ20671 (Accession NP_060394.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20671.

[28768] FLJ20700 (Accession NP_060402.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20700 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20700, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20700 BINDING SITE, designated SEQ ID:18943, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[28769] Another function of GAM189 is therefore inhibition of FLJ20700 (Accession NP_060402.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20700.

[28770] FLJ20813 (Accession NP_060431.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ20813 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20813 BINDING SITE, designated SEQ ID:10574, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28771] Another function of GAM189 is therefore inhibition of FLJ20813 (Accession NP_060431.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20813.

[28772] FLJ21128 (Accession NP_079359.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ21128

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21128 BINDING SITE, designated SEQ ID:17516, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28773] Another function of GAM189 is therefore inhibition of FLJ21128 (Accession NP_079359.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21128.

[28774] FLJ21603 (Accession NP_079038.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ21603 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21603 BINDING SITE, designated SEQ ID:15047, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28775] Another function of GAM189 is therefore inhibition of FLJ21603 (Accession NP_079038.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21603.

[28776] FLJ21673 (Accession NP_112160.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ21673 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ21673, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21673 BINDING SITE, designated SEQ ID:1435, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28777] Another function of GAM189 is therefore inhibition of FLJ21673 (Accession NP_112160.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21673.

[28778] FLJ21777 (Accession NP_115585.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ21777 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ21777, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21777 BINDING SITE, designated SEQ ID:4203, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28779] Another function of GAM189 is therefore inhibition of FLJ21777 (Accession NP_115585.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21777.

[28780] FLJ22329 (Accession NP_078932.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ22329 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22329 BINDING SITE, designated SEQ ID:9543, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28781] Another function of GAM189 is therefore inhibition of

FLJ22329 (Accession NP_078932.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22329.

[28782] FLJ22531 (Accession NP_078926.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ22531 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22531, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22531 BINDING SITE, designated SEQ ID:5636, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28783] Another function of GAM189 is therefore inhibition of FLJ22531 (Accession NP_078926.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22531.

[28784] FLJ22794 (Accession NP_071357.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ22794 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22794, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22794 BINDING SITE, designated SEQ ID:5559, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28785] Another function of GAM189 is therefore inhibition of FLJ22794 (Accession NP_071357.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22794.

[28786] FLJ22965 (Accession NP_071384.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ22965 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22965, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22965 BINDING SITE, designated SEQ ID:2808, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28787] Another function of GAM189 is therefore inhibition of FLJ22965 (Accession NP_071384.1) . Accordingly, utilities

of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22965.

[28788] FLJ23024 (Accession NP_079212.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ23024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23024 BINDING SITE, designated SEQ ID:9682, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28789] Another function of GAM189 is therefore inhibition of FLJ23024 (Accession NP_079212.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23024.

[28790] FLJ23053 (Accession NP_075058.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ23053 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23053, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23053 BINDING SITE, designated SEQ ID:8693, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28791] Another function of GAM189 is therefore inhibition of FLJ23053 (Accession NP_075058.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23053.

[28792] FLJ23186 (Accession NP_078892.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ23186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23186 BINDING SITE, designated SEQ ID:1340, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28793] Another function of GAM189 is therefore inhibition of FLJ23186 (Accession NP_078892.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ23186.

[28794] FLJ23263 (Accession NP_079391.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ23263 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ23263, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23263 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28795] Another function of GAM189 is therefore inhibition of FLJ23263 (Accession NP_079391.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23263.

[28796] FLJ23356 (Accession NP_115613.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ23356 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ23356 BINDING SITE, designated SEQ ID:12273, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28797] Another function of GAM189 is therefore inhibition of FLJ23356 (Accession NP_115613.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23356.

[28798] FLJ23392 (Accession NP_079060.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ23392 BINDING SITE1 through FLJ23392 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ23392, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23392 BINDING SITE1 through FLJ23392 BINDING SITE3, designated SEQ ID:5554, SEQ ID:9148 and SEQ ID:20052 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28799] Another function of GAM189 is therefore inhibition of FLJ23392 (Accession NP_079060.1) . Accordingly, utilities

of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23392.

[28800] FLJ23416 (Accession NP_115614.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ23416 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23416, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23416 BINDING SITE, designated SEQ ID:2152, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28801] Another function of GAM189 is therefore inhibition of FLJ23416 (Accession NP_115614.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23416.

[28802] FLJ23556 (Accession NP_079156.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ23556 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23556, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23556 BINDING SITE, designated SEQ ID:17969, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28803] Another function of GAM189 is therefore inhibition of FLJ23556 (Accession NP_079156.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23556.

[28804] FLJ23563 (Accession XP_041701.4) is another GAM189 target gene, herein designated TARGET GENE. FLJ23563 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23563 BINDING SITE, designated SEQ ID:15048, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28805] Another function of GAM189 is therefore inhibition of FLJ23563 (Accession XP_041701.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ23563.

[28806] FLJ23867 (Accession NP_689875.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ23867 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23867, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23867 BINDING SITE, designated SEQ ID:1374, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28807] Another function of GAM189 is therefore inhibition of FLJ23867 (Accession NP_689875.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23867.

[28808] FLJ25416 (Accession NP_659455.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ25416 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ25416, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ25416 BINDING SITE, designated SEQ ID:16915, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28809] Another function of GAM189 is therefore inhibition of FLJ25416 (Accession NP_659455.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25416.

[28810] FLJ25795 (Accession NP_689633.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ25795 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25795, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25795 BINDING SITE, designated SEQ ID:934, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28811] Another function of GAM189 is therefore inhibition of FLJ25795 (Accession NP_689633.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ25795.

[28812] FLJ30507 (Accession NP_694555.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ30507 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ30507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30507 BINDING SITE, designated SEQ ID:17957, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28813] Another function of GAM189 is therefore inhibition of FLJ30507 (Accession NP_694555.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30507.

[28814] FLJ30532 (Accession NP_653325.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ30532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ30532 BINDING SITE, designated SEQ ID:19834, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28815] Another function of GAM189 is therefore inhibition of FLJ30532 (Accession NP_653325.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30532.

[28816] FLJ31139 (Accession NP_775928.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ31139 BINDING SITE1 through FLJ31139 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ31139, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31139 BINDING SITE1 through FLJ31139 BINDING SITE3, designated SEQ ID:18868, SEQ ID:15200 and SEQ ID:3952 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28817] Another function of GAM189 is therefore inhibition of FLJ31139 (Accession NP_775928.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ31139.

[28818] FLJ31153 (Accession NP_653201.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ31153 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31153, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31153 BINDING SITE, designated SEQ ID:7373, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28819] Another function of GAM189 is therefore inhibition of FLJ31153 (Accession NP_653201.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31153.

[28820] FLJ31166 (Accession NP_694567.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ31166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ31166 BINDING SITE, designated SEQ ID:19301, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28821] Another function of GAM189 is therefore inhibition of FLJ31166 (Accession NP_694567.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31166.

[28822] FLJ31338 (Accession NP_689682.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ31338 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31338, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31338 BINDING SITE, designated SEQ ID:1672, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28823] Another function of GAM189 is therefore inhibition of FLJ31338 (Accession NP_689682.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ31338.

[28824] FLJ31384 (Accession NP_689685.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ31384 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31384, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31384 BINDING SITE, designated SEQ ID:14326, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28825] Another function of GAM189 is therefore inhibition of FLJ31384 (Accession NP_689685.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31384.

[28826] FLJ31393 (Accession NP_694569.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ31393 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ31393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ31393 BINDING SITE, designated SEQ ID:9670, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28827] Another function of GAM189 is therefore inhibition of FLJ31393 (Accession NP_694569.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31393.

[28828] FLJ31401 (Accession NP_689877.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ31401 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31401, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31401 BINDING SITE, designated SEQ ID:16543, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28829] Another function of GAM189 is therefore inhibition of FLJ31401 (Accession NP_689877.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31401.

[28830] FLJ32096 (Accession NP_776156.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ32096 BINDING SITE1 and FLJ32096 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ32096, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32096 BINDING SITE1 and FLJ32096 BINDING SITE2, designated SEQ ID:1025 and SEQ ID:16043 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28831] Another function of GAM189 is therefore inhibition of FLJ32096 (Accession NP_776156.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32096.

[28832] FLJ32130 (Accession NP_689671.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ32130 BINDING SITE1 through FLJ32130 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ32130, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32130 BINDING SITE1 through FLJ32130 BINDING SITE3, designated SEQ ID:4630, SEQ ID:15049 and SEQ ID:2061 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28833] Another function of GAM189 is therefore inhibition of FLJ32130 (Accession NP_689671.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32130.

[28834] FLJ32206 (Accession NP_689710.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ32206 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32206, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32206 BINDING SITE, designated SEQ ID:3860, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28835] Another function of GAM189 is therefore inhibition of FLJ32206 (Accession NP_689710.1) . Accordingly, utilities

of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32206.

[28836] FLJ32334 (Accession NP_653166.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ32334 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32334 BINDING SITE, designated SEQ ID:8493, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28837] Another function of GAM189 is therefore inhibition of FLJ32334 (Accession NP_653166.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32334.

[28838] FLJ32499 (Accession NP_653208.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ32499 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32499, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32499 BINDING SITE, designated SEQ ID:4681, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28839] Another function of GAM189 is therefore inhibition of FLJ32499 (Accession NP_653208.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32499.

[28840] FLJ32731 (Accession NP_689632.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ32731 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32731, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32731 BINDING SITE, designated SEQ ID:16099, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28841] Another function of GAM189 is therefore inhibition of FLJ32731 (Accession NP_689632.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ32731.

[28842] FLJ32803 (Accession NP_694584.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ32803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32803 BINDING SITE, designated SEQ ID:1856, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28843] Another function of GAM189 is therefore inhibition of FLJ32803 (Accession NP_694584.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32803.

[28844] FLJ32865 (Accession NP_653214.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ32865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ32865 BINDING SITE, designated SEQ ID:2146, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28845] Another function of GAM189 is therefore inhibition of FLJ32865 (Accession NP_653214.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865.

[28846] FLJ32894 (Accession NP_653268.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ32894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32894 BINDING SITE, designated SEQ ID:7467, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28847] Another function of GAM189 is therefore inhibition of FLJ32894 (Accession NP_653268.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ32894.

[28848] FLJ32932 (Accession NP_690873.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ32932 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32932, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32932 BINDING SITE, designated SEQ ID:9555, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28849] Another function of GAM189 is therefore inhibition of FLJ32932 (Accession NP_690873.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32932.

[28850] FLJ33505 (Accession NP_689530.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ33505 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33505, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ33505 BINDING SITE, designated SEQ ID:13693, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28851] Another function of GAM189 is therefore inhibition of FLJ33505 (Accession NP_689530.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33505.

[28852] FLJ33655 (Accession NP_775912.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ33655 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33655, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33655 BINDING SITE, designated SEQ ID:16113, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28853] Another function of GAM189 is therefore inhibition of FLJ33655 (Accession NP_775912.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33655.

[28854] FLJ34817 (Accession NP_689516.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ34817 BINDING SITE1 and FLJ34817 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ34817, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34817 BINDING SITE1 and FLJ34817 BINDING SITE2, designated SEQ ID:4004 and SEQ ID:7075 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28855] Another function of GAM189 is therefore inhibition of FLJ34817 (Accession NP_689516.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34817.

[28856] FLJ34922 (Accession NP_689483.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ34922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ34922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ34922 BINDING SITE, designated SEQ ID:18132, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28857] Another function of GAM189 is therefore inhibition of FLJ34922 (Accession NP_689483.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34922.

[28858] FLJ34969 (Accession XP_114353.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ34969 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ34969, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34969 BINDING SITE, designated SEQ ID:581, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28859] Another function of GAM189 is therefore inhibition of FLJ34969 (Accession XP_114353.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ34969.

[28860] FLJ35105 (Accession NP_689890.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ35105 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ35105, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35105 BINDING SITE, designated SEQ ID:18938, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28861] Another function of GAM189 is therefore inhibition of FLJ35105 (Accession NP_689890.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35105.

[28862] FLJ35681 (Accession NP_787096.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ35681 BINDING SITE1 and FLJ35681 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ35681, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of FLJ35681 BINDING SITE1 and FLJ35681 BINDING SITE2, designated SEQ ID:1653 and SEQ ID:11521 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28863] Another function of GAM189 is therefore inhibition of FLJ35681 (Accession NP_787096.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35681.

[28864] FLJ35848 (Accession XP_290755.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ35848 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35848, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35848 BINDING SITE, designated SEQ ID:14986, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28865] Another function of GAM189 is therefore inhibition of FLJ35848 (Accession XP_290755.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ35848.

[28866] FLJ36445 (Accession NP_694965.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ36445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36445 BINDING SITE, designated SEQ ID:2147, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28867] Another function of GAM189 is therefore inhibition of FLJ36445 (Accession NP_694965.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36445.

[28868] FLJ37045 (Accession NP_787085.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ37045 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ37045 BINDING SITE, designated SEQ ID:9497, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28869] Another function of GAM189 is therefore inhibition of FLJ37045 (Accession NP_787085.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37045.

[28870] FLJ37078 (Accession NP_694588.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ37078 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ37078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37078 BINDING SITE, designated SEQ ID:11528, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28871] Another function of GAM189 is therefore inhibition of FLJ37078 (Accession NP_694588.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ37078.

[28872] FLJ37433 (Accession NP_848612.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ37433 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37433, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37433 BINDING SITE, designated SEQ ID:8582, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28873] Another function of GAM189 is therefore inhibition of FLJ37433 (Accession NP_848612.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37433.

[28874] FLJ37543 (Accession NP_775938.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ37543 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37543, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ37543 BINDING SITE, designated SEQ ID:5495, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28875] Another function of GAM189 is therefore inhibition of FLJ37543 (Accession NP_775938.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37543.

[28876] FLJ38101 (Accession NP_694993.2) is another GAM189 target gene, herein designated TARGET GENE. FLJ38101 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38101 BINDING SITE, designated SEQ ID:5589, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28877] Another function of GAM189 is therefore inhibition of FLJ38101 (Accession NP_694993.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38101.

[28878] FLJ38149 (Accession XP_091919.5) is another GAM189 target gene, herein designated TARGET GENE. FLJ38149 BINDING SITE1 through FLJ38149 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ38149, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38149 BINDING SITE1 through FLJ38149 BINDING SITE3, designated SEQ ID:18971, SEQ ID:9373 and SEQ ID:15044 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28879] Another function of GAM189 is therefore inhibition of FLJ38149 (Accession XP_091919.5) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38149.

[28880] FLJ38281 (Accession NP_689814.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ38281 BINDING SITE1 and FLJ38281 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38281, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38281 BINDING SITE1 and FLJ38281 BINDING SITE2, designated SEQ ID:6885 and SEQ ID:9492 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28881] Another function of GAM189 is therefore inhibition of FLJ38281 (Accession NP_689814.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38281.

[28882] FLJ38607 (Accession NP_689867.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ38607 BINDING SITE1 and FLJ38607 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38607, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38607 BINDING SITE1 and FLJ38607 BINDING SITE2, designated SEQ ID:16688 and SEQ ID:7382 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28883] Another function of GAM189 is therefore inhibition of FLJ38607 (Accession NP_689867.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38607.

[28884] FLJ38792 (Accession NP_848615.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ38792 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38792, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38792 BINDING SITE, designated SEQ ID:14861, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28885] Another function of GAM189 is therefore inhibition of FLJ38792 (Accession NP_848615.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38792.

[28886] FLJ38819 (Accession NP_665872.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ38819 BINDING SITE1 and FLJ38819 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by FLJ38819, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38819 BINDING SITE1 and FLJ38819 BINDING SITE2, designated SEQ ID:18642 and SEQ ID:9791 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28887] Another function of GAM189 is therefore inhibition of FLJ38819 (Accession NP_665872.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38819.

[28888] FLJ38991 (Accession NP_776188.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ38991 BINDING SITE1 and FLJ38991 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38991, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38991 BINDING SITE1 and FLJ38991 BINDING SITE2, designated SEQ ID:10356 and

SEQ ID:14236 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28889] Another function of GAM189 is therefore inhibition of FLJ38991 (Accession NP_776188.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38991.

[28890] FLJ39415 (Accession NP_775952.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ39415 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39415, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39415 BINDING SITE, designated SEQ ID:11673, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28891] Another function of GAM189 is therefore inhibition of FLJ39415 (Accession NP_775952.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39415.

[28892] FLJ39599 (Accession NP_776164.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ39599 BINDING SITE1 and FLJ39599 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ39599, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39599 BINDING SITE1 and FLJ39599 BINDING SITE2, designated SEQ ID:16001 and SEQ ID:8232 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28893] Another function of GAM189 is therefore inhibition of FLJ39599 (Accession NP_776164.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39599.

[28894] FLJ39639 (Accession XP_290687.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ39639 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39639, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ39639 BINDING SITE, designated SEQ ID:9190, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28895] Another function of GAM189 is therefore inhibition of FLJ39639 (Accession XP_290687.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39639.

[28896] FLJ90231 (Accession NP_775852.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ90231 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90231, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90231 BINDING SITE, designated SEQ ID:10357, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28897] Another function of GAM189 is therefore inhibition of FLJ90231 (Accession NP_775852.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ90231.

[28898] FLJ90723 (Accession NP_787115.1) is another GAM189 target gene, herein designated TARGET GENE. FLJ90723 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90723, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90723 BINDING SITE, designated SEQ ID:19889, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28899] Another function of GAM189 is therefore inhibition of FLJ90723 (Accession NP_787115.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90723.

[28900] Formin binding protein 1 (FNBP1, Accession XP_052666.3) is another GAM189 target gene, herein designated TARGET GENE. FNBP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FNBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of FNBP1 BINDING SITE, designated SEQ ID:16354, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28901] Another function of GAM189 is therefore inhibition of Formin binding protein 1 (FNBP1, Accession XP_052666.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FNBP1.

[28902] Forkhead box e2 (FOXE2, Accession NP_036317.1) is another GAM189 target gene, herein designated TARGET GENE. FOXE2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FOXE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXE2 BINDING SITE, designated SEQ ID:15626, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28903] Another function of GAM189 is therefore inhibition of Forkhead box e2 (FOXE2, Accession NP_036317.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with FOXE2.

[28904] Forkhead box o1a (rhabdomyosarcoma) (FOXO1A, Accession NP_002006.2) is another GAM189 target gene, herein designated TARGET GENE. FOXO1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOXO1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXO1A BINDING SITE, designated SEQ ID:736, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28905] Another function of GAM189 is therefore inhibition of Forkhead box o1a (rhabdomyosarcoma) (FOXO1A, Accession NP_002006.2), a gene which is a probable transcription factor. and therefore may be associated with Alveolar rhabdomyosarcoma- 2. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Alveolar rhabdomyosarcoma- 2., and of other diseases and clinical conditions associated with FOXO1A.

[28906] The function of FOXO1A has been established by previous studies. In alveolar rhabdomyosarcoma, the translocation t(2;13)(q35;q14) is frequently found. Barr et al. (1993) de-

termined that PAX3 (OMIM Ref. No. 606597), which had previously been found to be mutated in Waardenburg syndrome (OMIM Ref. No. 193500), was affected by this t(2;13) in alveolar rhabdomyosarcoma (OMIM Ref. No. 268220). Galili et al. (1993) isolated the chromosome 13 gene that is fused with PAX3. The rearrangement breakpoints occurred within an intron downstream of the paired box and homeodomain- encoding regions. and identified it as a member of the forkhead domain family, which encodes transcription factors containing a conserved DNA-binding motif related to the Drosophila region- specific homeotic gene 'forkhead.' The distal half of the forkhead and the C- terminal region of the FKHR gene are involved in the chimeric transcript and fusion protein. (Because of the homology to 'forkhead,' the gene was symbolized FKHR, for 'forkhead' in rhabdomyosarcoma.) See human T- cell leukemia virus enhancer factor (OMIM Ref. No. 143089) and interleukin enhancer binding factor (OMIM Ref. No. 147685) for other members of the forkhead domain family of transcription factors. Fredericks et al. (1995) demonstrated expression of a 97- kD PAX3/FKHR fusion protein in a t(2;13)- positive rhabdomyosarcoma cell line and verified that a single polypeptide contained

epitopes derived from each protein. The fusion protein was localized to the nucleus in these cells, as was wildtype PAX3 in cells lacking the translocation. They found that DNA binding of the fusion protein was significantly impaired relative to that of PAX3 despite the fact that the 2 proteins had identical PAX DNA- binding domains. However, the fusion protein was a much more potent transcriptional activator than PAX3. Thus, the fusion protein may function as an oncogenic transcription factor by enhancing activation of normal PAX3 target genes.

[28907]

[28908] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28909] Barr, F. G.; Galili, N.; Holick, J.; Biegel, J. A.; Rovera, G.; Emanuel, B. S. : Rearrangement of the PAX3 paired box gene in the paediatric solid tumor alveolar rhabdomyosarcoma. Nature Genet. 3: 113- 117, 1993. ; and

[28910] Fredericks, W. J.; Galili, N.; Mukhopadhyay, S.; Rovera, G.; Bennicelli, J.; Barr, F. G.; Rauscher, F. J., III : The PAX3-FKHR fusion protein created by the t(2;13) translocation in alve.

[28911] Further studies establishing the function and utilities of

FOXO1A are found in John Hopkins OMIM database record ID 136533, and in cited publications listed in Table 5, which are hereby incorporated by reference.Fsh primary response (Irpr1 homolog, rat) 1 (FSHPRH1, Accession NP_006724.1) is another GAM189 target gene, herein designated TARGET GENE. FSHPRH1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FSHPRH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FSHPRH1 BINDING SITE, designated SEQ ID:11528, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28912] Another function of GAM189 is therefore inhibition of Fsh primary response (Irpr1 homolog, rat) 1 (FSHPRH1, Accession NP_006724.1), a gene which is involved in the response of gonadal tissues to follicle- stimulating hormone. and therefore may be associated with Hypergonadotropic ovarian dysgenesis (odg), x- linked disorders of gonadal development. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Hypergonadotropic ovarian dysgenesis (odg), x- linked disorders

of gonadal development, and of other diseases and clinical conditions associated with FSHPRH1.

[28913] The function of FSHPRH1 has been established by previous studies. Follicle- stimulating hormone (FSH; 136530), a gonadotropic hormone secreted by both the male and the female mammalian anterior pituitary gland, is responsible, with luteinizing hormone (OMIM Ref. No. 152780), for the regulation of follicular maturation and ovulation in females. Loss- of- function mutations in the FSH receptor gene (OMIM Ref. No. 136435) are associated with hypergonadotropic ovarian dysgenesis (ODG) in which inability of the gonads to respond to FSH results in failure of ovarian development with consequent primary amenorrhea; lack of negative feedback to the pituitary leads to the observed high levels of gonadotropins. Mutation of the gene for the beta subunit of FSH (136530.0001) has also been described in a patient with primary amenorrhea who was able to conceive after administration of FSH. Although there may be a role for FSH also in male gonadal development at puberty, fertility appears not to be compromised in known homozygous male relatives of ODG females (Aittomaki et al., 1995). Roberts et al. (1996) hypothesized that mutations in genes encoding other components

of the FSH signaling pathway might be responsible for other cases of female or even male disorders of gonadal development. The rat gene called leucine- rich primary response gene 1 (LRPR1) is rapidly transcriptionally activated in response to FSH stimulation of rat testicular Sertoli cells, both in vitro and in vivo (Slegtenhorst- Eegdeman et al., 1995). Roberts et al. (1996) characterized a human transcript that probably encodes the ortholog of the rat protein. The gene encodes a 756- amino acid polypeptide with 72% identity to rat LRPR1 at the amino acid level. The gene maps to human chromosome Xq22 and therefore is a potential candidate for human X- linked disorders of gonadal development. The human LRPR1 gene (also symbolized FSHPRH1) was isolated during characterization of a gene encoding dystrophin- related protein 2 (DRP2; 300052); searches of sequence databases using the BLAST program revealed the similarities to rat LRPR1. Other evidence indicated that LRPR1 and DRP2, which maps to Xq22, are closely situated. Roberts et al. (1996) found by hybridization to YACs and to cosmids isolated from that region that LRPR1 is transcribed in a proximal- to- distal direction and lies approximately 40 kb proximal to DRP2, while BTK (OMIM Ref. No. 300300),

the gene that is mutant and X- linked agammaglobuline-mia, lies approximately 300 kb distal.

[28914]

[28915] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28916] Aittomaki, K.; Lucena, J. L. D.; Pakarinen, P.; Sistonen, P.; Tapanainen, J.; Gromoll, J.; Kaskikari, R.; Sankila, E.- M.; Lehvaslaiho, H.; Engel, A. R.; Nieschlag, E.; Huhtaniemi, I.; de la Chapelle, A. : Mutation in the follicle- stimulating hormone receptor gene causes hereditary hyperg-onadotropic ovarian failure. Cell 82: 959- 968, 1995. ; and

[28917] Roberts, R. G.; Kendall, E.; Vetrie, D.; Bobrow, M. : Se-quence and chromosomal location of a human homologue of LRPR1, an FSH primary response gene. Genomics 37: 122- 124, 1996.

[28918] Further studies establishing the function and utilities of FSHPRH1 are found in John Hopkins OMIM database record ID 300065, and in cited publications listed in Table 5, which are hereby incorporated by refer-ence.Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype in-

cluded) (FUT1, Accession NP_000139.1) is another GAM189 target gene, herein designated TARGET GENE. FUT1 BINDING SITE1 and FUT1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FUT1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FUT1 BINDING SITE1 and FUT1 BINDING SITE2, designated SEQ ID:16365 and SEQ ID:11525 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28919] Another function of GAM189 is therefore inhibition of Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUT1.

[28920] Frizzled homolog 4 (drosophila) (FZD4, Accession NP_036325.2) is another GAM189 target gene, herein designated TARGET GENE. FZD4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by FZD4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FZD4 BINDING SITE, designated SEQ ID:4487, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28921] Another function of GAM189 is therefore inhibition of Frizzled homolog 4 (drosophila) (FZD4, Accession NP_036325.2), a gene which may function in cell polarity, cell fate specification and cancer; similar to frizzled receptor family, has seven transmembrane domains and therefore may be associated with Familial exudative vitreoretinopathy. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Familial exudative vitreoretinopathy., and of other diseases and clinical conditions associated with FZD4.

[28922] The function of FZD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.1.G2A (Accession NP_037477.1) is another GAM189 target gene, herein designated TARGET GENE. G2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G2A, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G2A BINDING SITE, designated SEQ ID:8714, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28923] Another function of GAM189 is therefore inhibition of G2A (Accession NP_037477.1), a gene which may mediate some of the effects of extracellular atp on insulin secretion. and therefore may be associated with Autoimmune disease. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Autoimmune disease., and of other diseases and clinical conditions associated with G2A.

[28924] The function of G2A has been established by previous studies. G2A belongs to a subfamily of GPCRs that bind to various glycolipids. Kabarowski et al. (2001) determined that expression of G2A induces signaling responses after exposure to lysophosphatidylcholine (LPC) and to sphingosylphosphorylcholine (SPC), a high- affinity ligand for OGR1 (GPR68; 601404). Scatchard analysis indicated that G2A binds LPC with high affinity and SPC with low affinity. Western blot analysis showed that both LPC and SPC acti-

vated ERK mitogen- activated protein kinase (see OMIM Ref. No. MAP3K4; 602425) in G2A- expressing CHO cells. LPC, but not SPC, stimulated transmigration of G2A- expressing T lymphocytes. The authors proposed that G2A may act as a sensor of LPC levels at sites of inflammation to limit the expansion of tissue- infiltrating cells promoting overt autoimmune disease.

[28925] Animal model experiments lend further support to the function of G2A. Le et al. (2001) showed that mice with a targeted disruption of G2a, apart from enhanced in vitro T- cell proliferative responses, initially appeared normal. With age, however, they developed a progressive secondary lymphoid organ enlargement associated with an abnormal polyclonal lymphocyte expansion. Older animals succumbed to a late- onset autoimmune wasting syndrome

[28926] It is appreciated that the abovementioned animal model for G2A is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[28927] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28928] Kabarowski, J. H. S.; Zhu, K.; Le, L. Q.; Witte, O. N.; Xu, Y. : Lysophosphatidylcholine as a ligand for the immunoregulatory receptor G2A. Science 293: 702- 705, 2001. ; and

[28929] Le, L. Q.; Kabarowski, J. H. S.; Weng, Z.; Satterthwaite, A. B.; Harvill, E. T.; Jensen, E. R.; Miller, J. F.; Witte, O. N. : Mice lacking the orphan G protein- coupled receptor G2A de.

[28930] Further studies establishing the function and utilities of G2A are found in John Hopkins OMIM database record ID 606167, and in cited publications listed in Table 5, which are hereby incorporated by reference.Glucose-6-phosphatase, catalytic (glycogen storage disease type i, von gierke disease) (G6PC, Accession NP_000142.1) is another GAM189 target gene, herein designated TARGET GENE. G6PC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G6PC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G6PC BINDING SITE, designated SEQ ID:4204, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28931] Another function of GAM189 is therefore inhibition of

Glucose-6-phosphatase, catalytic (glycogen storage disease type i, von gierke disease) (G6PC, Accession NP_000142.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G6PC.

[28932] GAL3ST-4 (Accession NP_078913.3) is another GAM189 target gene, herein designated TARGET GENE. GAL3ST-4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAL3ST-4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAL3ST-4 BINDING SITE, designated SEQ ID:4518, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28933] Another function of GAM189 is therefore inhibition of GAL3ST-4 (Accession NP_078913.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAL3ST-4.

[28934] Gata binding protein 2 (GATA2, Accession NP_116027.2) is another GAM189 target gene, herein designated TARGET GENE. GATA2 BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by GATA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GATA2 BINDING SITE, designated SEQ ID:16014, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28935] Another function of GAM189 is therefore inhibition of Gata binding protein 2 (GATA2, Accession NP_116027.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GATA2.

[28936] Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) is another GAM189 target gene, herein designated TARGET GENE. GGA2 BINDING SITE1 and GGA2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by GGA2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE1 and GGA2 BINDING SITE2, designated SEQ

ID:5631 and SEQ ID:5631 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28937] Another function of GAM189 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[28938] Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) is another GAM189 target gene, herein designated TARGET GENE. GGA2 BINDING SITE1 and GGA2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by GGA2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE1 and GGA2 BINDING SITE2, designated SEQ ID:6391 and SEQ ID:6391 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28939] Another function of GAM189 is therefore inhibition of

Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[28940] Gm2 ganglioside activator protein (GM2A, Accession NP_000396.1) is another GAM189 target gene, herein designated TARGET GENE. GM2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GM2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GM2A BINDING SITE, designated SEQ ID:11286, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28941] Another function of GAM189 is therefore inhibition of Gm2 ganglioside activator protein (GM2A, Accession NP_000396.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GM2A.

[28942] GNE (Accession NP_005467.1) is another GAM189 target gene, herein designated TARGET GENE. GNE BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by GNE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNE BINDING SITE, designated SEQ ID:8367, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28943] Another function of GAM189 is therefore inhibition of GNE (Accession NP_005467.1), a gene which has roles in sialic acid biosynthesis and regulates cell surface sialylation. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNE.

[28944] The function of GNE has been established by previous studies. Keppler et al. (1999) determined that UDP- GlcNAc 2- epimerase activity is rate- limiting for the biosynthesis of sialic acid and is required for sialylation in hematopoietic cells. The activity of the enzyme can be controlled at the transcriptional level and can affect the sialylation and function of specific cell surface molecules expressed on B cells and myeloid cells. In a Genbank submission (AJ238764), these authors reported the sequence

of a human UDP- GlcNAc 2- epimerase cDNA.

[28945] Animal model experiments lend further support to the function of GNE. Schwarzkopf et al. (2002) reported that inactivation of GNE (which is bifunctional and is the key enzyme of sialic acid biosynthesis) by gene targeting in mice caused early embryonic lethality, thereby emphasizing the fundamental role of the enzyme and sialylation during development. The need of the enzyme for a defined sialylation process is exemplified by the polysialylation of the neural cell adhesion molecule in embyronic stem cells.

[28946] It is appreciated that the abovementioned animal model for GNE is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[28947] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28948] Keppler, O. T.; Hinderlich, S.; Langner, J.; Schwartz- Albiez, R.; Reutter, W.; Pawlita, M. : UDP- GlcNAc 2- epimerase: a regulator of cell surface sialylation. Science 284: 1372- 1376, 1999. ; and

[28949] Schwarzkopf, M.; Knobeloch, K.- P.; Rohde, E.; Hinderlich,

S.; Wiechens, N.; Lucka, L.; Horak, I.; Reutter, W.; Horstkorte, R. : Sialylation is essential for early development in mice.

[28950] Further studies establishing the function and utilities of GNE are found in John Hopkins OMIM database record ID 603824, and in cited publications listed in Table 5, which are hereby incorporated by reference.Guanine nucleotide binding protein (g protein), gamma 4 (GNG4, Accession NP_004476.1) is another GAM189 target gene, herein designated TARGET GENE. GNG4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNG4 BINDING SITE, designated SEQ ID:559, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28951] Another function of GAM189 is therefore inhibition of Guanine nucleotide binding protein (g protein), gamma 4 (GNG4, Accession NP_004476.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNG4.

[28952] GNPNAT1 (Accession XP_085119.1) is another GAM189

target gene, herein designated TARGET GENE. GNPNAT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNPNAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNPNAT1 BINDING SITE, designated SEQ ID:8464, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28953] Another function of GAM189 is therefore inhibition of GNPNAT1 (Accession XP_085119.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNPNAT1.

[28954] GNRPX (Accession NP_060519.1) is another GAM189 target gene, herein designated TARGET GENE. GNRPX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNRPX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNRPX BINDING SITE, designated SEQ ID:12243, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA,

also designated SEQ ID:246.

[28955] Another function of GAM189 is therefore inhibition of GNRPX (Accession NP_060519.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNRPX.

[28956] Golgi autoantigen, golgin subfamily a, 3 (GOLGA3, Accession NP_005886.2) is another GAM189 target gene, herein designated TARGET GENE. GOLGA3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GOLGA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GOLGA3 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28957] Another function of GAM189 is therefore inhibition of Golgi autoantigen, golgin subfamily a, 3 (GOLGA3, Accession NP_005886.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLGA3.

[28958] Glycoprotein v (platelet) (GP5, Accession NP_004479.1) is another GAM189 target gene, herein designated TARGET

GENE. GP5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GP5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GP5 BINDING SITE, designated SEQ ID:5681, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28959] Another function of GAM189 is therefore inhibition of Glycoprotein v (platelet) (GP5, Accession NP_004479.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GP5.

[28960] GPP34R (Accession NP_060648.2) is another GAM189 target gene, herein designated TARGET GENE. GPP34R BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPP34R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPP34R BINDING SITE, designated SEQ ID:14203, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28961] Another function of GAM189 is therefore inhibition of GPP34R (Accession NP_060648.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPP34R.

[28962] G protein-coupled receptor 26 (GPR26, Accession NP_703143.1) is another GAM189 target gene, herein designated TARGET GENE. GPR26 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR26, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR26 BINDING SITE, designated SEQ ID:3010, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28963] Another function of GAM189 is therefore inhibition of G protein-coupled receptor 26 (GPR26, Accession NP_703143.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR26.

[28964] G protein-coupled receptor 4 (GPR4, Accession NP_005273.1) is another GAM189 target gene, herein designated TARGET GENE. GPR4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by GPR4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR4 BINDING SITE, designated SEQ ID:4965, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28965] Another function of GAM189 is therefore inhibition of G protein-coupled receptor 4 (GPR4, Accession NP_005273.1), a gene which stimulates to produce increased calcium by both SPC and LPC . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR4.

[28966] The function of GPR4 has been established by previous studies. Many cell membrane receptors are members of the G protein- coupled receptor (GPR) family. GPRs are characterized by the presence of 7 transmembrane domains and numerous conserved amino acids. Using degenerate PCR, Heiber et al. (1995) identified additional members of this family. Among these was GPR4, which encodes a putative 355- amino acid protein and was selected from a genomic DNA library using the PCR- derived product as a probe. GPR4 shares the greatest sequence

similarity with the human platelet- activating factor receptor (Ye et al., 1991). GPR4 is more than 50% identical to OGR1 (GPR68; 601404), a high- affinity receptor for the sphingosylphosphorylcholine (SPC) signaling molecule. Zhu et al. (2001) showed that cells expressing GPR4 are stimulated to produce increased calcium by both SPC and LPC (lysophosphatidylcholine), a ligand for G2A (OMIM Ref. No. 606167). RNA dot blot analysis revealed highest expression of GPR4 in ovary, liver, lung, kidney, lymph node, and subthalamic nucleus; in contrast, OGR1 is most highly expressed in lung, placenta, spleen, testis, small intestine, and peripheral blood leukocytes. Binding analysis determined that GPR4 interacts with SPC with high affinity and with LPC with lower affinity. Both ligands enhanced proliferation and ERK mitogen- activated protein kinase (see OMIM Ref. No. MAP3K4; 602425) activation in a GPR4- dependent and pertussis toxin (PTX)- sensitive manner, whereas ERK activation is PTX- insensitive in OGR1- mediated signaling. Cell migration analysis suggested that both LPC and SPC enhance chemotaxis, but not chemokinesis, through GPR4.

[28967]

[28968] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[28969] Heiber, M.; Docherty, J. M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H. H. Q.; Marchese, A.; Tsui, L.- C.; Shi, X.; George, S. R.; O'Dowd, B. F. : Isolation of three novel human genes encoding G protein- coupled receptors. DNA Cell Biol. 14: 25- 35, 1995. ; and

[28970] Zhu, K.; Baudhuin, L. M.; Hong, G.; Williams, F. S.; Cristina, K. L.; Kabarowski, J. H. S.; Witte, O. N.; Xu, Y. : Sphingosylphosphorylcholine and lysophosphatidylcholine are ligands f.

[28971] Further studies establishing the function and utilities of GPR4 are found in John Hopkins OMIM database record ID 600551, and in cited publications listed in Table 5, which are hereby incorporated by reference.G protein-coupled receptor 56 (GPR56, Accession NP_005673.2) is another GAM189 target gene, herein designated TARGET GENE. GPR56 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GPR56, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR56 BINDING SITE, designated SEQ ID:8622, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28972] Another function of GAM189 is therefore inhibition of G protein-coupled receptor 56 (GPR56, Accession NP_005673.2), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR56.

[28973] The function of GPR56 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.G protein-coupled receptor 66 (GPR66, Accession NP_006047.2) is another GAM189 target gene, herein designated TARGET GENE. GPR66 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR66, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR66 BINDING SITE, designated SEQ ID:19237, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28974] Another function of GAM189 is therefore inhibition of G protein-coupled receptor 66 (GPR66, Accession NP_006047.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR66.

[28975] G protein-coupled receptor 81 (GPR81, Accession NP_115943.1) is another GAM189 target gene, herein designated TARGET GENE. GPR81 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR81, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR81 BINDING SITE, designated SEQ ID:13260, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28976] Another function of GAM189 is therefore inhibition of G protein-coupled receptor 81 (GPR81, Accession NP_115943.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR81.

[28977] GR6 (Accession NP_031380.1) is another GAM189 target gene, herein designated TARGET GENE. GR6 BINDING SITE

is a target binding site found in the 5` untranslated region of mRNA encoded by GR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GR6 BINDING SITE, designated SEQ ID:2604, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28978] Another function of GAM189 is therefore inhibition of GR6 (Accession NP_031380.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GR6.

[28979] GRAF (Accession NP_055886.1) is another GAM189 target gene, herein designated TARGET GENE. GRAF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRAF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRAF BINDING SITE, designated SEQ ID:4362, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28980] Another function of GAM189 is therefore inhibition of

GRAF (Accession NP_055886.1), a gene which ia a GTPase activating protein for p21- rac and therefore may be associated with Juvenile myelomonocytic leukemia. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Juvenile myelomonocytic leukemia, and of other diseases and clinical conditions associated with GRAF.

[28981] The function of GRAF has been established by previous studies. Borkhardt et al. (2000) stated that mutual translocations involving 11q23 in acute leukemias had been demonstrated to show fusion between the mixed lineage leukemia (MLL; 159555) gene and a variety of different partner genes to a total of 23. The detection of a unique t(5;11)(q31;q23) in an infant with juvenile myelomonocytic leukemia and an MLL gene rearrangement provided an opportunity to clone another MLL fusion partner gene. By cloning the breakpoints in this translocation, Borkhardt et al. (2000) recovered a member of the GTPase- activating protein (GAP) family, which they identified as the human homolog of the avian GRAF gene (Hildebrand et al., 1996). Ishikawa et al. (1998) cloned a GRAF cDNA, which they designated KIAA0621, from a human brain cDNA library and found that it encodes a de-

duced 753- amino acid protein with a molecular mass of 87 kD. Hildebrand et al. (1996) determined that the GRAF gene is highly homologous to the BCR gene (OMIM Ref. No. 151410), which is also involved in a leukemia- associated translocation. The avian GRAF protein binds to the C- terminal domain of pp125(FAK), one of the tyrosine kinases predicted to be a critical component of the integrin signaling transduction pathway, in an SH3 domain- dependent manner and stimulates the GTPase activity of the GTP- binding protein RhoA. Thus, GRAF acts as a negative regulator of RhoA.

[28982]

[28983] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28984] Borkhardt, A.; Bojesen, S.; Haas, O. A.; Fuchs, U.; Bartelheimer, D.; Loncarevic, I. F.; Bohle, R. M.; Harbott, J.; Repp, R.; Jaeger, U.; Viehmann, S.; Henn, T.; Korth, P.; Scharr, D.; Lampert, F. : The human GRAF gene is fused to MLL in a unique t(5;11)(q31;q23) and both alleles are disrupted in three cases of myelodysplastic syndrome/acute myeloid leukemia with a deletion 5q. Proc. Nat. Acad. Sci. 97: 9168- 9173, 2000. ; and

[28985] Hildebrand, J. D.; Taylor, J. M.; Parsons, T. J. : An SH3 domain- containing GTPase- activating protein for Rho and Cdc42 associates with focal adhesion kinase. Molec. Cell. Biol. 16: 31.

[28986] Further studies establishing the function and utilities of GRAF are found in John Hopkins OMIM database record ID 605370, and in cited publications listed in Table 5, which are hereby incorporated by reference.GREB1 (Accession NP_055483.2) is another GAM189 target gene, herein designated TARGET GENE. GREB1 BINDING SITE1 through GREB1 BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by GREB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GREB1 BINDING SITE1 through GREB1 BINDING SITE3, designated SEQ ID:11815, SEQ ID:14861 and SEQ ID:9792 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28987] Another function of GAM189 is therefore inhibition of GREB1 (Accession NP_055483.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with GREB1.

[28988] Glutamate receptor, ionotropic, delta 1 (GRID1, Accession XP_043613.8) is another GAM189 target gene, herein designated TARGET GENE. GRID1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRID1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRID1 BINDING SITE, designated SEQ ID:17390, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28989] Another function of GAM189 is therefore inhibition of Glutamate receptor, ionotropic, delta 1 (GRID1, Accession XP_043613.8) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRID1.

[28990] Glutamate receptor, ionotropic, n-methyl d-aspartate-like 1a (GRINL1A, Accession NP_056347.1) is another GAM189 target gene, herein designated TARGET GENE. GRINL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRINL1A, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRINL1A BINDING SITE, designated SEQ ID:5433, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28991] Another function of GAM189 is therefore inhibition of Glutamate receptor, ionotropic, n-methyl d-aspartate-like 1a (GRINL1A, Accession NP_056347.1), a gene which plays a role in the development and function of the mammalian brain. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRINL1A.

[28992] The function of GRINL1A has been established by previous studies. The ionotropic glutamate receptors (e.g., GRIN1; 138249) play roles in the development and function of the mammalian brain. Roginski et al. (2001) isolated rat GRINL1 cDNA from a size- fractionated, directional rat brain cDNA library. They obtained human GRINL1A genomic DNA sequences by amplification with primers designed from the rat sequences. By fluorescence in situ hybridization, Roginski et al. (2001) mapped the GRINL1A gene to chromosome 15q22.1. By interspecific backcross analysis, Wydner et al. (2001) mapped the mouse Grinl1a

gene to chromosome 9 in a region that shares linkage conservation with human chromosome 15q21- q22.

[28993]

[28994] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[28995] Roginski, R. S.; Mohan Raj, B. K.; Finkernagel, S. W.; Sciorra, L. J. : Assignment of an ionotropic glutamate receptor- like gene (GRINL1A) to human chromosome 15q22.1 by in situ hybridization. Cytogenet. Cell Genet. 93: 143- 144, 2001. ; and

[28996] Wydner, K. S.; Mohan Raj, B. K.; Sciorra, L. J.; Roginski, R. S. : The mouse orthologue of the human ionotropic glutamate receptor- like gene (GRINL1A) maps to mouse chromosome 9. Cytog.

[28997] Further studies establishing the function and utilities of GRINL1A are found in John Hopkins OMIM database record ID 606485, and in cited publications listed in Table 5, which are hereby incorporated by reference.Glutamate receptor, metabotropic 6 (GRM6, Accession NP_000834.1) is another GAM189 target gene, herein designated TARGET GENE. GRM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRM6,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRM6 BINDING SITE, designated SEQ ID:10398, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[28998] Another function of GAM189 is therefore inhibition of Glutamate receptor, metabotropic 6 (GRM6, Accession NP_000834.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRM6.

[28999] GRWD (Accession NP_113673.2) is another GAM189 target gene, herein designated TARGET GENE. GRWD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRWD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRWD BINDING SITE, designated SEQ ID:7996, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29000] Another function of GAM189 is therefore inhibition of GRWD (Accession NP_113673.2) . Accordingly, utilities of

GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRWD.

[29001] GSDM (Accession NP_835465.1) is another GAM189 target gene, herein designated TARGET GENE. GSDM BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSDM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSDM BINDING SITE, designated SEQ ID:3199, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29002] Another function of GAM189 is therefore inhibition of GSDM (Accession NP_835465.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSDM.

[29003] GSDM (Accession XP_209009.1) is another GAM189 target gene, herein designated TARGET GENE. GSDM BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSDM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of GSDM BINDING SITE, designated SEQ ID:3199, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29004] Another function of GAM189 is therefore inhibition of GSDM (Accession XP_209009.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSDM.

[29005] Glutathione s-transferase m1 (GSTM1, Accession NP_666533.1) is another GAM189 target gene, herein designated TARGET GENE. GSTM1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSTM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSTM1 BINDING SITE, designated SEQ ID:12752, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29006] Another function of GAM189 is therefore inhibition of Glutathione s-transferase m1 (GSTM1, Accession NP_666533.1), a gene which is conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. and therefore may be as-

sociated with Aplastic anemia and cancer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Aplastic anemia and cancer, and of other diseases and clinical conditions associated with GSTM1.

[29007] The function of GSTM1 has been established by previous studies. The mu class glutathione transferase GSTM1 is absent from more than 50% of some populations (Board et al., 1990). This deficiency appears to be caused by the deletion of the GSTM1 gene (18,16:Seidegard et al., 1988, 1990); a null allele at the GSTM1 locus is found in 40 to 45% of Caucasians. GSTM1 deficiency may be a risk factor for cancer by providing increased sensitivity to particular chemical carcinogens (Strange et al., 1991; van Poppel et al., 1992). Seidegard et al. (1986, 1990) found an association between the GSTM1 null phenotype and susceptibility to lung cancer. Zhong et al. (1993) found a significant excess of 'nulled' individuals among cases of colorectal cancer: 56.1% compared with the control group value of 41.8%. More than 70% of individuals with a tumor in the proximal colon were GSTM1 nulled, in their terminology. Patients with reduced ability to metabolize environmental carcinogens or toxins may be at risk of developing aplastic anemia. GST has been implicated in detoxifying muta-

genic electrophilic compounds. Lee et al. (2001) investigated whether homozygous deletions of GSTM1 and GSTT1 affect the likelihood of developing aplastic anemia. They found that the incidence of GSTM1 and GSTT1 gene deletions was significantly higher for aplastic anemia patients than for healthy controls (odds ratio = 3.1, P = 0.01, and odds ratio = 3.1, P = 0.004, respectively). Among the aplastic anemia patients, 17.5% had chromosomal abnormalities at the time of diagnosis, and all aplastic anemia patients with chromosomal abnormalities showed GSTT1 gene deletions.

[29008]

[29009] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29010] van Poppel, G.; de Vogel, N.; van Bladeren, P. J.; Kok, F. J. : Increased cytogenetic damage in smokers deficient in glutathione S- transferase isozyme mu. Carcinogenesis 13: 303- 305, 1992. ; and

[29011] Lee, K. A.; Kim, S. H.; Woo, H. Y.; Hong, Y. J.; Cho, H. C. : Increased frequencies of glutathione S- transferase (GSTM1 and GSTT1) gene deletions in Korean patients with acquired aplasti.

[29012] Further studies establishing the function and utilities of GSTM1 are found in John Hopkins OMIM database record ID 138350, and in cited publications listed in Table 5, which are hereby incorporated by reference.Glutathione s-transferase m1 (GSTM1, Accession NP_000552.2) is another GAM189 target gene, herein designated TARGET GENE. GSTM1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSTM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSTM1 BINDING SITE, designated SEQ ID:12752, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29013] Another function of GAM189 is therefore inhibition of Glutathione s-transferase m1 (GSTM1, Accession NP_000552.2), a gene which is conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. and therefore may be associated with Aplastic anemia and cancer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Aplastic anemia and cancer, and of other

diseases and clinical conditions associated with GSTM1.

[29014] The function of GSTM1 has been established by previous studies. The mu class glutathione transferase GSTM1 is absent from more than 50% of some populations (Board et al., 1990). This deficiency appears to be caused by the deletion of the GSTM1 gene (18,16:Seidegard et al., 1988, 1990); a null allele at the GSTM1 locus is found in 40 to 45% of Caucasians. GSTM1 deficiency may be a risk factor for cancer by providing increased sensitivity to particular chemical carcinogens (Strange et al., 1991; van Poppel et al., 1992). Seidegard et al. (1986, 1990) found an association between the GSTM1 null phenotype and susceptibility to lung cancer. Zhong et al. (1993) found a significant excess of 'nulled' individuals among cases of colorectal cancer: 56.1% compared with the control group value of 41.8%. More than 70% of individuals with a tumor in the proximal colon were GSTM1 nulled, in their terminology. Patients with reduced ability to metabolize environmental carcinogens or toxins may be at risk of developing aplastic anemia. GST has been implicated in detoxifying mutagenic electrophilic compounds. Lee et al. (2001) investigated whether homozygous deletions of GSTM1 and GSTT1 affect the likelihood of developing aplastic anemia.

They found that the incidence of GSTM1 and GSTT1 gene deletions was significantly higher for aplastic anemia patients than for healthy controls (odds ratio = 3.1, P = 0.01, and odds ratio = 3.1, P = 0.004, respectively). Among the aplastic anemia patients, 17.5% had chromosomal abnormalities at the time of diagnosis, and all aplastic anemia patients with chromosomal abnormalities showed GSTT1 gene deletions.

[29015]

[29016] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29017] van Poppel, G.; de Vogel, N.; van Bladeren, P. J.; Kok, F. J. : Increased cytogenetic damage in smokers deficient in glutathione S- transferase isozyme mu. Carcinogenesis 13: 303- 305, 1992. ; and

[29018] Lee, K. A.; Kim, S. H.; Woo, H. Y.; Hong, Y. J.; Cho, H. C. : Increased frequencies of glutathione S- transferase (GSTM1 and GSTT1) gene deletions in Korean patients with acquired aplasti.

[29019] Further studies establishing the function and utilities of GSTM1 are found in John Hopkins OMIM database record ID 138350, and in cited publications listed in Table 5,

which are hereby incorporated by reference.Glutathione s-transferase m2 (muscle) (GSTM2, Accession NP_000839.1) is another GAM189 target gene, herein designated TARGET GENE. GSTM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GSTM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSTM2 BINDING SITE, designated SEQ ID:12752, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29020] Another function of GAM189 is therefore inhibition of Glutathione s-transferase m2 (muscle) (GSTM2, Accession NP_000839.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSTM2.

[29021] Glutathione s-transferase m4 (GSTM4, Accession NP_671490.1) is another GAM189 target gene, herein designated TARGET GENE. GSTM4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSTM4, corresponding to a target binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSTM4 BINDING SITE, designated SEQ ID:12752, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29022] Another function of GAM189 is therefore inhibition of Glutathione s-transferase m4 (GSTM4, Accession NP_671490.1), a gene which conjugates reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSTM4.

[29023] The function of GSTM4 has been established by previous studies. Glutathione S- transferases (GSTs) are a complex family of multifunctional enzymes thought to play a significant role in cellular detoxification. Cytosolic GSTs have been subdivided into 4 classes: alpha, mu, pi, and theta. Four isoenzymes of the mu class have been identified: GSTM1 (OMIM Ref. No. 138350), GSTM2 (OMIM Ref. No. 138380), GSTM3 (OMIM Ref. No. 138390), and GSTM4. Ross and Board (1993) cloned and characterized GSTM4. Ross et al. (1993) reported that a probe derived from GSTM4 cross- hybridizes with the other 3 known human

mu class GST genes. In situ hybridization with the GSTM4 probe localized a major region of hybridization on 1p13. An identical pattern of hybridization was observed in individuals with or without the GSTM1 gene. Taylor et al. (1991) found that GSTM4 and GSTM2 were located in the same cosmid. Comstock et al. (1993) reported the complete gene sequence and cDNA sequence of GSTM4. The deduced amino acid sequence of GSTM4 was 87% identical to GSTM1, 83% identical to GSTM2, and 70% identical to GSTM3. Using PCR amplification of a unique region of the GSTM4 gene from a panel of rodent- human somatic cell hybrid DNAs, Comstock et al. (1993) determined that the GSTM4 gene is located on chromosome 1.

[29024]

[29025] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29026] Ross, V. L.; Board, P. G. : Molecular cloning and heterologous expression of an alternatively spliced human mu class glutathione S- transferase transcript. Biochem. J. 294: 373- 380, 1993. ; and

[29027] Comstock, K. E.; Johnson, K. J.; Rifenbery, D.; Henner, W. D. : Isolation and analysis of the gene and cDNA for a hu-

man mu class glutathione S- transferase, GSTM4. J. Biol. Chem. 268: 169.

[29028] Further studies establishing the function and utilities of GSTM4 are found in John Hopkins OMIM database record ID 138333, and in cited publications listed in Table 5, which are hereby incorporated by reference.Glutathione s-transferase m4 (GSTM4, Accession NP_000841.1) is another GAM189 target gene, herein designated TARGET GENE. GSTM4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSTM4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSTM4 BINDING SITE, designated SEQ ID:12752, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29029] Another function of GAM189 is therefore inhibition of Glutathione s-transferase m4 (GSTM4, Accession NP_000841.1), a gene which conjugates reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with GSTM4.

[29030] The function of GSTM4 has been established by previous studies. Glutathione S- transferases (GSTs) are a complex family of multifunctional enzymes thought to play a significant role in cellular detoxification. Cytosolic GSTs have been subdivided into 4 classes: alpha, mu, pi, and theta. Four isoenzymes of the mu class have been identified: GSTM1 (OMIM Ref. No. 138350), GSTM2 (OMIM Ref. No. 138380), GSTM3 (OMIM Ref. No. 138390), and GSTM4. Ross and Board (1993) cloned and characterized GSTM4. Ross et al. (1993) reported that a probe derived from GSTM4 cross- hybridizes with the other 3 known human mu class GST genes. In situ hybridization with the GSTM4 probe localized a major region of hybridization on 1p13. An identical pattern of hybridization was observed in individuals with or without the GSTM1 gene. Taylor et al. (1991) found that GSTM4 and GSTM2 were located in the same cosmid. Comstock et al. (1993) reported the complete gene sequence and cDNA sequence of GSTM4. The deduced amino acid sequence of GSTM4 was 87% identical to GSTM1, 83% identical to GSTM2, and 70% identical to GSTM3. Using PCR amplification of a unique region of the GSTM4 gene from a panel of rodent- human somatic cell

hybrid DNAs, Comstock et al. (1993) determined that the GSTM4 gene is located on chromosome 1.

[29031]

[29032] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29033] Ross, V. L.; Board, P. G. : Molecular cloning and heterologous expression of an alternatively spliced human mu class glutathione S- transferase transcript. Biochem. J. 294: 373- 380, 1993. ; and

[29034] Comstock, K. E.; Johnson, K. J.; Rifenbery, D.; Henner, W. D. : Isolation and analysis of the gene and cDNA for a human mu class glutathione S- transferase, GSTM4. J. Biol. Chem. 268: 169.

[29035] Further studies establishing the function and utilities of GSTM4 are found in John Hopkins OMIM database record ID 138333, and in cited publications listed in Table 5, which are hereby incorporated by reference.General transcription factor iie, polypeptide 1, alpha 56kda (GTF2E1, Accession NP_005504.1) is another GAM189 target gene, herein designated TARGET GENE. GTF2E1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GTF2E1, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2E1 BINDING SITE, designated SEQ ID:15661, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29036] Another function of GAM189 is therefore inhibition of General transcription factor iie, polypeptide 1, alpha 56kda (GTF2E1, Accession NP_005504.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2E1.

[29037] GTF2IRD2 (Accession NP_115579.3) is another GAM189 target gene, herein designated TARGET GENE. GTF2IRD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GTF2IRD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2IRD2 BINDING SITE, designated SEQ ID:11522, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29038] Another function of GAM189 is therefore inhibition of GTF2IRD2 (Accession NP_115579.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2IRD2.

[29039] GTF2IRD2 (Accession NP_775808.1) is another GAM189 target gene, herein designated TARGET GENE. GTF2IRD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GTF2IRD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2IRD2 BINDING SITE, designated SEQ ID:11522, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29040] Another function of GAM189 is therefore inhibition of GTF2IRD2 (Accession NP_775808.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2IRD2.

[29041] GTPBG3 (Accession NP_116009.1) is another GAM189 target gene, herein designated TARGET GENE. GTPBG3 BIND-

ING SITE1 and GTPBG3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GTPBG3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTPBG3 BINDING SITE1 and GTPBG3 BINDING SITE2, designated SEQ ID:7812 and SEQ ID:10292 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29042] Another function of GAM189 is therefore inhibition of GTPBG3 (Accession NP_116009.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTPBG3.

[29043] Glycogenin (GYG, Accession NP_004121.2) is another GAM189 target gene, herein designated TARGET GENE. GYG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GYG BINDING SITE, designated SEQ ID:4258, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[29044] Another function of GAM189 is therefore inhibition of Glycogenin (GYG, Accession NP_004121.2), a gene which primes de novo glycogen synthesis. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GYG.

[29045] The function of GYG has been established by previous studies. Glycogenin is a self- glucosylating protein involved in the initiation reactions of glycogen synthesis. During initiation, the covalent attachment of a glucose residue to glycogenin is followed by elongation to form an oligosaccharide chain. Viskupic et al. (1992) isolated cDNAs encoding glycogenin from rabbit muscle, rat, and cow. Recombinant mammalian glycogenin was enzymatically active and capable of self- glucosylation. After incubation with UDP- glucose, the recombinant protein was able to serve as a substrate for glycogen synthase, leading to the production of high M(r) polysaccharide. Barbetti et al. (1996) identified a human glycogenin cDNA. The predicted 333- amino acid human protein shares 93% identity with rabbit muscle glycogenin. Northern blot analysis revealed that the 2.4- kb glycogenin mRNA was expressed prominently in human skeletal muscle and heart, and to a

lesser extent in several other tissues. Mu et al. (1997) isolated cDNAs encoding a related protein, which they designated glycogenin- 2 (OMIM Ref. No. 300198). They suggested that muscle glycogenin be referred to as glycogenin- 1.

[29046]

[29047] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29048] Barbetti, F.; Rocchi, M.; Bossolasco, M.; Cordera, R.; Sbraccia, P.; Finelli, P.; Consalez, G. G. : The human skeletal muscle glycogenin gene: cDNA, tissue expression, and chromosomal localization. Biochem. Biophys. Res. Commun. 220: 72- 77, 1996. ; and

[29049] Mu, J.; Skurat, A. V.; Roach, P. J. : Glycogenin- 2, a novel self- glucosylating protein involved in liver glycogen biosynthesis. J. Biol. Chem. 272: 27589- 27597, 1997.

[29050] Further studies establishing the function and utilities of GYG are found in John Hopkins OMIM database record ID 603942, and in cited publications listed in Table 5, which are hereby incorporated by reference.H-plk (Accession NP_056936.1) is another GAM189 target gene, herein designated TARGET GENE. H-plk BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by H-plk, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H-plk BINDING SITE, designated SEQ ID:12753, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29051] Another function of GAM189 is therefore inhibition of H-plk (Accession NP_056936.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H-plk.

[29052] H2AV (Accession NP_619541.1) is another GAM189 target gene, herein designated TARGET GENE. H2AV BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H2AV, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H2AV BINDING SITE, designated SEQ ID:18864, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29053] Another function of GAM189 is therefore inhibition of

H2AV (Accession NP_619541.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H2AV.

[29054] H63 (Accession NP_816929.1) is another GAM189 target gene, herein designated TARGET GENE. H63 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H63, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H63 BINDING SITE, designated SEQ ID:4554, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29055] Another function of GAM189 is therefore inhibition of H63 (Accession NP_816929.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H63.

[29056] H63 (Accession NP_612432.2) is another GAM189 target gene, herein designated TARGET GENE. H63 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H63, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of H63 BINDING SITE, designated SEQ ID:4554, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29057] Another function of GAM189 is therefore inhibition of H63 (Accession NP_612432.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H63.

[29058] Hepatitis a virus cellular receptor 2 (HAVCR2, Accession NP_116171.2) is another GAM189 target gene, herein designated TARGET GENE. HAVCR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HAVCR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HAVCR2 BINDING SITE, designated SEQ ID:16260, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29059] Another function of GAM189 is therefore inhibition of Hepatitis a virus cellular receptor 2 (HAVCR2, Accession NP_116171.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with HAVCR2.

[29060] HE9 (Accession NP_741997.1) is another GAM189 target gene, herein designated TARGET GENE. HE9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HE9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HE9 BINDING SITE, designated SEQ ID:7942, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29061] Another function of GAM189 is therefore inhibition of HE9 (Accession NP_741997.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HE9.

[29062] Hephaestin (HEPH, Accession NP_055614.1) is another GAM189 target gene, herein designated TARGET GENE. HEPH BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by HEPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HEPH BINDING SITE, designated

SEQ ID:15338, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29063] Another function of GAM189 is therefore inhibition of Hephaestin (HEPH, Accession NP_055614.1), a gene which is thought to be a membrane- bound protein responsible for transport of dietary iron from epithelial cells of the intestinal lumen into the circulatory system. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEPH.

[29064] The function of HEPH has been established by previous studies. Vulpe et al. (1999) found that Heph expression contrasts that of Cp, which is highly expressed in liver and expressed to a lesser extent in other tissues, including brain and lung, but is not expressed in intestine, where the highest expression of Heph is found. In situ hybridization studies indicated that intestinal expression of Heph is limited to villi, with almost no signal observed in crypt cells. Iron absorption occurs in villi. Vulpe et al. (1999) found that sla mice have a deletion of 582 nucleotides from the Heph gene, predicting an in- frame omission of 194 amino acids in the gene product. On the

basis of its homology with ceruloplasmin, Vulpe et al. (1999) proposed that hephaestin is a ferroxidase necessary for iron release from intestinal epithelial cells. Since it contains only 1 putative membrane- spanning domain, it is unlikely to be a transmembrane iron carrier itself; hephaestin may interact with an iron- transport protein to facilitate the movement of iron across the membrane. Hephaestin represents a link between copper and iron metabolism in mammals and offers a basis for the iron-deficiency anemia associated with copper deficiency. Copper deficiency results in the decreased absorption of dietary iron, which enters intestinal epithelium normally but cannot exit into the circulation. Indeed, intestinal iron accumulation in copper- deficient swine is similar to the iron accumulation seen in sla mice (Lee et al., 1968). The administration of copper, but not iron, to copper- deficient pigs alleviates the anemia and facilitates the egress of iron from tissues, including intestine.

[29065]

[29066] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29067] Vulpe, C. D.; Kuo, Y.- M.; Murphy, T. L.; Cowley, L.;

Askwith, C.; Libina, N.; Gitschier, J.; Anderson, G. J. : Hephaestin, a ceruloplasmin homologue implicated in intestinal iron transport, is defective in the sla mouse. Nature Genet. 21: 195- 199, 1999. ; and

[29068] Lee, G. R.; Nacht, S.; Lukens, J. N.; Cartwright, G. E. : Iron metabolism in copper- deficient swine. J. Clin. Invest. 47: 2058- 2069, 1968.

[29069] Further studies establishing the function and utilities of HEPH are found in John Hopkins OMIM database record ID 300167, and in cited publications listed in Table 5, which are hereby incorporated by reference.Hexosaminidase a (alpha polypeptide) (HEXA, Accession NP_000511.1) is another GAM189 target gene, herein designated TARGET GENE. HEXA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HEXA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HEXA BINDING SITE, designated SEQ ID:14035, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29070] Another function of GAM189 is therefore inhibition of Hexosaminidase a (alpha polypeptide) (HEXA, Accession

NP_000511.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEXA.

[29071] Holocarboxylase synthetase (biotin-[proprionyl-coenzyme a-carboxylase (atp-hydrolysing)] ligase) (HLCS, Accession NP_000402.2) is another GAM189 target gene, herein designated TARGET GENE. HLCS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HLCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:2142, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29072] Another function of GAM189 is therefore inhibition of Holocarboxylase synthetase (biotin-[proprionyl-coenzyme a-carboxylase (atp-hydrolysing)] ligase) (HLCS, Accession NP_000402.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLCS.

[29073] High-mobility group 20a (HMG20A, Accession NP_060670.1) is another GAM189 target gene, herein designated TARGET GENE. HMG20A BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by HMG20A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HMG20A BINDING SITE, designated SEQ ID:5040, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29074] Another function of GAM189 is therefore inhibition of High-mobility group 20a (HMG20A, Accession NP_060670.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMG20A.

[29075] HPRN (Accession NP_071938.1) is another GAM189 target gene, herein designated TARGET GENE. HPRN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HPRN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HPRN BINDING SITE, designated SEQ ID:12916, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29076] Another function of GAM189 is therefore inhibition of HPRN (Accession NP_071938.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HPRN.

[29077] Histamine receptor h4 (HRH4, Accession NP_067637.2) is another GAM189 target gene, herein designated TARGET GENE. HRH4 BINDING SITE1 and HRH4 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HRH4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HRH4 BINDING SITE1 and HRH4 BINDING SITE2, designated SEQ ID:3116 and SEQ ID:18211 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29078] Another function of GAM189 is therefore inhibition of Histamine receptor h4 (HRH4, Accession NP_067637.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRH4.

[29079] Hmt1 hnrnp methyltransferase-like 3 (s. cerevisiae) (HRMT1L3, Accession NP_062828.2) is another GAM189

target gene, herein designated TARGET GENE. HRMT1L3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HRMT1L3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HRMT1L3 BINDING SITE, designated SEQ ID:18437, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29080] Another function of GAM189 is therefore inhibition of Hmt1 hnrnp methyltransferase-like 3 (s. cerevisiae) (HRMT1L3, Accession NP_062828.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRMT1L3.

[29081] HSD3B7 (Accession NP_079469.2) is another GAM189 target gene, herein designated TARGET GENE. HSD3B7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSD3B7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSD3B7 BINDING SITE, designated SEQ ID:2674, to the nucleotide

sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29082] Another function of GAM189 is therefore inhibition of HSD3B7 (Accession NP_079469.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSD3B7.

[29083] HSMPP8 (Accession XP_167894.1) is another GAM189 target gene, herein designated TARGET GENE. HSMPP8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSMPP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSMPP8 BINDING SITE, designated SEQ ID:7797, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29084] Another function of GAM189 is therefore inhibition of HSMPP8 (Accession XP_167894.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSMPP8.

[29085] Heat shock 70kda protein 4 (HSPA4, Accession

XP_114482.1) is another GAM189 target gene, herein designated TARGET GENE. HSPA4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSPA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPA4 BINDING SITE, designated SEQ ID:15189, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29086] Another function of GAM189 is therefore inhibition of Heat shock 70kda protein 4 (HSPA4, Accession XP_114482.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPA4.

[29087] HSPC065 (Accession NP_054876.2) is another GAM189 target gene, herein designated TARGET GENE. HSPC065 BINDING SITE1 and HSPC065 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HSPC065, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPC065 BINDING SITE1 and

HSPC065 BINDING SITE2, designated SEQ ID:4676 and SEQ ID:713 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29088] Another function of GAM189 is therefore inhibition of HSPC065 (Accession NP_054876.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC065.

[29089] 5-hydroxytryptamine (serotonin) receptor 1d (HTR1D, Accession NP_000855.1) is another GAM189 target gene, herein designated TARGET GENE. HTR1D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR1D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR1D BINDING SITE, designated SEQ ID:2563, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29090] Another function of GAM189 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 1d (HTR1D, Accession NP_000855.1), a gene which belongs to g- pro-

tein coupled receptor. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR1D.

[29091] The function of HTR1D has been established by previous studies. The serotonin 1D receptor was initially characterized by radioligand binding procedures using membranes derived from bovine caudate nucleus. The 5- HT- 1D receptor is known to be a G protein- coupled receptor. Sumatriptan, an agent effective in the treatment of acute migraine, is the only ligand yet identified that is selective for the 5- HT- 1D receptor. Weinshank et al. (1992) reported the cloning, deduced amino acid sequences, pharmacologic properties, and second- messenger coupling of a pair of human 5- HT- 1D receptor genes, which they designated alpha and beta due to their strong similarities. Both genes have no introns in their coding regions, are expressed in the human cerebral cortex, and can couple to inhibition of adenylate cyclase activity. Their pharmacologic binding properties match closely those of human, bovine, and guinea pig 5- HT- 1D sites. Libert et al. (1991) obtained cDNA clones encoding 4 receptors of the G protein- coupled receptor family by selective amplification and cloning from thyroid cDNA. One of these clones,

termed RDC4 by them, showed close structural similarity with the serotonin 5HT1A receptor (OMIM Ref. No. 109760). By in situ hybridization, they demonstrated that the gene (HTR1D) is located on chromosome 1 at 1p36.3-p34.3. By Southern blot analysis of a hybrid cell panel, Jin et al. (1992) showed that the HTR1D gene is located on chromosome 1. Wilkie et al. (1993) showed that the homologous gene in the mouse is located on chromosome 4.

[29092]

[29093] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29094] Weinshank, R. L.; Zgombick, J. M.; Macchi, M. J.; Branchek, T. A.; Hartig, P. R. : Human serotonin 1D receptor is encoded by a subfamily of two distinct genes: 5- HT(1D- alpha) and 5- HT(1D- beta). Proc. Nat. Acad. Sci. 89: 3630-3634, 1992. ; and

[29095] Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.; Simon, M. I.; Copeland, N. G.; Jenkins, N. A. : Identification, chromosomal location, and genome organization of mammalian.

[29096] Further studies establishing the function and utilities of

HTR1D are found in John Hopkins OMIM database record ID 182133, and in cited publications listed in Table 5, which are hereby incorporated by reference.Hormonally upregulated neu-associated kinase (HUNK, Accession NP_055401.1) is another GAM189 target gene, herein designated TARGET GENE. HUNK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HUNK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUNK BINDING SITE, designated SEQ ID:17952, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29097] Another function of GAM189 is therefore inhibition of Hormonally upregulated neu-associated kinase (HUNK, Accession NP_055401.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUNK.

[29098] Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1) is another GAM189 target gene, herein designated TARGET GENE. HUS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by HUS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUS1 BINDING SITE, designated SEQ ID:14238, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29099] Another function of GAM189 is therefore inhibition of Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1), a gene which May form DNA damage- responsive protein complex . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUS1.

[29100] The function of HUS1 has been established by previous studies. The S. pombe 'checkpoint rad' genes hus1, rad1 (OMIM Ref. No. 603153), rad3, rad9 (OMIM Ref. No. 603761), rad17 (OMIM Ref. No. 603139), and rad26 are essential for both the incomplete DNA replication (S- M) and DNA damage checkpoints. An early step in the DNA damage checkpoint response appears to involve activation of the rad3 phosphatidylinositol 3- kinase- related (PIK-R) checkpoint kinase (see OMIM Ref. No. AT; 208900) by the other 5 checkpoint rad gene products. Kostrub et al.

(1998) found that the fission yeast hus1 and rad1 proteins form a stable complex, and that the formation of this complex is dependent on rad9, suggesting that these 3 proteins may exist in a discrete complex in the absence of checkpoint activation. Hus1 is phosphorylated in response to DNA damage, and this phosphorylation requires rad3 and the other checkpoint rad genes. By searching EST databases, Kostrub et al. (1998) and Dean et al. (1998) each identified mouse and human cDNAs encoding hus1 homologs. Kostrub et al. (1998) reported that the predicted 281- amino acid human protein shares 30% and 86% identity with S. pombe hus1 and mouse Hus1, respectively. However, neither mammalian gene complemented a fission yeast hus1 mutation. Volkmer and Karnitz (1999) demonstrated that the human RAD1 and HUS1 proteins associate in a complex that interacts with a highly modified form of RAD9. They concluded that these 3 proteins are central components of a DNA damage- responsive protein complex in human cells. AU- rich elements (AREs) are cis- acting sequences typically found in 3- prime untranslated regions of many labile mRNAs. AREs either mediate rapid degradation of mRNA or inhibit its translation. Dominguez et al. (1998) identified EE2-

16C, a HUS1 cDNA, among a collection of ARE- containing mRNAs.

[29101]

[29102] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29103] Kostrub, C. F.; Knudsen, K.; Subramani, S.; Enoch, T. : Hus1p, a conserved fission yeast checkpoint protein, interacts with Rad1p and is phosphorylated in response to DNA damage. EMBO J. 17: 2055- 2066, 1998. ; and

[29104] Volkmer, E.; Karnitz, L. M. : Human homologs of Schizosaccharomyces pombe Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J. Biol. Chem. 274: 567- 570, 1999.

[29105] Further studies establishing the function and utilities of HUS1 are found in John Hopkins OMIM database record ID 603760, and in cited publications listed in Table 5, which are hereby incorporated by reference.Hyaluronoglucosaminidase 4 (HYAL4, Accession NP_036401.1) is another GAM189 target gene, herein designated TARGET GENE. HYAL4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HYAL4, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HYAL4 BINDING SITE, designated SEQ ID:2143, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29106] Another function of GAM189 is therefore inhibition of Hyaluronoglucosaminidase 4 (HYAL4, Accession NP_036401.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HYAL4.

[29107] HYPB (Accession NP_036403.1) is another GAM189 target gene, herein designated TARGET GENE. HYPB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by HYPB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HYPB BINDING SITE, designated SEQ ID:14422, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29108] Another function of GAM189 is therefore inhibition of HYPB (Accession NP_036403.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with HYPB.

[29109] Intercellular adhesion molecule 1 (cd54), human rhinovirus receptor (ICAM1, Accession NP_000192.1) is another GAM189 target gene, herein designated TARGET GENE. ICAM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ICAM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICAM1 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29110] Another function of GAM189 is therefore inhibition of Intercellular adhesion molecule 1 (cd54), human rhinovirus receptor (ICAM1, Accession NP_000192.1), a gene which binds the integrin LFA- 1 (ITGB2) and promotes adhesion; member of the immunoglobulin superfamily and therefore may be associated with Malaria, cerebral, susceptibility to. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Malaria, cerebral, susceptibility to, and of other diseases and clinical conditions associated with ICAM1.

[29111] The function of ICAM1 has been established by previous

studies. Intercellular adhesion molecule- 1 (ICAM1) is a ligand for lymphocyte- function associated (LFA) antigens (see OMIM Ref. No. 116920). Simmons et al. (1988) analyzed a cDNA clone of the ICAM1 gene and found that it showed homology to the neural cell adhesion molecule NCAM (OMIM Ref. No. 116930). Greve et al. (1989) demonstrated that the ICAM1 protein is the major human rhinovirus receptor. Bella et al. (1998) analyzed the structural features of the ICAM1 molecule that underlie its function as a receptor for the major group of human rhinoviruses and as a ligand for LFA- 1. Expression of HLA-DR antigen (see OMIM Ref. No. 142860) and ICAM1 in human conjunctival epithelium is upregulated in patients with dry eyes associated with Sjogren syndrome (OMIM Ref. No. 270150). Tsubota et al. (1999) reported that this upregulation in Sjogren syndrome patients may be controlled by interferon- gamma (OMIM Ref. No. 147570) through the activation of transcription factor NFKB (nuclear OMIM Ref. No. 164011). Pisella et al. (2000) reported that a significant increase of HLA- DR and ICAM1 expression by epithelial cells was consistently found in patients with keratoconjunctivitis sicca (Sjogren syndrome) compared with expression in normal eyes. These 2

markers were well correlated with each other and correlated inversely with tear break- up time and tear production as measured by the Schirmer test. The percentage of conjunctival goblet cells was significantly decreased in dry eye patients with a significant negative correlation with both HLA- DR and ICAM1 markers. Lu and Cyster (2002) studied the mechanisms that control localization of marginal zone B cells. They demonstrated that marginal zone B cells express elevated levels of the integrins LFA-1 (see OMIM Ref. No. 153370) and alpha- 4- beta- 1 (see OMIM Ref. No. 192975 and 135630), and that the marginal zone B cells bind to the ligands ICAM1 and VCAM1 (OMIM Ref. No. 192225). These ligands are expressed within the marginal zone in a lymphotoxin- dependent manner. Combined inhibition of LFA- 1 and alpha- 4- beta- 1 causes a rapid and selective release of B cells from the marginal zone. Furthermore, lipopolysaccharide- triggered marginal zone B cell relocalization involves downregulation of integrin- mediated adhesion. Lu and Cyster (2002) concluded that their studies identified key requirements for marginal zone B cell localization and established a role for integrins in peripheral lymphoid tissue compartmentalization.

[29112] Animal model experiments lend further support to the function of ICAM1. To test the role of Icam1 in intact animals, Sligh et al. (1993) disrupted the gene in murine embryonic stem cells by gene targeting. Homozygous deficient animals developed normally, were fertile, and had a moderate granulocytosis. Studies were consistent with complete loss of surface expression of the protein. Deficient mice exhibited prominent abnormalities of inflammatory responses including impaired neutrophil emigration in response to chemical peritonitis and decreased contact hypersensitivity to 2,4- dinitrofluorobenzene. Mutant cells provided negligible stimulation in the mixed lymphocyte reaction, although they proliferated normally as responder cells

[29113] It is appreciated that the abovementioned animal model for ICAM1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[29114] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29115] Sligh, J. E., Jr.; Ballantyne, C. M.; Rich, S. S.; Hawkins, H. K.; Smith, C. W.; Bradley, A.; Beaudet, A. L. : Inflammatory and

immune responses are impaired in mice deficient in intercellular adhesion molecule 1. Proc. Nat. Acad. Sci. 90: 8529- 8533, 1993. ; and

[29116] Lu, T. T.; Cyster, J. G. : Integrin- mediated long- term B cell retention in the splenic marginal zone. Science 297: 409- 412, 2002.

[29117] Further studies establishing the function and utilities of ICAM1 are found in John Hopkins OMIM database record ID 147840, and in cited publications listed in Table 5, which are hereby incorporated by reference.ICK (Accession NP_055735.1) is another GAM189 target gene, herein designated TARGET GENE. ICK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ICK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29118] Another function of GAM189 is therefore inhibition of ICK (Accession NP_055735.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with ICK.

[29119] ICK (Accession NP_057597.2) is another GAM189 target gene, herein designated TARGET GENE. ICK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ICK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29120] Another function of GAM189 is therefore inhibition of ICK (Accession NP_057597.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK.

[29121] Insulin-like growth factor 1 (somatomedin c) (IGF1, Accession NP_000609.1) is another GAM189 target gene, herein designated TARGET GENE. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IGF1 BINDING SITE, desig-

nated SEQ ID:6279, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29122] Another function of GAM189 is therefore inhibition of Insulin-like growth factor 1 (somatomedin c) (IGF1, Accession NP_000609.1), a gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore may be associated with Growth retardation with sensorineural deafness and mental retardation. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Growth retardation with sensorineural deafness and mental retardation, and of other diseases and clinical conditions associated with IGF1.

[29123] The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Immunoglobulin mu binding protein 2 (IGHMBP2, Accession NP_002171.1) is another GAM189 target gene, herein designated TARGET GENE. IGHMBP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IGHMBP2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IGHMBP2 BINDING SITE, designated SEQ ID:17385, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29124] Another function of GAM189 is therefore inhibition of Immunoglobulin mu binding protein 2 (IGHMBP2, Accession NP_002171.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IGHMBP2.

[29125] Immunoglobulin lambda-like polypeptide 1 (IGLL1, Accession NP_690594.1) is another GAM189 target gene, herein designated TARGET GENE. IGLL1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by IGLL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IGLL1 BINDING SITE, designated SEQ ID:4573, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29126] Another function of GAM189 is therefore inhibition of Immunoglobulin lambda-like polypeptide 1 (IGLL1, Acces-

sion NP_690594.1), a gene which expressed only in pre-b- cells and a special b- cell line (which is surface ig negative). and therefore may be associated with Agammaglobulinemia, autosomal recessive. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Agammaglobulinemia, autosomal recessive, and of other diseases and clinical conditions associated with IGLL1.

[29127] The function of IGLL1 has been established by previous studies. The VpreB (OMIM Ref. No. 605141) and lambda-5 genes encode the iota and omega polypeptide chains, respectively (Pillai and Baltimore, 1988), which associate with the immunoglobulin (Ig) mu chain to form a molecular complex that is expressed on the surface of pre- B cells. This complex presumably regulates Ig gene rearrangements in the early steps of B- cell differentiation. In the mouse the 2 genes are simultaneously expressed in pre- B cells, are only 4.6 kb apart, and belong to the same transcription unit. A primary transcript is synthesized from which the pre- B and lambda- 5 mRNAs are derived by alternative splicing. In the human, however, Mattei et al. (1991) concluded that the 2 genes, designated VPREB1 and IGLL1, are separate. Schiff et al. (1989) isolated from

a human fetal liver cDNA library clones that were only 85% homologous to the functional C- lambda genes (IGLC; 147220) and showed that they represent additional non-allelic members of a C- lambda- like family. Using pulsed field gel electrophoresis, the genes were shown to be present on a 200- kb DNA fragment, distinct from the C-lambda cluster. A splicing event accounted for differences between the 2 cDNAs. By in situ hybridization, Mattei et al. (1991) demonstrated that the pre- B- specific lambda-like cluster is located in the 22q11.2- q12.3 region, distal to the IgC lambda locus. B- cell precursors transiently express a pre- B cell receptor complex consisting of a rearranged mu heavy chain, a surrogate light chain composed of lambda- 5/14.1 and VpreB, and the immunoglobulin-associated signal transducing chains, Ig- alpha and Ig-beta. Mutations in the mu heavy chain are associated with complete failure of B- cell development in both humans and mice. In humans, the picture is that of autosomal recessive agammaglobulinemia (147020.0001 ff). Mutations in murine lambda- 5 result in a 'leaky' phenotype with detectable humoral responses. In evaluating patients with agammaglobulinemia and markedly reduced numbers of B cells, Minegishi et al. (1998) identified a boy with muta-

tions on both alleles of the gene encoding lambda-5/14.1. The maternal allele carried a premature stop codon in the first exon of the gene and the paternal allele demonstrated 3- bp substitutions in a 33- bp sequence in exon 3. The 3 substitutions corresponded to the sequence in the lambda- 5/14.1 pseudogene 16.1 and resulted in an amino acid substitution at an invariant proline. When expressed in COS cells, the allele carrying the pseudogene sequence resulted in defective folding and secretion of mutant lambda- 5/14.1. These findings indicated that expression of the functional lambda- 5/14.1 is critical for B-cell development in the human

[29128]

[29129] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29130] Kudo, A.; Melchers, F. : A second gene, Vpre- B in the lambda 5 locus of the mouse, which appears to be selectively expressed in pre- B lymphocytes. EMBO J. 6: 2267-2272, 1987. ; and

[29131] Mattei, M.- G.; Fumoux, F.; Roeckel, N.; Fougereau, M.; Schiff, C. : The human pre- B- specific lambda- like cluster is located in the 22q11.2- 22q12.3 region, distal to

the IgC- lambda locus.

[29132] Further studies establishing the function and utilities of IGLL1 are found in John Hopkins OMIM database record ID 146770, and in cited publications listed in Table 5, which are hereby incorporated by reference.Immunoglobulin lambda-like polypeptide 1 (IGLL1, Accession NP_064455.1) is another GAM189 target gene, herein designated TARGET GENE. IGLL1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by IGLL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IGLL1 BINDING SITE, designated SEQ ID:4573, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29133] Another function of GAM189 is therefore inhibition of Immunoglobulin lambda-like polypeptide 1 (IGLL1, Accession NP_064455.1), a gene which expressed only in pre-b- cells and a special b- cell line (which is surface ig negative). and therefore may be associated with Agammaglobulinemia, autosomal recessive. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of Agammaglobulinemia, autosomal recessive, and of other diseases and clinical conditions associated with IGLL1.

[29134] The function of IGLL1 has been established by previous studies. The VpreB (OMIM Ref. No. 605141) and lambda-5 genes encode the iota and omega polypeptide chains, respectively (Pillai and Baltimore, 1988), which associate with the immunoglobulin (Ig) mu chain to form a molecular complex that is expressed on the surface of pre- B cells. This complex presumably regulates Ig gene rearrangements in the early steps of B- cell differentiation. In the mouse the 2 genes are simultaneously expressed in pre- B cells, are only 4.6 kb apart, and belong to the same transcription unit. A primary transcript is synthesized from which the pre- B and lambda- 5 mRNAs are derived by alternative splicing. In the human, however, Mattei et al. (1991) concluded that the 2 genes, designated VPREB1 and IGLL1, are separate. Schiff et al. (1989) isolated from a human fetal liver cDNA library clones that were only 85% homologous to the functional C- lambda genes (IGLC; 147220) and showed that they represent additional non-allelic members of a C- lambda- like family. Using pulsed field gel electrophoresis, the genes were shown to be

present on a 200- kb DNA fragment, distinct from the C-lambda cluster. A splicing event accounted for differences between the 2 cDNAs. By in situ hybridization, Mattei et al. (1991) demonstrated that the pre- B- specific lambda-like cluster is located in the 22q11.2- q12.3 region, distal to the IgC lambda locus. B- cell precursors transiently express a pre- B cell receptor complex consisting of a rearranged mu heavy chain, a surrogate light chain composed of lambda- 5/14.1 and VpreB, and the immunoglobulin-associated signal transducing chains, Ig- alpha and Ig-beta. Mutations in the mu heavy chain are associated with complete failure of B- cell development in both humans and mice. In humans, the picture is that of autosomal recessive agammaglobulinemia (147020.0001 ff). Mutations in murine lambda- 5 result in a 'leaky' phenotype with detectable humoral responses. In evaluating patients with agammaglobulinemia and markedly reduced numbers of B cells, Minegishi et al. (1998) identified a boy with mutations on both alleles of the gene encoding lambda-5/14.1. The maternal allele carried a premature stop codon in the first exon of the gene and the paternal allele demonstrated 3- bp substitutions in a 33- bp sequence in exon 3. The 3 substitutions corresponded to the sequence

in the lambda- 5/14.1 pseudogene 16.1 and resulted in an amino acid substitution at an invariant proline. When expressed in COS cells, the allele carrying the pseudogene sequence resulted in defective folding and secretion of mutant lambda- 5/14.1. These findings indicated that expression of the functional lambda- 5/14.1 is critical for B-cell development in the human

[29135]

[29136] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29137] Kudo, A.; Melchers, F. : A second gene, Vpre- B in the lambda 5 locus of the mouse, which appears to be selectively expressed in pre- B lymphocytes. EMBO J. 6: 2267-2272, 1987. ; and

[29138] Mattei, M.- G.; Fumoux, F.; Roeckel, N.; Fougereau, M.; Schiff, C. : The human pre- B- specific lambda- like cluster is located in the 22q11.2- 22q12.3 region, distal to the IgC- lambda locus.

[29139] Further studies establishing the function and utilities of IGLL1 are found in John Hopkins OMIM database record ID 146770, and in cited publications listed in Table 5, which are hereby incorporated by reference.Interleukin 11 (IL11,

Accession NP_000632.1) is another GAM189 target gene, herein designated TARGET GENE. IL11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL11 BINDING SITE, designated SEQ ID:11544, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29140] Another function of GAM189 is therefore inhibition of Interleukin 11 (IL11, Accession NP_000632.1), a gene which stimulates the proliferation of hematopoietic stem cells and megakaryocyte progenitor cells and induces megakaryocyte maturation. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL11.

[29141] The function of IL11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM41.1.Interleukin 12 receptor, beta 1 (IL12RB1, Accession NP_714912.1) is another GAM189 target gene, herein designated TARGET GENE. IL12RB1 BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL12RB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL12RB1 BINDING SITE, designated SEQ ID:10756, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29142] Another function of GAM189 is therefore inhibition of Interleukin 12 receptor, beta 1 (IL12RB1, Accession NP_714912.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL12RB1.

[29143] Interleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NP_757366.1) is another GAM189 target gene, herein designated TARGET GENE. IL16 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by IL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL16 BINDING SITE, designated SEQ ID:19554, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[29144] Another function of GAM189 is therefore inhibition of Interleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NP_757366.1), a gene which modulates T- cell activation. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL16.

[29145] The function of IL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Interleukin 21 receptor (IL21R, Accession NP_851564.1) is another GAM189 target gene, herein designated TARGET GENE. IL21R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL21R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL21R BINDING SITE, designated SEQ ID:498, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29146] Another function of GAM189 is therefore inhibition of Interleukin 21 receptor (IL21R, Accession NP_851564.1), a

gene which is involved in receptor mediated endocytosis and transduces the mitogenic signals of il- 2. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL21R.

[29147] The function of IL21R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Interleukin 21 receptor (IL21R, Accession NP_851565.1) is another GAM189 target gene, herein designated TARGET GENE. IL21R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL21R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL21R BINDING SITE, designated SEQ ID:498, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29148] Another function of GAM189 is therefore inhibition of Interleukin 21 receptor (IL21R, Accession NP_851565.1), a gene which is involved in receptor mediated endocytosis and transduces the mitogenic signals of il- 2. Accordingly,

utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL21R.

[29149] The function of IL21R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Interleukin 21 receptor (IL21R, Accession NP_068570.1) is another GAM189 target gene, herein designated TARGET GENE. IL21R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL21R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL21R BINDING SITE, designated SEQ ID:498, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29150] Another function of GAM189 is therefore inhibition of Interleukin 21 receptor (IL21R, Accession NP_068570.1), a gene which is involved in receptor mediated endocytosis and transduces the mitogenic signals of il- 2. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with IL21R.

[29151] The function of IL21R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Interleukin 28 receptor, alpha (IL28RA, Accession NP_775087.1) is another GAM189 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:7046, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29152] Another function of GAM189 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_775087.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[29153] Interleukin 28 receptor, alpha (IL28RA, Accession NP_734464.1) is another GAM189 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:7046, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29154] Another function of GAM189 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_734464.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[29155] Interleukin 28 receptor, alpha (IL28RA, Accession NP_775088.1) is another GAM189 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:7046, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[29156] Another function of GAM189 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_775088.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[29157] Interleukin 5 receptor, alpha (IL5RA, Accession NP_783853.1) is another GAM189 target gene, herein designated TARGET GENE. IL5RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL5RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL5RA BINDING SITE, designated SEQ ID:8557, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29158] Another function of GAM189 is therefore inhibition of Interleukin 5 receptor, alpha (IL5RA, Accession NP_783853.1), a gene which is the receptor for interleukin- 5. the alpha chain binds to il- 5. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

IL5RA.

[29159] The function of IL5RA has been established by previous studies. Tavernier et al. (1991) isolated cDNA clones encoding 2 receptor proteins involved in the binding of human interleukin- 5 (IL5; 147850). The major transcript of this receptor gene, as analyzed in both eosinophilic sublines of human promyelocytic cells and in eosinophilic myelocytes grown from cord blood, encodes a secreted form of this receptor. A second component of the receptor was found to be identical to the beta chain of the human granulocyte- macrophage colony- stimulating factor high affinity receptor (CSF2RB; 138981). The finding that IL5 and CSF2 share a receptor subunit provides a molecular basis for the observation that these cytokines can partially interfere with each other's binding and have highly overlapping biologic activities on eosinophils. The common use of the same receptor component is reminiscent of the structural relatedness of IL3 (OMIM Ref. No. 147740), IL5, and GM- CSF (CSF2; 138960). The homology at the C terminus may indicate a related binding domain. The common origin of all 3 cytokines is also suggested by their clustered chromosomal localization and by the structure of their genes. Using a yeast 2- hybrid screen of a granu-

locyte cDNA library with the cytoplasmic domain of IL5RA as bait, Geijsen et al. (2001) identified an interaction of IL5RA with syntenin (SDCBP; 602217). GST pull- down, BI-Acore, coimmunoprecipitation, and deletion mutant analyses confirmed an association of syntenin with the last 15 C- terminal residues of IL5RA; syntenin did not interact with CFS2RB. Within this 15- residue stretch of IL5RA, the C- terminal phenylalanine is critical. Deletion of either of the 2 tandem PDZ domains of syntenin, which are known to interact with C- terminal peptide sequences, abrogated the IL5RA- syntenin interaction. A second 2- hybrid screen identified the mouse transcriptional factor Sox4 (OMIM Ref. No. 184430) as a binding partner for syntenin but not for IL5RA. The syntenin- Sox4 interaction occurs outside of the PDZ domains of syntenin. Luciferase reporter analysis and fluorescence microscopy showed that IL5, but not IL3, induces cytoplasmic and nuclear expression of syntenin and, in a syntenin- and cytoplasmic IL5RA- dependent manner, of Sox4. Geijsen et al. (2001) concluded that syntenin acts as an adaptor molecule in the IL5RA- mediated activation of SOX4. They also noted that mice lacking either Il5ra or Sox4 have defects in B-cell development

[29160]

[29161] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29162] Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers, W.; Plaetinck, G. : A human high affinity interleukin- 5 receptor (IL5R) is composed of an IL5- specific alpha chain and a beta chain shared with the receptor for GM- CSF. Cell 66: 1175- 1184, 1991. ; and

[29163] Geijsen, N.; Uings, I. J.; Pals, C.; Armstrong, J.; McKinnon, M.; Raaijmakers, J. A. M.; Lammers, J.- W. J.; Koenderman, L.; Coffer, P. J. : Cytokine- specific transcriptional regulation t.

[29164] Further studies establishing the function and utilities of IL5RA are found in John Hopkins OMIM database record ID 147851, and in cited publications listed in Table 5, which are hereby incorporated by reference.Interleukin 5 receptor, alpha (IL5RA, Accession NP_000555.2) is another GAM189 target gene, herein designated TARGET GENE. IL5RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL5RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL5RA BINDING SITE, designated SEQ ID:8557, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29165] Another function of GAM189 is therefore inhibition of Interleukin 5 receptor, alpha (IL5RA, Accession NP_000555.2), a gene which is the receptor for interleukin- 5. the alpha chain binds to il- 5. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL5RA.

[29166] The function of IL5RA has been established by previous studies. Tavernier et al. (1991) isolated cDNA clones encoding 2 receptor proteins involved in the binding of human interleukin- 5 (IL5; 147850). The major transcript of this receptor gene, as analyzed in both eosinophilic sublines of human promyelocytic cells and in eosinophilic myelocytes grown from cord blood, encodes a secreted form of this receptor. A second component of the receptor was found to be identical to the beta chain of the human granulocyte- macrophage colony- stimulating factor high affinity receptor (CSF2RB; 138981). The finding that IL5 and CSF2 share a receptor subunit provides a molecular

basis for the observation that these cytokines can partially interfere with each other's binding and have highly overlapping biologic activities on eosinophils. The common use of the same receptor component is reminiscent of the structural relatedness of IL3 (OMIM Ref. No. 147740), IL5, and GM- CSF (CSF2; 138960). The homology at the C terminus may indicate a related binding domain. The common origin of all 3 cytokines is also suggested by their clustered chromosomal localization and by the structure of their genes. Using a yeast 2- hybrid screen of a granulocyte cDNA library with the cytoplasmic domain of IL5RA as bait, Geijsen et al. (2001) identified an interaction of IL5RA with syntenin (SDCBP; 602217). GST pull- down, BIAcore, coimmunoprecipitation, and deletion mutant analyses confirmed an association of syntenin with the last 15 C- terminal residues of IL5RA; syntenin did not interact with CFS2RB. Within this 15- residue stretch of IL5RA, the C- terminal phenylalanine is critical. Deletion of either of the 2 tandem PDZ domains of syntenin, which are known to interact with C- terminal peptide sequences, abrogated the IL5RA- syntenin interaction. A second 2- hybrid screen identified the mouse transcriptional factor Sox4 (OMIM Ref. No. 184430) as a binding partner for syntenin

but not for IL5RA. The syntenin- Sox4 interaction occurs outside of the PDZ domains of syntenin. Luciferase reporter analysis and fluorescence microscopy showed that IL5, but not IL3, induces cytoplasmic and nuclear expression of syntenin and, in a syntenin- and cytoplasmic IL5RA- dependent manner, of Sox4. Geijsen et al. (2001) concluded that syntenin acts as an adaptor molecule in the IL5RA- mediated activation of SOX4. They also noted that mice lacking either Il5ra or Sox4 have defects in B-cell development

[29167]

[29168] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29169] Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers, W.; Plaetinck, G. : A human high affinity interleukin- 5 receptor (IL5R) is composed of an IL5- specific alpha chain and a beta chain shared with the receptor for GM- CSF. Cell 66: 1175- 1184, 1991. ; and

[29170] Geijsen, N.; Uings, I. J.; Pals, C.; Armstrong, J.; McKinnon, M.; Raaijmakers, J. A. M.; Lammers, J.- W. J.; Koenderman, L.; Coffer, P. J. : Cytokine- specific transcriptional regulation t.

[29171] Further studies establishing the function and utilities of IL5RA are found in John Hopkins OMIM database record ID 147851, and in cited publications listed in Table 5, which are hereby incorporated by reference.Interleukin enhancer binding factor 3, 90kda (ILF3, Accession NP_036350.2) is another GAM189 target gene, herein designated TARGET GENE. ILF3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ILF3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ILF3 BINDING SITE, designated SEQ ID:17287, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29172] Another function of GAM189 is therefore inhibition of Interleukin enhancer binding factor 3, 90kda (ILF3, Accession NP_036350.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ILF3.

[29173] IMPACT (Accession NP_060909.1) is another GAM189 target gene, herein designated TARGET GENE. IMPACT BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by IMPACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IMPACT BINDING SITE, designated SEQ ID:8975, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29174] Another function of GAM189 is therefore inhibition of IMPACT (Accession NP_060909.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMPACT.

[29175] INHBE (Accession NP_113667.1) is another GAM189 target gene, herein designated TARGET GENE. INHBE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INHBE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INHBE BINDING SITE, designated SEQ ID:16283, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29176] Another function of GAM189 is therefore inhibition of INHBE (Accession NP_113667.1) . Accordingly, utilities of

GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INHBE.

[29177] Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) is another GAM189 target gene, herein designated TARGET GENE. INMT BINDING SITE1 and INMT BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by INMT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INMT BINDING SITE1 and INMT BINDING SITE2, designated SEQ ID:9149 and SEQ ID:11523 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29178] Another function of GAM189 is therefore inhibition of Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INMT.

[29179] Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) is another GAM189 target gene, herein designated TARGET GENE. IRF4 BINDING SITE1 and IRF4 BINDING SITE2 are target binding sites found in untrans-

lated regions of mRNA encoded by IRF4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRF4 BINDING SITE1 and IRF4 BINDING SITE2, designated SEQ ID:2698 and SEQ ID:1517 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29180] Another function of GAM189 is therefore inhibition of Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRF4.

[29181] Integrin, alpha x (antigen cd11c (p150), alpha polypeptide) (ITGAX, Accession NP_000878.1) is another GAM189 target gene, herein designated TARGET GENE. ITGAX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITGAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITGAX BINDING SITE, designated SEQ ID:559, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[29182] Another function of GAM189 is therefore inhibition of Integrin, alpha x (antigen cd11c (p150), alpha polypeptide) (ITGAX, Accession NP_000878.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAX.

[29183] Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3, Accession NP_000206.1) is another GAM189 target gene, herein designated TARGET GENE. JAK3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JAK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JAK3 BINDING SITE, designated SEQ ID:18060, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29184] Another function of GAM189 is therefore inhibition of Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3, Accession NP_000206.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAK3.

[29185] JM11 (Accession NP_296375.1) is another GAM189 target

gene, herein designated TARGET GENE. JM11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JM11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JM11 BINDING SITE, designated SEQ ID:10197, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29186] Another function of GAM189 is therefore inhibition of JM11 (Accession NP_296375.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JM11.

[29187] Jerky homolog (mouse) (JRK, Accession NP_003715.1) is another GAM189 target gene, herein designated TARGET GENE. JRK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JRK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JRK BINDING SITE, designated SEQ ID:3927, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29188] Another function of GAM189 is therefore inhibition of Jerky homolog (mouse) (JRK, Accession NP_003715.1), a gene which might function as a DNA- binding protein. and therefore may be associated with Absence epilepsy. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Absence epilepsy, and of other diseases and clinical conditions associated with JRK.

[29189] The function of JRK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.2.Potassium inwardly-rectifying channel, subfamily j, member 11 (KCNJ11, Accession NP_000516.2) is another GAM189 target gene, herein designated TARGET GENE. KCNJ11 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KCNJ11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ11 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29190] Another function of GAM189 is therefore inhibition of

Potassium inwardly-rectifying channel, subfamily j, member 11 (KCNJ11, Accession NP_000516.2), a gene which is controlled by g proteins. inward rectifier k+ channels are characterized by a greater tendancy to allow potassium to flow into the cell rather than out of it. and therefore is associated with Persistent hyperinsulinemic hypoglycemia of infancy. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Persistent hyperinsulinemic hypoglycemia of infancy, and of other diseases and clinical conditions associated with KCNJ11.

[29191] The function of KCNJ11 has been established by previous studies. ATP- sensitive potassium currents, I(KATP), were discovered in cardiac muscle and later found in pancreatic beta cells, pituitary tissue, skeletal muscle, brain, and vascular and nonvascular smooth muscle. I(KATP) functions in secretion and muscle contraction by coupling metabolic activity to membrane potential. In pancreatic beta cells, ATP- potassium channels are crucial for the regulation of glucose- induced insulin secretion and are the target for the sulfonylureas, oral hypoglycemic agents widely used in the treatment of noninsulin- dependent diabetes mellitus (NIDDM; 125853), and for diazoxide, a potassium channel opener. The sulfonylurea receptor SUR

(OMIM Ref. No. 600509) is a member of the ATP- binding cassette superfamily with multiple transmembrane- spanning domains and 2 potential nucleotide- binding folds. Truncation of SUR that removes the second nucleotide-binding fold causes familial persistent hyperinsulinemic hypoglycemia of infancy (see, OMIM Ref. No., for example, 600509.0001), a rare disorder of glucose homeostasis characterized by unregulated insulin secretion despite severe hypoglycemia. Although these observations imply that SUR is closely associated with, or even a subunit of, K(ATP) channels, expression of SUR alone had not produced a measurable I(KATP). Inagaki et al. (1995) cloned a member of the inwardly rectifying potassium channel family, which they called BIR or Kir6.2, in the nomenclature of Chandy and Gutman (1993). The channel was expressed in large amounts in rat pancreatic islets and glucose- responsive insulin- secreting cell lines. The sequence showed a single open reading frame encoding a 390- amino acid protein with 2 putative transmembrane segments. The mouse homolog also had a single open reading frame encoding a 390- amino acid protein with 96% amino acid identity with human BIR, thus confirming that the gene encoding human BIR is intronless in the

protein- coding region. Several other genes encoding inward rectifiers lack introns. This gene is also symbolized KCNJ11.

[29192] Animal model experiments lend further support to the function of KCNJ11. ATP- sensitive potassium channels are activated by various metabolic stresses, including hypoxia. The substantia nigra pars reticulata, the area with the highest expression of ATP- sensitive potassium channels in the brain, plays a pivotal role in the control of seizures. Yamada et al. (2001) studied mutant mice lacking the Kir6.2 subunit of ATP- sensitive potassium channels and found that they were susceptible to generalized seizures after brief hypoxia. In normal mice, the substantia nigra pars reticulata neuron activity was inactivated during hypoxia by the opening of the postsynaptic ATP-sensitive potassium channels, whereas in knockout mice, the activity of these neurons was enhanced. ATP- sensitive potassium channels exert a depressant effect on substantia nigra pars reticulata neuronal activity during hypoxia and may be involved in the nigral protection mechanism against generalized seizures

[29193] It is appreciated that the abovementioned animal model for KCNJ11 is acknowledged by those skilled in the art as

a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[29194] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29195] Thomas, P. M.; Cote, G. J.; Hallman, D. M.; Mathew, P. M. : Homozygosity mapping, to chromosome 11p, of the gene for familial persistent hyperinsulinemic hypoglycemia of infancy. Am. J. Hum. Genet. 56: 416- 421, 1995. ; and

[29196] Yamada, K.; Ji, J. J.; Yuan, H.; Miki, T.; Sata, S.; Horimoto, N.; Shimizu, T.; Seino, S.; Inagaki, N. : Protective role of ATP- sensitive potassium channels in hypoxia- induced generalize.

[29197] Further studies establishing the function and utilities of KCNJ11 are found in John Hopkins OMIM database record ID 600937, and in cited publications listed in Table 5, which are hereby incorporated by reference.Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_061128.1) is another GAM189 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNJ16, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:2456, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29198] Another function of GAM189 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_061128.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[29199] Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733937.1) is another GAM189 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNJ16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:2456, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29200] Another function of GAM189 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733937.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[29201] Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733938.1) is another GAM189 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNJ16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:2456, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29202] Another function of GAM189 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733938.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with KCNJ16.

[29203] KENAE (Accession NP_789786.1) is another GAM189 target gene, herein designated TARGET GENE. KENAE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KENAE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KENAE BINDING SITE, designated SEQ ID:14862, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29204] Another function of GAM189 is therefore inhibition of KENAE (Accession NP_789786.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KENAE.

[29205] KIAA0063 (Accession NP_055691.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0063 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0063, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0063 BINDING SITE, designated SEQ ID:5884, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29206] Another function of GAM189 is therefore inhibition of KIAA0063 (Accession NP_055691.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0063.

[29207] KIAA0082 (Accession NP_055865.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0082 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0082, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0082 BINDING SITE, designated SEQ ID:18751, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29208] Another function of GAM189 is therefore inhibition of KIAA0082 (Accession NP_055865.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0082.

[29209] KIAA0087 (Accession NP_055584.1) is another GAM189

target gene, herein designated TARGET GENE. KIAA0087 BINDING SITE1 and KIAA0087 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0087, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0087 BINDING SITE1 and KIAA0087 BINDING SITE2, designated SEQ ID:10179 and SEQ ID:7956 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29210] Another function of GAM189 is therefore inhibition of KIAA0087 (Accession NP_055584.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0087.

[29211] KIAA0117 (Accession XP_290939.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA0117 BINDING SITE, designated SEQ ID:9255, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29212] Another function of GAM189 is therefore inhibition of KIAA0117 (Accession XP_290939.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0117.

[29213] KIAA0182 (Accession XP_050495.4) is another GAM189 target gene, herein designated TARGET GENE. KIAA0182 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0182, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0182 BINDING SITE, designated SEQ ID:2218, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29214] Another function of GAM189 is therefore inhibition of KIAA0182 (Accession XP_050495.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0182.

[29215] KIAA0186 (Accession NP_066545.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0186 BINDING SITE, designated SEQ ID:2625, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29216] Another function of GAM189 is therefore inhibition of KIAA0186 (Accession NP_066545.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0186.

[29217] KIAA0205 (Accession NP_055688.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0205 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0205, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0205 BINDING SITE, designated SEQ ID:3429, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29218] Another function of GAM189 is therefore inhibition of KIAA0205 (Accession NP_055688.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0205.

[29219] KIAA0237 (Accession NP_055562.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0237 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0237, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0237 BINDING SITE, designated SEQ ID:17386, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29220] Another function of GAM189 is therefore inhibition of KIAA0237 (Accession NP_055562.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0237.

[29221] KIAA0295 (Accession XP_042833.2) is another GAM189

target gene, herein designated TARGET GENE. KIAA0295 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0295, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0295 BINDING SITE, designated SEQ ID:10742, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29222] Another function of GAM189 is therefore inhibition of KIAA0295 (Accession XP_042833.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0295.

[29223] KIAA0435 (Accession NP_055616.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0435 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0435, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0435 BINDING SITE, designated SEQ ID:5041, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[29224] Another function of GAM189 is therefore inhibition of KIAA0435 (Accession NP_055616.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0435.

[29225] KIAA0446 (Accession XP_044155.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0446 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0446, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0446 BINDING SITE, designated SEQ ID:1475, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29226] Another function of GAM189 is therefore inhibition of KIAA0446 (Accession XP_044155.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0446.

[29227] KIAA0459 (Accession XP_027862.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0459

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:4531, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29228] Another function of GAM189 is therefore inhibition of KIAA0459 (Accession XP_027862.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459.

[29229] KIAA0469 (Accession NP_055666.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0469 BINDING SITE1 and KIAA0469 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0469, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0469 BINDING SITE1 and KIAA0469 BINDING SITE2, designated SEQ ID:9147 and SEQ ID:9493 respectively, to the nucleotide sequence of

GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29230] Another function of GAM189 is therefore inhibition of KIAA0469 (Accession NP_055666.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469.

[29231] KIAA0475 (Accession NP_055679.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0475 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:16940, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29232] Another function of GAM189 is therefore inhibition of KIAA0475 (Accession NP_055679.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475.

[29233] KIAA0493 (Accession XP_034717.1) is another GAM189

target gene, herein designated TARGET GENE. KIAA0493 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0493 BINDING SITE, designated SEQ ID:17206, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29234] Another function of GAM189 is therefore inhibition of KIAA0493 (Accession XP_034717.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0493.

[29235] KIAA0495 (Accession XP_031397.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0495 BINDING SITE1 and KIAA0495 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0495, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0495 BINDING SITE1 and KIAA0495 BINDING SITE2, designated SEQ ID:14759 and

SEQ ID:5442 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29236] Another function of GAM189 is therefore inhibition of KIAA0495 (Accession XP_031397.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0495.

[29237] KIAA0513 (Accession NP_055547.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0513 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0513, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE, designated SEQ ID:3931, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29238] Another function of GAM189 is therefore inhibition of KIAA0513 (Accession NP_055547.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513.

[29239] KIAA0527 (Accession XP_171054.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0527 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0527, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0527 BINDING SITE, designated SEQ ID:19745, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29240] Another function of GAM189 is therefore inhibition of KIAA0527 (Accession XP_171054.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0527.

[29241] KIAA0532 (Accession XP_047659.6) is another GAM189 target gene, herein designated TARGET GENE. KIAA0532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0532 BINDING SITE, designated SEQ ID:12455, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29242] Another function of GAM189 is therefore inhibition of KIAA0532 (Accession XP_047659.6) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0532.

[29243] KIAA0555 (Accession NP_055605.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0555 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0555, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0555 BINDING SITE, designated SEQ ID:5555, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29244] Another function of GAM189 is therefore inhibition of KIAA0555 (Accession NP_055605.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0555.

[29245] KIAA0561 (Accession XP_038150.2) is another GAM189

target gene, herein designated TARGET GENE. KIAA0561 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0561, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0561 BINDING SITE, designated SEQ ID:9629, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29246] Another function of GAM189 is therefore inhibition of KIAA0561 (Accession XP_038150.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0561.

[29247] KIAA0562 (Accession NP_055519.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0562 BINDING SITE, designated SEQ ID:16544, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[29248] Another function of GAM189 is therefore inhibition of KIAA0562 (Accession NP_055519.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0562.

[29249] KIAA0563 (Accession NP_055649.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0563 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0563 BINDING SITE, designated SEQ ID:16377, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29250] Another function of GAM189 is therefore inhibition of KIAA0563 (Accession NP_055649.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0563.

[29251] KIAA0682 (Accession NP_055667.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0682

BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA0682, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0682 BINDING SITE, designated SEQ ID:6522, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29252] Another function of GAM189 is therefore inhibition of KIAA0682 (Accession NP_055667.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0682.

[29253] KIAA0804 (Accession XP_291080.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0804 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0804, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0804 BINDING SITE, designated SEQ ID:14656, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29254] Another function of GAM189 is therefore inhibition of KIAA0804 (Accession XP_291080.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0804.

[29255] KIAA0831 (Accession NP_055739.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0831 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0831, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0831 BINDING SITE, designated SEQ ID:3260, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29256] Another function of GAM189 is therefore inhibition of KIAA0831 (Accession NP_055739.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0831.

[29257] KIAA0841 (Accession XP_049237.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0841 BINDING SITE1 and KIAA0841 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by KIAA0841, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0841 BINDING SITE1 and KIAA0841 BINDING SITE2, designated SEQ ID:8185 and SEQ ID:5490 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29258] Another function of GAM189 is therefore inhibition of KIAA0841 (Accession XP_049237.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0841.

[29259] KIAA0861 (Accession NP_055893.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA0861 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0861, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0861 BINDING SITE, designated SEQ ID:2153, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[29260] Another function of GAM189 is therefore inhibition of KIAA0861 (Accession NP_055893.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0861.

[29261] KIAA0889 (Accession NP_056192.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0889 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA0889, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0889 BINDING SITE, designated SEQ ID:13271, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29262] Another function of GAM189 is therefore inhibition of KIAA0889 (Accession NP_056192.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0889.

[29263] KIAA0924 (Accession NP_055712.1) is another GAM189

target gene, herein designated TARGET GENE. KIAA0924 BINDING SITE1 and KIAA0924 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0924, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0924 BINDING SITE1 and KIAA0924 BINDING SITE2, designated SEQ ID:13297 and SEQ ID:7655 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29264] Another function of GAM189 is therefore inhibition of KIAA0924 (Accession NP_055712.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0924.

[29265] KIAA0931 (Accession XP_041191.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA0931 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0931, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA0931 BINDING SITE, designated SEQ ID:14272, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29266] Another function of GAM189 is therefore inhibition of KIAA0931 (Accession XP_041191.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0931.

[29267] KIAA0935 (Accession XP_052620.6) is another GAM189 target gene, herein designated TARGET GENE. KIAA0935 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0935, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0935 BINDING SITE, designated SEQ ID:11958, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29268] Another function of GAM189 is therefore inhibition of KIAA0935 (Accession XP_052620.6) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0935.

[29269] KIAA0962 (Accession XP_290942.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA0962 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0962, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0962 BINDING SITE, designated SEQ ID:8976, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29270] Another function of GAM189 is therefore inhibition of KIAA0962 (Accession XP_290942.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0962.

[29271] KIAA1002 (Accession XP_290584.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1002 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1002, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1002 BINDING SITE, designated SEQ ID:12518, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29272] Another function of GAM189 is therefore inhibition of KIAA1002 (Accession XP_290584.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1002.

[29273] KIAA1040 (Accession XP_051091.3) is another GAM189 target gene, herein designated TARGET GENE. KIAA1040 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1040, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1040 BINDING SITE, designated SEQ ID:11846, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29274] Another function of GAM189 is therefore inhibition of KIAA1040 (Accession XP_051091.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1040.

[29275] KIAA1041 (Accession NP_055762.1) is another GAM189

target gene, herein designated TARGET GENE. KIAA1041 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1041, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1041 BINDING SITE, designated SEQ ID:3653, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29276] Another function of GAM189 is therefore inhibition of KIAA1041 (Accession NP_055762.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1041.

[29277] KIAA1054 (Accession XP_043493.5) is another GAM189 target gene, herein designated TARGET GENE. KIAA1054 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1054, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1054 BINDING SITE, designated SEQ ID:14832, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[29278] Another function of GAM189 is therefore inhibition of KIAA1054 (Accession XP_043493.5) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1054.

[29279] KIAA1115 (Accession NP_055746.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1115 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1115, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1115 BINDING SITE, designated SEQ ID:9842, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29280] Another function of GAM189 is therefore inhibition of KIAA1115 (Accession NP_055746.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1115.

[29281] KIAA1128 (Accession NP_061872.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1128

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1128 BINDING SITE, designated SEQ ID:5783, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29282] Another function of GAM189 is therefore inhibition of KIAA1128 (Accession NP_061872.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1128.

[29283] KIAA1143 (Accession XP_044014.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1143 BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29284] Another function of GAM189 is therefore inhibition of KIAA1143 (Accession XP_044014.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1143.

[29285] KIAA1145 (Accession NP_065749.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1145 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1145, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1145 BINDING SITE, designated SEQ ID:17532, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29286] Another function of GAM189 is therefore inhibition of KIAA1145 (Accession NP_065749.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1145.

[29287] KIAA1155 (Accession XP_030864.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1155 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1155, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1155 BINDING SITE, designated SEQ ID:2664, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29288] Another function of GAM189 is therefore inhibition of KIAA1155 (Accession XP_030864.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1155.

[29289] KIAA1170 (Accession XP_045907.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1170 BINDING SITE, designated SEQ ID:10162, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29290] Another function of GAM189 is therefore inhibition of

KIAA1170 (Accession XP_045907.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1170.

[29291] KIAA1185 (Accession NP_065761.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1185 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1185, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1185 BINDING SITE, designated SEQ ID:5755, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29292] Another function of GAM189 is therefore inhibition of KIAA1185 (Accession NP_065761.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1185.

[29293] KIAA1193 (Accession XP_041843.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1193, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1193 BINDING SITE, designated SEQ ID:17517, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29294] Another function of GAM189 is therefore inhibition of KIAA1193 (Accession XP_041843.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1193.

[29295] KIAA1198 (Accession NP_065765.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE5 are target binding sites found in untranslated regions of mRNA encoded by KIAA1198, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE5, designated SEQ ID:13749, SEQ ID:16471, SEQ ID:12389, SEQ ID:16088 and SEQ ID:12478 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA,

also designated SEQ ID:246.

[29296] Another function of GAM189 is therefore inhibition of KIAA1198 (Accession NP_065765.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1198.

[29297] KIAA1209 (Accession XP_027307.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1209 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1209, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1209 BINDING SITE, designated SEQ ID:8271, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29298] Another function of GAM189 is therefore inhibition of KIAA1209 (Accession XP_027307.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1209.

[29299] KIAA1210 (Accession XP_172801.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1210

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1210, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1210 BINDING SITE, designated SEQ ID:9144, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29300] Another function of GAM189 is therefore inhibition of KIAA1210 (Accession XP_172801.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1210.

[29301] KIAA1257 (Accession XP_031577.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1257 BINDING SITE1 and KIAA1257 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1257, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1257 BINDING SITE1 and KIAA1257 BINDING SITE2, designated SEQ ID:11523 and SEQ ID:9032 respectively, to the nucleotide sequence of

GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29302] Another function of GAM189 is therefore inhibition of KIAA1257 (Accession XP_031577.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1257.

[29303] KIAA1268 (Accession XP_291055.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1268 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1268 BINDING SITE, designated SEQ ID:3236, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29304] Another function of GAM189 is therefore inhibition of KIAA1268 (Accession XP_291055.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1268.

[29305] KIAA1273 (Accession XP_300760.1) is another GAM189

target gene, herein designated TARGET GENE. KIAA1273 BINDING SITE1 and KIAA1273 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1273, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1273 BINDING SITE1 and KIAA1273 BINDING SITE2, designated SEQ ID:7374 and SEQ ID:4555 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29306] Another function of GAM189 is therefore inhibition of KIAA1273 (Accession XP_300760.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1273.

[29307] KIAA1276 (Accession XP_039169.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1276 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1276, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1276 BINDING SITE, designated SEQ ID:1905, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29308] Another function of GAM189 is therefore inhibition of KIAA1276 (Accession XP_039169.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1276.

[29309] KIAA1287 (Accession NP_065799.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1287 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1287, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1287 BINDING SITE, designated SEQ ID:9573, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29310] Another function of GAM189 is therefore inhibition of KIAA1287 (Accession NP_065799.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1287.

[29311] KIAA1393 (Accession XP_050793.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1393 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1393 BINDING SITE, designated SEQ ID:10123, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29312] Another function of GAM189 is therefore inhibition of KIAA1393 (Accession XP_050793.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1393.

[29313] KIAA1443 (Accession NP_065885.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1443 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1443, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1443 BINDING SITE, designated SEQ ID:15171, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29314] Another function of GAM189 is therefore inhibition of KIAA1443 (Accession NP_065885.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1443.

[29315] KIAA1456 (Accession XP_040100.3) is another GAM189 target gene, herein designated TARGET GENE. KIAA1456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1456 BINDING SITE, designated SEQ ID:5529, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29316] Another function of GAM189 is therefore inhibition of KIAA1456 (Accession XP_040100.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1456.

[29317] KIAA1463 (Accession XP_051160.2) is another GAM189

target gene, herein designated TARGET GENE. KIAA1463 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1463, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1463 BINDING SITE, designated SEQ ID:1667, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29318] Another function of GAM189 is therefore inhibition of KIAA1463 (Accession XP_051160.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1463.

[29319] KIAA1465 (Accession XP_027396.4) is another GAM189 target gene, herein designated TARGET GENE. KIAA1465 BINDING SITE1 and KIAA1465 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1465, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1465 BINDING SITE1 and KIAA1465 BINDING SITE2, designated SEQ ID:18838 and

SEQ ID:18992 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29320] Another function of GAM189 is therefore inhibition of KIAA1465 (Accession XP_027396.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1465.

[29321] KIAA1493 (Accession XP_034415.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1493 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1493 BINDING SITE, designated SEQ ID:15045, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29322] Another function of GAM189 is therefore inhibition of KIAA1493 (Accession XP_034415.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1493.

[29323] KIAA1508 (Accession XP_290952.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1508 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1508, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1508 BINDING SITE, designated SEQ ID:8820, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29324] Another function of GAM189 is therefore inhibition of KIAA1508 (Accession XP_290952.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1508.

[29325] KIAA1518 (Accession XP_170889.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1518 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA1518, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1518 BINDING SITE, designated

SEQ ID:13383, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29326] Another function of GAM189 is therefore inhibition of KIAA1518 (Accession XP_170889.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1518.

[29327] KIAA1530 (Accession XP_042661.5) is another GAM189 target gene, herein designated TARGET GENE. KIAA1530 BINDING SITE1 and KIAA1530 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1530, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1530 BINDING SITE1 and KIAA1530 BINDING SITE2, designated SEQ ID:4028 and SEQ ID:15284 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29328] Another function of GAM189 is therefore inhibition of KIAA1530 (Accession XP_042661.5) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA1530.

[29329] KIAA1550 (Accession XP_039393.3) is another GAM189 target gene, herein designated TARGET GENE. KIAA1550 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1550, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1550 BINDING SITE, designated SEQ ID:3790, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29330] Another function of GAM189 is therefore inhibition of KIAA1550 (Accession XP_039393.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1550.

[29331] KIAA1559 (Accession XP_054472.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1559 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1559, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA1559 BINDING SITE, designated SEQ ID:4029, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29332] Another function of GAM189 is therefore inhibition of KIAA1559 (Accession XP_054472.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1559.

[29333] KIAA1571 (Accession XP_027744.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1571 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1571, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1571 BINDING SITE, designated SEQ ID:14154, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29334] Another function of GAM189 is therefore inhibition of KIAA1571 (Accession XP_027744.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1571.

[29335] KIAA1615 (Accession NP_066002.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1615, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2, designated SEQ ID:10111 and SEQ ID:8549 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29336] Another function of GAM189 is therefore inhibition of KIAA1615 (Accession NP_066002.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1615.

[29337] KIAA1671 (Accession XP_037809.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1671 BINDING SITE1 and KIAA1671 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1671, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1671 BINDING SITE1 and KIAA1671 BINDING SITE2, designated SEQ ID:17191 and SEQ ID:7194 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29338] Another function of GAM189 is therefore inhibition of KIAA1671 (Accession XP_037809.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1671.

[29339] KIAA1712 (Accession XP_041497.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by KIAA1712, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2, designated SEQ ID:1142 and SEQ ID:14165 respectively, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29340] Another function of GAM189 is therefore inhibition of KIAA1712 (Accession XP_041497.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1712.

[29341] KIAA1712 (Accession XP_041497.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by KIAA1712, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2, designated SEQ ID:14165 and SEQ ID:1142 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29342] Another function of GAM189 is therefore inhibition of KIAA1712 (Accession XP_041497.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1712.

[29343] KIAA1724 (Accession XP_040280.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1724 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1724, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1724 BINDING SITE, designated SEQ ID:14630, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29344] Another function of GAM189 is therefore inhibition of KIAA1724 (Accession XP_040280.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1724.

[29345] KIAA1737 (Accession NP_219494.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1737 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1737, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1737 BINDING SITE, designated SEQ ID:10602, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29346] Another function of GAM189 is therefore inhibition of KIAA1737 (Accession NP_219494.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1737.

[29347] KIAA1775 (Accession NP_149091.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1775 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1775, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1775 BINDING SITE, designated SEQ ID:1618, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29348] Another function of GAM189 is therefore inhibition of KIAA1775 (Accession NP_149091.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1775.

[29349] KIAA1784 (Accession NP_115820.1) is another GAM189

target gene, herein designated TARGET GENE. KIAA1784 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1784, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1784 BINDING SITE, designated SEQ ID:11058, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29350] Another function of GAM189 is therefore inhibition of KIAA1784 (Accession NP_115820.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1784.

[29351] KIAA1822 (Accession XP_041566.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1822 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1822 BINDING SITE, designated SEQ ID:10095, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[29352] Another function of GAM189 is therefore inhibition of KIAA1822 (Accession XP_041566.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1822.

[29353] KIAA1827 (Accession XP_290834.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1827 BINDING SITE1 and KIAA1827 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1827, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1827 BINDING SITE1 and KIAA1827 BINDING SITE2, designated SEQ ID:2143 and SEQ ID:12636 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29354] Another function of GAM189 is therefore inhibition of KIAA1827 (Accession XP_290834.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1827.

[29355] KIAA1829 (Accession XP_030378.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1829 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1829, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1829 BINDING SITE, designated SEQ ID:14863, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29356] Another function of GAM189 is therefore inhibition of KIAA1829 (Accession XP_030378.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1829.

[29357] KIAA1836 (Accession XP_114087.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1836 BINDING SITE, designated SEQ ID:12627, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29358] Another function of GAM189 is therefore inhibition of KIAA1836 (Accession XP_114087.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1836.

[29359] KIAA1853 (Accession XP_045184.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1853 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1853, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1853 BINDING SITE, designated SEQ ID:19095, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29360] Another function of GAM189 is therefore inhibition of KIAA1853 (Accession XP_045184.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1853.

[29361] KIAA1904 (Accession XP_056282.1) is another GAM189

target gene, herein designated TARGET GENE. KIAA1904 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1904, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1904 BINDING SITE, designated SEQ ID:16492, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29362] Another function of GAM189 is therefore inhibition of KIAA1904 (Accession XP_056282.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1904.

[29363] KIAA1922 (Accession XP_057040.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1922 BINDING SITE, designated SEQ ID:7553, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[29364] Another function of GAM189 is therefore inhibition of KIAA1922 (Accession XP_057040.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1922.

[29365] KIAA1924 (Accession NP_694971.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA1924 BINDING SITE1 and KIAA1924 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1924, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1924 BINDING SITE1 and KIAA1924 BINDING SITE2, designated SEQ ID:1857 and SEQ ID:8341 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29366] Another function of GAM189 is therefore inhibition of KIAA1924 (Accession NP_694971.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1924.

[29367] KIAA1937 (Accession XP_057107.3) is another GAM189 target gene, herein designated TARGET GENE. KIAA1937 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1937, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1937 BINDING SITE, designated SEQ ID:2983, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29368] Another function of GAM189 is therefore inhibition of KIAA1937 (Accession XP_057107.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1937.

[29369] KIAA1971 (Accession XP_058720.4) is another GAM189 target gene, herein designated TARGET GENE. KIAA1971 BINDING SITE1 and KIAA1971 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1971, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1971 BINDING SITE1 and

KIAA1971 BINDING SITE2, designated SEQ ID:6902 and SEQ ID:11506 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29370] Another function of GAM189 is therefore inhibition of KIAA1971 (Accession XP_058720.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1971.

[29371] KIAA1987 (Accession XP_113870.1) is another GAM189 target gene, herein designated TARGET GENE. KIAA1987 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1987, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1987 BINDING SITE, designated SEQ ID:7554, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29372] Another function of GAM189 is therefore inhibition of KIAA1987 (Accession XP_113870.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1987.

[29373] KIAA2028 (Accession XP_059415.2) is another GAM189 target gene, herein designated TARGET GENE. KIAA2028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA2028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA2028 BINDING SITE, designated SEQ ID:12100, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29374] Another function of GAM189 is therefore inhibition of KIAA2028 (Accession XP_059415.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2028.

[29375] Kruppel-like factor 12 (KLF12, Accession NP_009180.3) is another GAM189 target gene, herein designated TARGET GENE. KLF12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLF12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of KLF12 BINDING SITE, designated SEQ ID:1127, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29376] Another function of GAM189 is therefore inhibition of Kruppel-like factor 12 (KLF12, Accession NP_009180.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF12.

[29377] Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_002253.1) is another GAM189 target gene, herein designated TARGET GENE. KLRD1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLRD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLRD1 BINDING SITE, designated SEQ ID:2353, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29378] Another function of GAM189 is therefore inhibition of Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_002253.1), a gene which is a re-

ceptor for the recognition of mhc class i hla- e molecules by nk cells and some cytotoxic t- cells. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLRD1.

[29379] The function of KLRD1 has been established by previous studies. Natural killer (NK) cells are a distinct lineage of lymphocytes that mediate cytotoxic activity and secrete cytokines upon immune stimulation. Several genes of the C- type lectin superfamily, including members of the NKG2 family, are expressed by NK cells and may be involved in the regulation of NK cell function. See NKG2A, 161555. To study CD94, an antigen preferentially expressed on NK cells, Chang et al. (1995) used an expression cloning strategy to isolate an IL2- activated polyclonal NK cell line cDNA encoding CD94. Northern blot analysis revealed that CD94 is expressed as 3 major transcripts of 0.8, 1.8, and 3.5 kb and a minor transcript of 5.5 kb in NK cell lines. The predicted protein contains a 147- amino acid extracellular domain with several motifs characteristic of C- type lectins, a 26- amino acid transmembrane domain, and a 7- amino acid cytoplasmic domain. CD94 is classified as a type II membrane protein

because it has an external C terminus. The amino acid sequence of CD94 is 27 to 32% identical to those of NKG2 family members NKG2A, NKG2C (KLRC2; 602891), NKG2D (OMIM Ref. No. 602893), and NKG2E (KLRC3; 602892). Chang et al. (1995) stated that the virtual absence of a cytoplasmic domain implies that CD94 function requires association with other receptors. Lazetic et al. (1996) demonstrated that CD94 forms disulfide- bonded heterodimers with NKG2A, NKG2C, and NKG2E. Rodriguez et al. (1998) reported that the CD94 gene contains 6 exons. Using S1 nuclease protection and primer extension assays, they found that transcription initiation in CD94 is heterogeneous, but is restricted to a 60- bp region around the major initiation site. Chang et al. (1995) mapped the CD94 gene to chromosome 12 using a somatic cell hybrid panel. By analysis of a cosmid contig, Plougastel and Trowsdale (1998) found that the CD94 gene is located at 12p13.2- p12.3, within the NK complex, a cluster of C- type lectin genes preferentially expressed in NK cells.

[29380]

[29381] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[29382] Plougastel, B.; Trowsdale, J. : Sequence analysis of a 62-kb region overlapping the human KLRC cluster of genes. Genomics 49: 193- 199, 1998. ; and

[29383] Rodriguez, A.; Carretero, M.; Glienke, J.; Bellon, T.; Ramirez, A.; Lehrach, H.; Francis, F.; Lopez- Botet, M. : Structure of the human CD94 C- type lectin gene. Immunogenetics 47: 305- 309.

[29384] Further studies establishing the function and utilities of KLRD1 are found in John Hopkins OMIM database record ID 602894, and in cited publications listed in Table 5, which are hereby incorporated by reference.Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_031360.1) is another GAM189 target gene, herein designated TARGET GENE. KLRD1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLRD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLRD1 BINDING SITE, designated SEQ ID:2353, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29385] Another function of GAM189 is therefore inhibition of Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_031360.1), a gene which is a receptor for the recognition of mhc class i hla- e molecules by nk cells and some cytotoxic t- cells. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLRD1.

[29386] The function of KLRD1 has been established by previous studies. Natural killer (NK) cells are a distinct lineage of lymphocytes that mediate cytotoxic activity and secrete cytokines upon immune stimulation. Several genes of the C- type lectin superfamily, including members of the NKG2 family, are expressed by NK cells and may be involved in the regulation of NK cell function. See NKG2A, 161555. To study CD94, an antigen preferentially expressed on NK cells, Chang et al. (1995) used an expression cloning strategy to isolate an IL2- activated polyclonal NK cell line cDNA encoding CD94. Northern blot analysis revealed that CD94 is expressed as 3 major transcripts of 0.8, 1.8, and 3.5 kb and a minor transcript of 5.5 kb in NK cell lines. The predicted protein contains a 147- amino acid extracellular domain with several motifs

characteristic of C- type lectins, a 26- amino acid transmembrane domain, and a 7- amino acid cytoplasmic domain. CD94 is classified as a type II membrane protein because it has an external C terminus. The amino acid sequence of CD94 is 27 to 32% identical to those of NKG2 family members NKG2A, NKG2C (KLRC2; 602891), NKG2D (OMIM Ref. No. 602893), and NKG2E (KLRC3; 602892). Chang et al. (1995) stated that the virtual absence of a cytoplasmic domain implies that CD94 function requires association with other receptors. Lazetic et al. (1996) demonstrated that CD94 forms disulfide- bonded heterodimers with NKG2A, NKG2C, and NKG2E. Rodriguez et al. (1998) reported that the CD94 gene contains 6 exons. Using S1 nuclease protection and primer extension assays, they found that transcription initiation in CD94 is heterogeneous, but is restricted to a 60- bp region around the major initiation site. Chang et al. (1995) mapped the CD94 gene to chromosome 12 using a somatic cell hybrid panel. By analysis of a cosmid contig, Plougastel and Trowsdale (1998) found that the CD94 gene is located at 12p13.2- p12.3, within the NK complex, a cluster of C- type lectin genes preferentially expressed in NK cells.

[29387]

[29388] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[29389] Plougastel, B.; Trowsdale, J. : Sequence analysis of a 62- kb region overlapping the human KLRC cluster of genes. Genomics 49: 193- 199, 1998. ; and

[29390] Rodriguez, A.; Carretero, M.; Glienke, J.; Bellon, T.; Ramirez, A.; Lehrach, H.; Francis, F.; Lopez- Botet, M. : Structure of the human CD94 C- type lectin gene. Immunogenetics 47: 305- 309.

[29391] Further studies establishing the function and utilities of KLRD1 are found in John Hopkins OMIM database record ID 602894, and in cited publications listed in Table 5, which are hereby incorporated by reference.Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NP_003670.1) is another GAM189 target gene, herein designated TARGET GENE. KMO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KMO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KMO BINDING SITE,

designated SEQ ID:6338, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29392] Another function of GAM189 is therefore inhibition of Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NP_003670.1), a gene which may play a role in encephalic photoreception. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KMO.

[29393] The function of KMO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) is another GAM189 target gene, herein designated TARGET GENE. LAMP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAMP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMP3 BINDING SITE, designated SEQ ID:17760, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA,

also designated SEQ ID:246.

[29394] Another function of GAM189 is therefore inhibition of Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP3.

[29395] Leucyl-trna synthetase (LARS, Accession NP_064502.8) is another GAM189 target gene, herein designated TARGET GENE. LARS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LARS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LARS BINDING SITE, designated SEQ ID:2620, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29396] Another function of GAM189 is therefore inhibition of Leucyl-trna synthetase (LARS, Accession NP_064502.8) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LARS.

[29397] Lim and sh3 protein 1 (LASP1, Accession NP_006139.1) is another GAM189 target gene, herein designated TARGET

GENE. LASP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LASP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LASP1 BINDING SITE, designated SEQ ID:17709, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29398] Another function of GAM189 is therefore inhibition of Lim and sh3 protein 1 (LASP1, Accession NP_006139.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LASP1.

[29399] Lipocalin 7 (LCN7, Accession NP_071447.1) is another GAM189 target gene, herein designated TARGET GENE. LCN7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCN7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCN7 BINDING SITE, designated SEQ ID:15937, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29400] Another function of GAM189 is therefore inhibition of Lipocalin 7 (LCN7, Accession NP_071447.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCN7.

[29401] Leucine zipper-ef-hand containing transmembrane protein 1 (LETM1, Accession NP_036450.1) is another GAM189 target gene, herein designated TARGET GENE. LETM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LETM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LETM1 BINDING SITE, designated SEQ ID:18695, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29402] Another function of GAM189 is therefore inhibition of Leucine zipper-ef-hand containing transmembrane protein 1 (LETM1, Accession NP_036450.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LETM1.

[29403] LGP2 (Accession NP_077024.1) is another GAM189 target

gene, herein designated TARGET GENE. LGP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LGP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LGP2 BINDING SITE, designated SEQ ID:8032, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29404] Another function of GAM189 is therefore inhibition of LGP2 (Accession NP_077024.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGP2.

[29405] Lim homeobox protein 2 (LHX2, Accession NP_004780.3) is another GAM189 target gene, herein designated TARGET GENE. LHX2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LHX2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LHX2 BINDING SITE, designated SEQ ID:4178, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29406] Another function of GAM189 is therefore inhibition of Lim homeobox protein 2 (LHX2, Accession NP_004780.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHX2.

[29407] LIN-28 (Accession NP_078950.1) is another GAM189 target gene, herein designated TARGET GENE. LIN-28 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LIN-28, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LIN-28 BINDING SITE, designated SEQ ID:4726, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29408] Another function of GAM189 is therefore inhibition of LIN-28 (Accession NP_078950.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIN-28.

[29409] Link-GEFII (Accession NP_057423.1) is another GAM189 target gene, herein designated TARGET GENE. Link-GEFII BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Link-GEFII, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Link-GEFII BINDING SITE, designated SEQ ID:19936, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29410] Another function of GAM189 is therefore inhibition of Link-GEFII (Accession NP_057423.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Link-GEFII.

[29411] Lipase, member h (LIPH, Accession NP_640341.1) is another GAM189 target gene, herein designated TARGET GENE. LIPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LIPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LIPH BINDING SITE, designated SEQ ID:10379, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29412] Another function of GAM189 is therefore inhibition of Lipase, member h (LIPH, Accession NP_640341.1) . Accord-

ingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIPH.

[29413] Lethal giant larvae homolog 2 (drosophila) (LLGL2, Accession NP_004515.1) is another GAM189 target gene, herein designated TARGET GENE. LLGL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LLGL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LLGL2 BINDING SITE, designated SEQ ID:15172, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29414] Another function of GAM189 is therefore inhibition of Lethal giant larvae homolog 2 (drosophila) (LLGL2, Accession NP_004515.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LLGL2.

[29415] LNK (Accession NP_005466.1) is another GAM189 target gene, herein designated TARGET GENE. LNK BINDING SITE1 and LNK BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LNK,

corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LNK BINDING SITE1 and LNK BINDING SITE2, designated SEQ ID:13992 and SEQ ID:1866 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29416] Another function of GAM189 is therefore inhibition of LNK (Accession NP_005466.1), a gene which links T- cell receptor activation signal to phospholipase c- gamma- 1, grb- 2 and phosphatidylinositol 3- kinase (by similarity). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNK.

[29417] The function of LNK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.LOC112687 (Accession XP_053145.1) is another GAM189 target gene, herein designated TARGET GENE. LOC112687 BINDING SITE1 through LOC112687 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC112687, corresponding to target binding sites such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112687 BINDING SITE1 through LOC112687 BINDING SITE3, designated SEQ ID:16673, SEQ ID:793 and SEQ ID:7988 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29418] Another function of GAM189 is therefore inhibition of LOC112687 (Accession XP_053145.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112687.

[29419] LOC112817 (Accession NP_612422.2) is another GAM189 target gene, herein designated TARGET GENE. LOC112817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112817 BINDING SITE, designated SEQ ID:16256, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29420] Another function of GAM189 is therefore inhibition of

LOC112817 (Accession NP_612422.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112817.

[29421] LOC113444 (Accession NP_612437.2) is another GAM189 target gene, herein designated TARGET GENE. LOC113444 BINDING SITE1 through LOC113444 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC113444, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC113444 BINDING SITE1 through LOC113444 BINDING SITE3, designated SEQ ID:18294, SEQ ID:5336 and SEQ ID:15899 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29422] Another function of GAM189 is therefore inhibition of LOC113444 (Accession NP_612437.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113444.

[29423] LOC113828 (Accession NP_612444.1) is another GAM189 target gene, herein designated TARGET GENE. LOC113828

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC113828, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC113828 BINDING SITE, designated SEQ ID:5632, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29424] Another function of GAM189 is therefore inhibition of LOC113828 (Accession NP_612444.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113828.

[29425] LOC115123 (Accession XP_055276.1) is another GAM189 target gene, herein designated TARGET GENE. LOC115123 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC115123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115123 BINDING SITE, designated SEQ ID:15271, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29426] Another function of GAM189 is therefore inhibition of LOC115123 (Accession XP_055276.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115123.

[29427] LOC115219 (Accession XP_055499.2) is another GAM189 target gene, herein designated TARGET GENE. LOC115219 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC115219, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115219 BINDING SITE, designated SEQ ID:12422, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29428] Another function of GAM189 is therefore inhibition of LOC115219 (Accession XP_055499.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115219.

[29429] LOC115648 (Accession NP_663299.1) is another GAM189 target gene, herein designated TARGET GENE. LOC115648 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC115648, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115648 BINDING SITE, designated SEQ ID:7429, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29430] Another function of GAM189 is therefore inhibition of LOC115648 (Accession NP_663299.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115648.

[29431] LOC116411 (Accession XP_058095.1) is another GAM189 target gene, herein designated TARGET GENE. LOC116411 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC116411, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC116411 BINDING SITE, designated SEQ ID:14720, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29432] Another function of GAM189 is therefore inhibition of

LOC116411 (Accession XP_058095.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116411.

[29433] LOC118490 (Accession XP_060981.3) is another GAM189 target gene, herein designated TARGET GENE. LOC118490 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC118490, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118490 BINDING SITE, designated SEQ ID:456, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29434] Another function of GAM189 is therefore inhibition of LOC118490 (Accession XP_060981.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118490.

[29435] LOC118812 (Accession NP_849154.1) is another GAM189 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded

by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:2649, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29436] Another function of GAM189 is therefore inhibition of LOC118812 (Accession NP_849154.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118812.

[29437] LOC118812 (Accession XP_058346.2) is another GAM189 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:2649, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29438] Another function of GAM189 is therefore inhibition of LOC118812 (Accession XP_058346.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118812.

[29439] LOC119395 (Accession XP_061446.3) is another GAM189 target gene, herein designated TARGET GENE. LOC119395 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC119395, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC119395 BINDING SITE, designated SEQ ID:745, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29440] Another function of GAM189 is therefore inhibition of LOC119395 (Accession XP_061446.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC119395.

[29441] LOC120526 (Accession XP_058475.1) is another GAM189 target gene, herein designated TARGET GENE. LOC120526 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC120526, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC120526 BINDING SITE, designated SEQ ID:17112, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29442] Another function of GAM189 is therefore inhibition of LOC120526 (Accession XP_058475.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120526.

[29443] LOC121952 (Accession XP_062872.2) is another GAM189 target gene, herein designated TARGET GENE. LOC121952 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC121952, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC121952 BINDING SITE, designated SEQ ID:9891, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29444] Another function of GAM189 is therefore inhibition of

LOC121952 (Accession XP_062872.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121952.

[29445] LOC124221 (Accession XP_058785.3) is another GAM189 target gene, herein designated TARGET GENE. LOC124221 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC124221, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC124221 BINDING SITE, designated SEQ ID:14576, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29446] Another function of GAM189 is therefore inhibition of LOC124221 (Accession XP_058785.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124221.

[29447] LOC125061 (Accession XP_058889.3) is another GAM189 target gene, herein designated TARGET GENE. LOC125061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC125061, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC125061 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29448] Another function of GAM189 is therefore inhibition of LOC125061 (Accession XP_058889.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125061.

[29449] LOC126669 (Accession XP_060121.4) is another GAM189 target gene, herein designated TARGET GENE. LOC126669 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC126669, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126669 BINDING SITE, designated SEQ ID:3477, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29450] Another function of GAM189 is therefore inhibition of LOC126669 (Accession XP_060121.4) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126669.

[29451] LOC127253 (Accession XP_059122.1) is another GAM189 target gene, herein designated TARGET GENE. LOC127253 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC127253, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC127253 BINDING SITE, designated SEQ ID:18918, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29452] Another function of GAM189 is therefore inhibition of LOC127253 (Accession XP_059122.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127253.

[29453] LOC127841 (Accession XP_059184.1) is another GAM189 target gene, herein designated TARGET GENE. LOC127841 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC127841, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC127841 BINDING SITE, designated SEQ ID:18516, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29454] Another function of GAM189 is therefore inhibition of LOC127841 (Accession XP_059184.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127841.

[29455] LOC128387 (Accession XP_059243.2) is another GAM189 target gene, herein designated TARGET GENE. LOC128387 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC128387, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC128387 BINDING SITE, designated SEQ ID:15173, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29456] Another function of GAM189 is therefore inhibition of LOC128387 (Accession XP_059243.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC128387.

[29457] LOC132241 (Accession XP_059583.1) is another GAM189 target gene, herein designated TARGET GENE. LOC132241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC132241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC132241 BINDING SITE, designated SEQ ID:509, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29458] Another function of GAM189 is therefore inhibition of LOC132241 (Accession XP_059583.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132241.

[29459] LOC135293 (Accession XP_072402.4) is another GAM189 target gene, herein designated TARGET GENE. LOC135293 BINDING SITE1 and LOC135293 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC135293, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135293 BINDING SITE1 and LOC135293 BINDING SITE2, designated SEQ ID:3512 and SEQ ID:10443 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29460] Another function of GAM189 is therefore inhibition of LOC135293 (Accession XP_072402.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135293.

[29461] LOC135763 (Accession NP_612639.1) is another GAM189 target gene, herein designated TARGET GENE. LOC135763 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135763, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135763 BINDING SITE, designated SEQ ID:17207, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29462] Another function of GAM189 is therefore inhibition of LOC135763 (Accession NP_612639.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135763.

[29463] LOC135818 (Accession XP_059804.4) is another GAM189 target gene, herein designated TARGET GENE. LOC135818 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135818 BINDING SITE, designated SEQ ID:19136, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29464] Another function of GAM189 is therefore inhibition of LOC135818 (Accession XP_059804.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135818.

[29465] LOC137886 (Accession XP_059929.3) is another GAM189 target gene, herein designated TARGET GENE. LOC137886 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC137886, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC137886 BINDING SITE, designated SEQ ID:19990, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29466] Another function of GAM189 is therefore inhibition of LOC137886 (Accession XP_059929.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137886.

[29467] LOC139422 (Accession XP_066687.2) is another GAM189 target gene, herein designated TARGET GENE. LOC139422 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC139422, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC139422 BINDING SITE, designated SEQ ID:9489, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29468] Another function of GAM189 is therefore inhibition of LOC139422 (Accession XP_066687.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC139422.

[29469] LOC143241 (Accession NP_620167.1) is another GAM189 target gene, herein designated TARGET GENE. LOC143241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC143241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143241 BINDING SITE, designated SEQ ID:15574, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29470] Another function of GAM189 is therefore inhibition of LOC143241 (Accession NP_620167.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143241.

[29471] LOC144248 (Accession XP_084786.1) is another GAM189 target gene, herein designated TARGET GENE. LOC144248 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC144248 BINDING SITE, designated SEQ ID:3159, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29472] Another function of GAM189 is therefore inhibition of LOC144248 (Accession XP_084786.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144248.

[29473] LOC144266 (Accession XP_084795.1) is another GAM189 target gene, herein designated TARGET GENE. LOC144266 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144266, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144266 BINDING SITE, designated SEQ ID:17498, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29474] Another function of GAM189 is therefore inhibition of LOC144266 (Accession XP_084795.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC144266.

[29475] LOC144404 (Accession XP_084852.6) is another GAM189 target gene, herein designated TARGET GENE. LOC144404 BINDING SITE1 through LOC144404 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC144404, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144404 BINDING SITE1 through LOC144404 BINDING SITE3, designated SEQ ID:5897, SEQ ID:1633 and SEQ ID:15352 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29476] Another function of GAM189 is therefore inhibition of LOC144404 (Accession XP_084852.6) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144404.

[29477] LOC144467 (Accession NP_612482.1) is another GAM189 target gene, herein designated TARGET GENE. LOC144467 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144467, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144467 BINDING SITE, designated SEQ ID:5733, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29478] Another function of GAM189 is therefore inhibition of LOC144467 (Accession NP_612482.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144467.

[29479] LOC144481 (Accession XP_096611.2) is another GAM189 target gene, herein designated TARGET GENE. LOC144481 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144481, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144481 BINDING SITE, designated SEQ ID:19220, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29480] Another function of GAM189 is therefore inhibition of LOC144481 (Accession XP_096611.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC144481.

[29481] LOC144667 (Accession XP_096648.1) is another GAM189 target gene, herein designated TARGET GENE. LOC144667 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144667, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144667 BINDING SITE, designated SEQ ID:12712, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29482] Another function of GAM189 is therefore inhibition of LOC144667 (Accession XP_096648.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144667.

[29483] LOC144742 (Accession XP_084949.1) is another GAM189 target gene, herein designated TARGET GENE. LOC144742 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144742, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC144742 BINDING SITE, designated SEQ ID:17736, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29484] Another function of GAM189 is therefore inhibition of LOC144742 (Accession XP_084949.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144742.

[29485] LOC144766 (Accession XP_084963.2) is another GAM189 target gene, herein designated TARGET GENE. LOC144766 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144766, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144766 BINDING SITE, designated SEQ ID:8972, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29486] Another function of GAM189 is therefore inhibition of LOC144766 (Accession XP_084963.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC144766.

[29487] LOC144776 (Accession XP_084964.1) is another GAM189 target gene, herein designated TARGET GENE. LOC144776 BINDING SITE1 and LOC144776 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC144776, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144776 BINDING SITE1 and LOC144776 BINDING SITE2, designated SEQ ID:444 and SEQ ID:16275 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29488] Another function of GAM189 is therefore inhibition of LOC144776 (Accession XP_084964.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144776.

[29489] LOC144817 (Accession XP_084972.1) is another GAM189 target gene, herein designated TARGET GENE. LOC144817 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144817, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144817 BINDING SITE, designated SEQ ID:12065, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29490] Another function of GAM189 is therefore inhibition of LOC144817 (Accession XP_084972.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144817.

[29491] LOC144962 (Accession XP_084990.1) is another GAM189 target gene, herein designated TARGET GENE. LOC144962 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144962, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144962 BINDING SITE, designated SEQ ID:12130, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29492] Another function of GAM189 is therefore inhibition of LOC144962 (Accession XP_084990.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC144962.

[29493] LOC145098 (Accession XP_085022.1) is another GAM189 target gene, herein designated TARGET GENE. LOC145098 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145098, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145098 BINDING SITE, designated SEQ ID:675, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29494] Another function of GAM189 is therefore inhibition of LOC145098 (Accession XP_085022.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145098.

[29495] LOC145231 (Accession XP_096740.1) is another GAM189 target gene, herein designated TARGET GENE. LOC145231 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145231, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC145231 BINDING SITE, designated SEQ ID:6417, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29496] Another function of GAM189 is therefore inhibition of LOC145231 (Accession XP_096740.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145231.

[29497] LOC145268 (Accession XP_085072.1) is another GAM189 target gene, herein designated TARGET GENE. LOC145268 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145268 BINDING SITE, designated SEQ ID:18805, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29498] Another function of GAM189 is therefore inhibition of LOC145268 (Accession XP_085072.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC145268.

[29499] LOC145725 (Accession XP_085211.1) is another GAM189 target gene, herein designated TARGET GENE. LOC145725 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145725 BINDING SITE, designated SEQ ID:4773, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29500] Another function of GAM189 is therefore inhibition of LOC145725 (Accession XP_085211.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145725.

[29501] LOC145757 (Accession XP_085227.1) is another GAM189 target gene, herein designated TARGET GENE. LOC145757 BINDING SITE1 and LOC145757 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC145757, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC145757 BINDING SITE1 and LOC145757 BINDING SITE2, designated SEQ ID:11523 and SEQ ID:7370 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29502] Another function of GAM189 is therefore inhibition of LOC145757 (Accession XP_085227.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145757.

[29503] LOC145783 (Accession XP_085231.2) is another GAM189 target gene, herein designated TARGET GENE. LOC145783 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145783, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145783 BINDING SITE, designated SEQ ID:2196, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29504] Another function of GAM189 is therefore inhibition of LOC145783 (Accession XP_085231.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC145783.

[29505] LOC145813 (Accession XP_096873.1) is another GAM189 target gene, herein designated TARGET GENE. LOC145813 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145813 BINDING SITE, designated SEQ ID:16256, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29506] Another function of GAM189 is therefore inhibition of LOC145813 (Accession XP_096873.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145813.

[29507] LOC145988 (Accession XP_085290.3) is another GAM189 target gene, herein designated TARGET GENE. LOC145988 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145988, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC145988 BINDING SITE, designated SEQ ID:11009, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29508] Another function of GAM189 is therefore inhibition of LOC145988 (Accession XP_085290.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145988.

[29509] LOC146177 (Accession NP_778229.1) is another GAM189 target gene, herein designated TARGET GENE. LOC146177 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146177 BINDING SITE, designated SEQ ID:16175, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29510] Another function of GAM189 is therefore inhibition of LOC146177 (Accession NP_778229.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC146177.

[29511] LOC146229 (Accession XP_085387.1) is another GAM189 target gene, herein designated TARGET GENE. LOC146229 BINDING SITE1 through LOC146229 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC146229, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146229 BINDING SITE1 through LOC146229 BINDING SITE4, designated SEQ ID:8706, SEQ ID:5672, SEQ ID:5551 and SEQ ID:1644 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29512] Another function of GAM189 is therefore inhibition of LOC146229 (Accession XP_085387.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146229.

[29513] LOC146346 (Accession XP_085430.1) is another GAM189 target gene, herein designated TARGET GENE. LOC146346 BINDING SITE1 and LOC146346 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by LOC146346, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146346 BINDING SITE1 and LOC146346 BINDING SITE2, designated SEQ ID:17670 and SEQ ID:5798 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29514] Another function of GAM189 is therefore inhibition of LOC146346 (Accession XP_085430.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146346.

[29515] LOC146429 (Accession XP_096998.2) is another GAM189 target gene, herein designated TARGET GENE. LOC146429 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146429, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146429 BINDING SITE, designated SEQ ID:2457, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29516] Another function of GAM189 is therefore inhibition of LOC146429 (Accession XP_096998.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146429.

[29517] LOC146443 (Accession XP_085461.6) is another GAM189 target gene, herein designated TARGET GENE. LOC146443 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146443, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146443 BINDING SITE, designated SEQ ID:813, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29518] Another function of GAM189 is therefore inhibition of LOC146443 (Accession XP_085461.6) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146443.

[29519] LOC146475 (Accession XP_097006.1) is another GAM189 target gene, herein designated TARGET GENE. LOC146475 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC146475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146475 BINDING SITE, designated SEQ ID:9246, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29520] Another function of GAM189 is therefore inhibition of LOC146475 (Accession XP_097006.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146475.

[29521] LOC146513 (Accession XP_097013.1) is another GAM189 target gene, herein designated TARGET GENE. LOC146513 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146513, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146513 BINDING SITE, designated SEQ ID:3374, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29522] Another function of GAM189 is therefore inhibition of

LOC146513 (Accession XP_097013.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146513.

[29523] LOC146603 (Accession XP_085514.2) is another GAM189 target gene, herein designated TARGET GENE. LOC146603 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146603 BINDING SITE, designated SEQ ID:7382, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29524] Another function of GAM189 is therefore inhibition of LOC146603 (Accession XP_085514.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146603.

[29525] LOC146784 (Accession XP_085588.1) is another GAM189 target gene, herein designated TARGET GENE. LOC146784 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146784, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146784 BINDING SITE, designated SEQ ID:13448, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29526] Another function of GAM189 is therefore inhibition of LOC146784 (Accession XP_085588.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146784.

[29527] LOC146839 (Accession XP_097107.1) is another GAM189 target gene, herein designated TARGET GENE. LOC146839 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146839, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146839 BINDING SITE, designated SEQ ID:1745, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29528] Another function of GAM189 is therefore inhibition of LOC146839 (Accession XP_097107.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146839.

[29529] LOC146894 (Accession NP_660316.1) is another GAM189 target gene, herein designated TARGET GENE. LOC146894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146894 BINDING SITE, designated SEQ ID:8315, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29530] Another function of GAM189 is therefore inhibition of LOC146894 (Accession NP_660316.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146894.

[29531] LOC146895 (Accession XP_097120.1) is another GAM189 target gene, herein designated TARGET GENE. LOC146895 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146895, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146895 BINDING SITE, designated SEQ ID:8232, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29532] Another function of GAM189 is therefore inhibition of LOC146895 (Accession XP_097120.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146895.

[29533] LOC146901 (Accession XP_097121.1) is another GAM189 target gene, herein designated TARGET GENE. LOC146901 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146901, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146901 BINDING SITE, designated SEQ ID:6392, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29534] Another function of GAM189 is therefore inhibition of LOC146901 (Accession XP_097121.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC146901.

[29535] LOC146909 (Accession XP_085634.2) is another GAM189 target gene, herein designated TARGET GENE. LOC146909 BINDING SITE1 and LOC146909 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC146909, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146909 BINDING SITE1 and LOC146909 BINDING SITE2, designated SEQ ID:19550 and SEQ ID:9492 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29536] Another function of GAM189 is therefore inhibition of LOC146909 (Accession XP_085634.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146909.

[29537] LOC147071 (Accession XP_054031.5) is another GAM189 target gene, herein designated TARGET GENE. LOC147071 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147071, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147071 BINDING SITE, designated SEQ ID:16699, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29538] Another function of GAM189 is therefore inhibition of LOC147071 (Accession XP_054031.5) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147071.

[29539] LOC147080 (Accession XP_097182.1) is another GAM189 target gene, herein designated TARGET GENE. LOC147080 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147080, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147080 BINDING SITE, designated SEQ ID:12558, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29540] Another function of GAM189 is therefore inhibition of LOC147080 (Accession XP_097182.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147080.

[29541] LOC147166 (Accession XP_085722.2) is another GAM189 target gene, herein designated TARGET GENE. LOC147166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147166 BINDING SITE, designated SEQ ID:10618, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29542] Another function of GAM189 is therefore inhibition of LOC147166 (Accession XP_085722.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147166.

[29543] LOC147381 (Accession XP_097230.2) is another GAM189 target gene, herein designated TARGET GENE. LOC147381 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147381, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147381 BINDING SITE, designated SEQ ID:19915, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29544] Another function of GAM189 is therefore inhibition of LOC147381 (Accession XP_097230.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147381.

[29545] LOC147407 (Accession XP_084000.1) is another GAM189 target gene, herein designated TARGET GENE. LOC147407 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147407, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147407 BINDING SITE, designated SEQ ID:12065, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29546] Another function of GAM189 is therefore inhibition of LOC147407 (Accession XP_084000.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147407.

[29547] LOC147817 (Accession XP_085903.1) is another GAM189 target gene, herein designated TARGET GENE. LOC147817 BINDING SITE1 and LOC147817 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC147817, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147817 BINDING SITE1 and LOC147817 BINDING SITE2, designated SEQ ID:1634 and SEQ ID:19233 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29548] Another function of GAM189 is therefore inhibition of LOC147817 (Accession XP_085903.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147817.

[29549] LOC147841 (Accession XP_085924.2) is another GAM189 target gene, herein designated TARGET GENE. LOC147841 BINDING SITE1 and LOC147841 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by LOC147841, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147841 BINDING SITE1 and LOC147841 BINDING SITE2, designated SEQ ID:12065 and SEQ ID:8642 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29550] Another function of GAM189 is therefore inhibition of LOC147841 (Accession XP_085924.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147841.

[29551] LOC147947 (Accession XP_085974.1) is another GAM189 target gene, herein designated TARGET GENE. LOC147947 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147947, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147947 BINDING SITE, designated SEQ ID:17952, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29552] Another function of GAM189 is therefore inhibition of LOC147947 (Accession XP_085974.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147947.

[29553] LOC148137 (Accession NP_653293.1) is another GAM189 target gene, herein designated TARGET GENE. LOC148137 BINDING SITE1 and LOC148137 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC148137, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148137 BINDING SITE1 and LOC148137 BINDING SITE2, designated SEQ ID:5784 and SEQ ID:17935 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29554] Another function of GAM189 is therefore inhibition of LOC148137 (Accession NP_653293.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148137.

[29555] LOC148198 (Accession XP_047554.4) is another GAM189

target gene, herein designated TARGET GENE. LOC148198 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148198, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148198 BINDING SITE, designated SEQ ID:11563, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29556] Another function of GAM189 is therefore inhibition of LOC148198 (Accession XP_047554.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148198.

[29557] LOC148708 (Accession XP_086286.4) is another GAM189 target gene, herein designated TARGET GENE. LOC148708 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148708 BINDING SITE, designated SEQ ID:15671, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29558] Another function of GAM189 is therefore inhibition of LOC148708 (Accession XP_086286.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148708.

[29559] LOC148709 (Accession XP_086281.1) is another GAM189 target gene, herein designated TARGET GENE. LOC148709 BINDING SITE1 and LOC148709 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC148709, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148709 BINDING SITE1 and LOC148709 BINDING SITE2, designated SEQ ID:9201 and SEQ ID:6922 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29560] Another function of GAM189 is therefore inhibition of LOC148709 (Accession XP_086281.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148709.

[29561] LOC149149 (Accession XP_097598.1) is another GAM189 target gene, herein designated TARGET GENE. LOC149149 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149149 BINDING SITE, designated SEQ ID:2184, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29562] Another function of GAM189 is therefore inhibition of LOC149149 (Accession XP_097598.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149149.

[29563] LOC149194 (Accession XP_086458.1) is another GAM189 target gene, herein designated TARGET GENE. LOC149194 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149194 BINDING SITE, designated SEQ ID:12637, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29564] Another function of GAM189 is therefore inhibition of LOC149194 (Accession XP_086458.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149194.

[29565] LOC149371 (Accession NP_787072.1) is another GAM189 target gene, herein designated TARGET GENE. LOC149371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149371 BINDING SITE, designated SEQ ID:13354, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29566] Another function of GAM189 is therefore inhibition of LOC149371 (Accession NP_787072.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149371.

[29567] LOC149466 (Accession XP_086546.1) is another GAM189

target gene, herein designated TARGET GENE. LOC149466 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149466, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149466 BINDING SITE, designated SEQ ID:16260, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29568] Another function of GAM189 is therefore inhibition of LOC149466 (Accession XP_086546.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149466.

[29569] LOC149478 (Accession XP_086536.1) is another GAM189 target gene, herein designated TARGET GENE. LOC149478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149478, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149478 BINDING SITE, designated SEQ ID:5016, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29570] Another function of GAM189 is therefore inhibition of LOC149478 (Accession XP_086536.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149478.

[29571] LOC149506 (Accession XP_097661.1) is another GAM189 target gene, herein designated TARGET GENE. LOC149506 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149506, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE, designated SEQ ID:2139, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29572] Another function of GAM189 is therefore inhibition of LOC149506 (Accession XP_097661.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149506.

[29573] LOC149606 (Accession XP_086600.1) is another GAM189 target gene, herein designated TARGET GENE. LOC149606 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149606, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149606 BINDING SITE, designated SEQ ID:8887, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29574] Another function of GAM189 is therefore inhibition of LOC149606 (Accession XP_086600.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149606.

[29575] LOC149692 (Accession XP_097706.1) is another GAM189 target gene, herein designated TARGET GENE. LOC149692 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC149692, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149692 BINDING SITE, designated SEQ ID:11025, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29576] Another function of GAM189 is therefore inhibition of LOC149692 (Accession XP_097706.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149692.

[29577] LOC149703 (Accession XP_097719.1) is another GAM189 target gene, herein designated TARGET GENE. LOC149703 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149703, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149703 BINDING SITE, designated SEQ ID:10508, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29578] Another function of GAM189 is therefore inhibition of

LOC149703 (Accession XP_097719.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149703.

[29579] LOC149832 (Accession XP_097733.1) is another GAM189 target gene, herein designated TARGET GENE. LOC149832 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149832, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149832 BINDING SITE, designated SEQ ID:17917, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29580] Another function of GAM189 is therefore inhibition of LOC149832 (Accession XP_097733.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149832.

[29581] LOC150054 (Accession XP_097797.1) is another GAM189 target gene, herein designated TARGET GENE. LOC150054 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150054, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150054 BINDING SITE, designated SEQ ID:5157, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29582] Another function of GAM189 is therefore inhibition of LOC150054 (Accession XP_097797.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150054.

[29583] LOC150225 (Accession XP_097870.1) is another GAM189 target gene, herein designated TARGET GENE. LOC150225 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150225, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150225 BINDING SITE, designated SEQ ID:7207, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29584] Another function of GAM189 is therefore inhibition of LOC150225 (Accession XP_097870.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150225.

[29585] LOC150384 (Accession XP_097894.1) is another GAM189 target gene, herein designated TARGET GENE. LOC150384 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150384, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150384 BINDING SITE, designated SEQ ID:7485, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29586] Another function of GAM189 is therefore inhibition of LOC150384 (Accession XP_097894.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150384.

[29587] LOC150397 (Accession XP_086907.1) is another GAM189 target gene, herein designated TARGET GENE. LOC150397 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150397, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150397 BINDING SITE, designated SEQ ID:19467, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29588] Another function of GAM189 is therefore inhibition of LOC150397 (Accession XP_086907.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150397.

[29589] LOC150587 (Accession XP_097917.1) is another GAM189 target gene, herein designated TARGET GENE. LOC150587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150587 BINDING SITE, designated SEQ ID:16940, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29590] Another function of GAM189 is therefore inhibition of LOC150587 (Accession XP_097917.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC150587.

[29591] LOC151057 (Accession XP_097998.1) is another GAM189 target gene, herein designated TARGET GENE. LOC151057 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151057, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151057 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29592] Another function of GAM189 is therefore inhibition of LOC151057 (Accession XP_097998.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151057.

[29593] LOC151196 (Accession XP_098019.1) is another GAM189 target gene, herein designated TARGET GENE. LOC151196 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151196, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC151196 BINDING SITE, designated SEQ ID:19774, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29594] Another function of GAM189 is therefore inhibition of LOC151196 (Accession XP_098019.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151196.

[29595] LOC151201 (Accession XP_098021.1) is another GAM189 target gene, herein designated TARGET GENE. LOC151201 BINDING SITE1 and LOC151201 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC151201, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE1 and LOC151201 BINDING SITE2, designated SEQ ID:2572 and SEQ ID:12725 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29596] Another function of GAM189 is therefore inhibition of LOC151201 (Accession XP_098021.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151201.

[29597] LOC151475 (Accession XP_098063.1) is another GAM189 target gene, herein designated TARGET GENE. LOC151475 BINDING SITE1 and LOC151475 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC151475, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151475 BINDING SITE1 and LOC151475 BINDING SITE2, designated SEQ ID:4174 and SEQ ID:4371 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29598] Another function of GAM189 is therefore inhibition of LOC151475 (Accession XP_098063.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151475.

[29599] LOC151610 (Accession XP_087245.1) is another GAM189 target gene, herein designated TARGET GENE. LOC151610 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC151610, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151610 BINDING SITE, designated SEQ ID:2599, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29600] Another function of GAM189 is therefore inhibition of LOC151610 (Accession XP_087245.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151610.

[29601] LOC151636 (Accession NP_612144.1) is another GAM189 target gene, herein designated TARGET GENE. LOC151636 BINDING SITE1 through LOC151636 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC151636, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151636 BINDING SITE1 through LOC151636 BINDING SITE3, designated SEQ ID:4151, SEQ ID:14731 and SEQ ID:2693 respectively, to the nucleotide sequence of GAM189 RNA,

herein designated GAM RNA, also designated SEQ ID:246.

[29602] Another function of GAM189 is therefore inhibition of LOC151636 (Accession NP_612144.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151636.

[29603] LOC151657 (Accession XP_098100.2) is another GAM189 target gene, herein designated TARGET GENE. LOC151657 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151657, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151657 BINDING SITE, designated SEQ ID:4248, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29604] Another function of GAM189 is therefore inhibition of LOC151657 (Accession XP_098100.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151657.

[29605] LOC151877 (Accession XP_098132.1) is another GAM189 target gene, herein designated TARGET GENE. LOC151877

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151877, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151877 BINDING SITE, designated SEQ ID:4677, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29606] Another function of GAM189 is therefore inhibition of LOC151877 (Accession XP_098132.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151877.

[29607] LOC152245 (Accession XP_098182.1) is another GAM189 target gene, herein designated TARGET GENE. LOC152245 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152245, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152245 BINDING SITE, designated SEQ ID:9470, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29608] Another function of GAM189 is therefore inhibition of LOC152245 (Accession XP_098182.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152245.

[29609] LOC152445 (Accession XP_098231.1) is another GAM189 target gene, herein designated TARGET GENE. LOC152445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE, designated SEQ ID:2922, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29610] Another function of GAM189 is therefore inhibition of LOC152445 (Accession XP_098231.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152445.

[29611] LOC152620 (Accession XP_011108.2) is another GAM189 target gene, herein designated TARGET GENE. LOC152620 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC152620, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152620 BINDING SITE, designated SEQ ID:1745, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29612] Another function of GAM189 is therefore inhibition of LOC152620 (Accession XP_011108.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152620.

[29613] LOC152719 (Accession XP_098257.1) is another GAM189 target gene, herein designated TARGET GENE. LOC152719 BINDING SITE1 and LOC152719 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC152719, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152719 BINDING SITE1 and LOC152719 BINDING SITE2, designated SEQ ID:17637 and SEQ ID:11919 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA,

also designated SEQ ID:246.

[29614] Another function of GAM189 is therefore inhibition of LOC152719 (Accession XP_098257.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152719.

[29615] LOC152794 (Accession XP_087525.1) is another GAM189 target gene, herein designated TARGET GENE. LOC152794 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152794, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152794 BINDING SITE, designated SEQ ID:2010, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29616] Another function of GAM189 is therefore inhibition of LOC152794 (Accession XP_087525.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152794.

[29617] LOC152804 (Accession XP_098266.2) is another GAM189 target gene, herein designated TARGET GENE. LOC152804

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152804, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152804 BINDING SITE, designated SEQ ID:9568, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29618] Another function of GAM189 is therefore inhibition of LOC152804 (Accession XP_098266.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152804.

[29619] LOC153077 (Accession XP_098307.1) is another GAM189 target gene, herein designated TARGET GENE. LOC153077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153077 BINDING SITE, designated SEQ ID:5304, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29620] Another function of GAM189 is therefore inhibition of LOC153077 (Accession XP_098307.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153077.

[29621] LOC153811 (Accession XP_087779.2) is another GAM189 target gene, herein designated TARGET GENE. LOC153811 BINDING SITE1 through LOC153811 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC153811, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153811 BINDING SITE1 through LOC153811 BINDING SITE3, designated SEQ ID:9683, SEQ ID:17512 and SEQ ID:19665 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29622] Another function of GAM189 is therefore inhibition of LOC153811 (Accession XP_087779.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153811.

[29623] LOC153883 (Accession XP_087798.1) is another GAM189

target gene, herein designated TARGET GENE. LOC153883 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153883, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153883 BINDING SITE, designated SEQ ID:15929, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29624] Another function of GAM189 is therefore inhibition of LOC153883 (Accession XP_087798.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153883.

[29625] LOC153910 (Accession XP_087801.1) is another GAM189 target gene, herein designated TARGET GENE. LOC153910 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153910, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153910 BINDING SITE, designated SEQ ID:2882, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29626] Another function of GAM189 is therefore inhibition of LOC153910 (Accession XP_087801.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153910.

[29627] LOC154282 (Accession XP_098505.1) is another GAM189 target gene, herein designated TARGET GENE. LOC154282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154282 BINDING SITE, designated SEQ ID:4307, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29628] Another function of GAM189 is therefore inhibition of LOC154282 (Accession XP_098505.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154282.

[29629] LOC154822 (Accession XP_098618.3) is another GAM189 target gene, herein designated TARGET GENE. LOC154822

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154822 BINDING SITE, designated SEQ ID:19205, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29630] Another function of GAM189 is therefore inhibition of LOC154822 (Accession XP_098618.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154822.

[29631] LOC154877 (Accession XP_098626.1) is another GAM189 target gene, herein designated TARGET GENE. LOC154877 BINDING SITE1 through LOC154877 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC154877, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE1 through LOC154877 BINDING SITE3, designated SEQ ID:17731, SEQ ID:3200 and SEQ ID:16089 re-

spectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29632] Another function of GAM189 is therefore inhibition of LOC154877 (Accession XP_098626.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877.

[29633] LOC155066 (Accession XP_088142.4) is another GAM189 target gene, herein designated TARGET GENE. LOC155066 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC155066, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC155066 BINDING SITE, designated SEQ ID:17980, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29634] Another function of GAM189 is therefore inhibition of LOC155066 (Accession XP_088142.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155066.

[29635] LOC158014 (Accession XP_088442.1) is another GAM189

target gene, herein designated TARGET GENE. LOC158014 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158014, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158014 BINDING SITE, designated SEQ ID:2542, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29636] Another function of GAM189 is therefore inhibition of LOC158014 (Accession XP_088442.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158014.

[29637] LOC158228 (Accession XP_098903.4) is another GAM189 target gene, herein designated TARGET GENE. LOC158228 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158228, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158228 BINDING SITE, designated SEQ ID:5779, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29638] Another function of GAM189 is therefore inhibition of LOC158228 (Accession XP_098903.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158228.

[29639] LOC158310 (Accession XP_098919.1) is another GAM189 target gene, herein designated TARGET GENE. LOC158310 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158310, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158310 BINDING SITE, designated SEQ ID:14859, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29640] Another function of GAM189 is therefore inhibition of LOC158310 (Accession XP_098919.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158310.

[29641] LOC158381 (Accession XP_048461.1) is another GAM189 target gene, herein designated TARGET GENE. LOC158381

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158381, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158381 BINDING SITE, designated SEQ ID:6212, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29642] Another function of GAM189 is therefore inhibition of LOC158381 (Accession XP_048461.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158381.

[29643] LOC158402 (Accession XP_098936.1) is another GAM189 target gene, herein designated TARGET GENE. LOC158402 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158402, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158402 BINDING SITE, designated SEQ ID:17964, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29644] Another function of GAM189 is therefore inhibition of LOC158402 (Accession XP_098936.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158402.

[29645] LOC158436 (Accession XP_098942.1) is another GAM189 target gene, herein designated TARGET GENE. LOC158436 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158436 BINDING SITE, designated SEQ ID:1263, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29646] Another function of GAM189 is therefore inhibition of LOC158436 (Accession XP_098942.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158436.

[29647] LOC158476 (Accession XP_098955.1) is another GAM189 target gene, herein designated TARGET GENE. LOC158476 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC158476, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158476 BINDING SITE, designated SEQ ID:935, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29648] Another function of GAM189 is therefore inhibition of LOC158476 (Accession XP_098955.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158476.

[29649] LOC158572 (Accession XP_088608.1) is another GAM189 target gene, herein designated TARGET GENE. LOC158572 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158572, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158572 BINDING SITE, designated SEQ ID:12003, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29650] Another function of GAM189 is therefore inhibition of

LOC158572 (Accession XP_088608.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158572.

[29651] LOC158668 (Accession XP_045161.1) is another GAM189 target gene, herein designated TARGET GENE. LOC158668 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158668, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158668 BINDING SITE, designated SEQ ID:16260, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29652] Another function of GAM189 is therefore inhibition of LOC158668 (Accession XP_045161.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158668.

[29653] LOC160897 (Accession XP_090573.3) is another GAM189 target gene, herein designated TARGET GENE. LOC160897 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC160897, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC160897 BINDING SITE, designated SEQ ID:17208, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29654] Another function of GAM189 is therefore inhibition of LOC160897 (Accession XP_090573.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160897.

[29655] LOC162427 (Accession XP_091549.3) is another GAM189 target gene, herein designated TARGET GENE. LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC162427, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2, designated SEQ ID:12068 and SEQ ID:12068 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29656] Another function of GAM189 is therefore inhibition of LOC162427 (Accession XP_091549.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162427.

[29657] LOC162427 (Accession XP_091549.3) is another GAM189 target gene, herein designated TARGET GENE. LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC162427, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2, designated SEQ ID:8231 and SEQ ID:8231 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29658] Another function of GAM189 is therefore inhibition of LOC162427 (Accession XP_091549.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162427.

[29659] LOC162962 (Accession XP_091886.7) is another GAM189

target gene, herein designated TARGET GENE. LOC162962 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC162962, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162962 BINDING SITE, designated SEQ ID:3249, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29660] Another function of GAM189 is therefore inhibition of LOC162962 (Accession XP_091886.7) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162962.

[29661] LOC162967 (Accession XP_091890.6) is another GAM189 target gene, herein designated TARGET GENE. LOC162967 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC162967, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162967 BINDING SITE, designated SEQ ID:13831, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29662] Another function of GAM189 is therefore inhibition of LOC162967 (Accession XP_091890.6) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162967.

[29663] LOC163227 (Accession NP_775802.1) is another GAM189 target gene, herein designated TARGET GENE. LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC163227, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2, designated SEQ ID:9147 and SEQ ID:11854 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29664] Another function of GAM189 is therefore inhibition of LOC163227 (Accession NP_775802.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163227.

[29665] LOC164091 (Accession XP_089356.1) is another GAM189 target gene, herein designated TARGET GENE. LOC164091 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC164091, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC164091 BINDING SITE, designated SEQ ID:7989, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29666] Another function of GAM189 is therefore inhibition of LOC164091 (Accession XP_089356.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164091.

[29667] LOC168451 (Accession XP_095114.2) is another GAM189 target gene, herein designated TARGET GENE. LOC168451 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC168451, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC168451 BINDING SITE, designated SEQ ID:19786, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29668] Another function of GAM189 is therefore inhibition of LOC168451 (Accession XP_095114.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168451.

[29669] LOC170409 (Accession XP_096330.1) is another GAM189 target gene, herein designated TARGET GENE. LOC170409 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC170409, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC170409 BINDING SITE, designated SEQ ID:15561, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29670] Another function of GAM189 is therefore inhibition of LOC170409 (Accession XP_096330.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170409.

[29671] LOC196264 (Accession XP_113683.1) is another GAM189

target gene, herein designated TARGET GENE. LOC196264 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196264, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196264 BINDING SITE, designated SEQ ID:2452, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29672] Another function of GAM189 is therefore inhibition of LOC196264 (Accession XP_113683.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196264.

[29673] LOC197342 (Accession XP_113869.1) is another GAM189 target gene, herein designated TARGET GENE. LOC197342 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC197342, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC197342 BINDING SITE, designated SEQ ID:2432, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29674] Another function of GAM189 is therefore inhibition of LOC197342 (Accession XP_113869.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197342.

[29675] LOC197358 (Accession XP_113872.2) is another GAM189 target gene, herein designated TARGET GENE. LOC197358 BINDING SITE1 and LOC197358 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC197358, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC197358 BINDING SITE1 and LOC197358 BINDING SITE2, designated SEQ ID:6387 and SEQ ID:4625 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29676] Another function of GAM189 is therefore inhibition of LOC197358 (Accession XP_113872.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197358.

[29677] LOC199725 (Accession XP_117119.1) is another GAM189 target gene, herein designated TARGET GENE. LOC199725 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC199725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199725 BINDING SITE, designated SEQ ID:10884, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29678] Another function of GAM189 is therefore inhibition of LOC199725 (Accession XP_117119.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199725.

[29679] LOC199899 (Accession XP_117153.1) is another GAM189 target gene, herein designated TARGET GENE. LOC199899 BINDING SITE1 and LOC199899 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC199899, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199899 BINDING SITE1

and LOC199899 BINDING SITE2, designated SEQ ID:8292 and SEQ ID:5253 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29680] Another function of GAM189 is therefore inhibition of LOC199899 (Accession XP_117153.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199899.

[29681] LOC199906 (Accession XP_114052.1) is another GAM189 target gene, herein designated TARGET GENE. LOC199906 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC199906, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199906 BINDING SITE, designated SEQ ID:19756, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29682] Another function of GAM189 is therefore inhibition of LOC199906 (Accession XP_114052.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC199906.

[29683] LOC200169 (Accession XP_117200.1) is another GAM189 target gene, herein designated TARGET GENE. LOC200169 BINDING SITE1 and LOC200169 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC200169, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200169 BINDING SITE1 and LOC200169 BINDING SITE2, designated SEQ ID:6122 and SEQ ID:5066 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29684] Another function of GAM189 is therefore inhibition of LOC200169 (Accession XP_117200.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200169.

[29685] LOC200844 (Accession XP_114306.1) is another GAM189 target gene, herein designated TARGET GENE. LOC200844 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC200844, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200844 BINDING SITE, designated SEQ ID:16540, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29686] Another function of GAM189 is therefore inhibition of LOC200844 (Accession XP_114306.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200844.

[29687] LOC200860 (Accession XP_117289.1) is another GAM189 target gene, herein designated TARGET GENE. LOC200860 BINDING SITE1 and LOC200860 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC200860, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200860 BINDING SITE1 and LOC200860 BINDING SITE2, designated SEQ ID:12075 and SEQ ID:4175 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29688] Another function of GAM189 is therefore inhibition of

LOC200860 (Accession XP_117289.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200860.

[29689] LOC200895 (Accession NP_789785.1) is another GAM189 target gene, herein designated TARGET GENE. LOC200895 BINDING SITE1 and LOC200895 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC200895, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200895 BINDING SITE1 and LOC200895 BINDING SITE2, designated SEQ ID:17681 and SEQ ID:11863 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29690] Another function of GAM189 is therefore inhibition of LOC200895 (Accession NP_789785.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200895.

[29691] LOC200916 (Accession XP_114317.3) is another GAM189 target gene, herein designated TARGET GENE. LOC200916

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200916, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200916 BINDING SITE, designated SEQ ID:3465, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29692] Another function of GAM189 is therefore inhibition of LOC200916 (Accession XP_114317.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200916.

[29693] LOC201164 (Accession NP_849158.1) is another GAM189 target gene, herein designated TARGET GENE. LOC201164 BINDING SITE1 and LOC201164 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC201164, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201164 BINDING SITE1 and LOC201164 BINDING SITE2, designated SEQ ID:16993 and SEQ ID:13384 re-

spectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29694] Another function of GAM189 is therefore inhibition of LOC201164 (Accession NP_849158.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201164.

[29695] LOC201292 (Accession NP_775818.1) is another GAM189 target gene, herein designated TARGET GENE. LOC201292 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201292, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201292 BINDING SITE, designated SEQ ID:4556, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29696] Another function of GAM189 is therefore inhibition of LOC201292 (Accession NP_775818.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201292.

[29697] LOC201562 (Accession XP_114343.2) is another GAM189

target gene, herein designated TARGET GENE. LOC201562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201562 BINDING SITE, designated SEQ ID:15044, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29698] Another function of GAM189 is therefore inhibition of LOC201562 (Accession XP_114343.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201562.

[29699] LOC201725 (Accession XP_114370.1) is another GAM189 target gene, herein designated TARGET GENE. LOC201725 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201725 BINDING SITE, designated SEQ ID:5492, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29700] Another function of GAM189 is therefore inhibition of LOC201725 (Accession XP_114370.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201725.

[29701] LOC202400 (Accession XP_117397.1) is another GAM189 target gene, herein designated TARGET GENE. LOC202400 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC202400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202400 BINDING SITE, designated SEQ ID:9145, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29702] Another function of GAM189 is therefore inhibition of LOC202400 (Accession XP_117397.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202400.

[29703] LOC202404 (Accession XP_114481.4) is another GAM189 target gene, herein designated TARGET GENE. LOC202404

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC202404, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202404 BINDING SITE, designated SEQ ID:18628, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29704] Another function of GAM189 is therefore inhibition of LOC202404 (Accession XP_114481.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202404.

[29705] LOC202460 (Accession XP_114493.1) is another GAM189 target gene, herein designated TARGET GENE. LOC202460 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC202460, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202460 BINDING SITE, designated SEQ ID:16450, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29706] Another function of GAM189 is therefore inhibition of LOC202460 (Accession XP_114493.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202460.

[29707] LOC202934 (Accession XP_117486.2) is another GAM189 target gene, herein designated TARGET GENE. LOC202934 BINDING SITE1 and LOC202934 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC202934, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE1 and LOC202934 BINDING SITE2, designated SEQ ID:4820 and SEQ ID:1729 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29708] Another function of GAM189 is therefore inhibition of LOC202934 (Accession XP_117486.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934.

[29709] LOC203547 (Accession XP_114719.1) is another GAM189

target gene, herein designated TARGET GENE. LOC203547 BINDING SITE1 and LOC203547 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC203547, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC203547 BINDING SITE1 and LOC203547 BINDING SITE2, designated SEQ ID:9545 and SEQ ID:2351 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29710] Another function of GAM189 is therefore inhibition of LOC203547 (Accession XP_114719.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203547.

[29711] LOC204288 (Accession XP_115295.1) is another GAM189 target gene, herein designated TARGET GENE. LOC204288 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC204288, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC204288 BINDING SITE, designated SEQ ID:10724, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29712] Another function of GAM189 is therefore inhibition of LOC204288 (Accession XP_115295.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC204288.

[29713] LOC219293 (Accession XP_166599.2) is another GAM189 target gene, herein designated TARGET GENE. LOC219293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219293 BINDING SITE, designated SEQ ID:19361, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29714] Another function of GAM189 is therefore inhibition of LOC219293 (Accession XP_166599.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219293.

[29715] LOC219700 (Accession XP_167570.1) is another GAM189 target gene, herein designated TARGET GENE. LOC219700 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC219700, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219700 BINDING SITE, designated SEQ ID:2410, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29716] Another function of GAM189 is therefore inhibition of LOC219700 (Accession XP_167570.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219700.

[29717] LOC219731 (Accession XP_167596.1) is another GAM189 target gene, herein designated TARGET GENE. LOC219731 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC219731, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219731 BINDING SITE, designated SEQ ID:4678, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29718] Another function of GAM189 is therefore inhibition of LOC219731 (Accession XP_167596.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219731.

[29719] LOC219735 (Accession XP_167601.1) is another GAM189 target gene, herein designated TARGET GENE. LOC219735 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219735 BINDING SITE, designated SEQ ID:18913, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29720] Another function of GAM189 is therefore inhibition of LOC219735 (Accession XP_167601.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219735.

[29721] LOC219894 (Accession XP_167782.1) is another GAM189

target gene, herein designated TARGET GENE. LOC219894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219894 BINDING SITE, designated SEQ ID:14588, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29722] Another function of GAM189 is therefore inhibition of LOC219894 (Accession XP_167782.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219894.

[29723] LOC220074 (Accession NP_660352.1) is another GAM189 target gene, herein designated TARGET GENE. LOC220074 BINDING SITE1 through LOC220074 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC220074, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220074 BINDING SITE1 through LOC220074 BINDING SITE3, des-

ignated SEQ ID:16838, SEQ ID:6497 and SEQ ID:9147 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29724] Another function of GAM189 is therefore inhibition of LOC220074 (Accession NP_660352.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220074.

[29725] LOC221174 (Accession XP_167915.1) is another GAM189 target gene, herein designated TARGET GENE. LOC221174 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221174, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221174 BINDING SITE, designated SEQ ID:17256, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29726] Another function of GAM189 is therefore inhibition of LOC221174 (Accession XP_167915.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221174.

[29727] LOC221663 (Accession XP_168131.1) is another GAM189 target gene, herein designated TARGET GENE. LOC221663 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221663 BINDING SITE, designated SEQ ID:1939, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29728] Another function of GAM189 is therefore inhibition of LOC221663 (Accession XP_168131.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221663.

[29729] LOC221946 (Accession XP_168340.1) is another GAM189 target gene, herein designated TARGET GENE. LOC221946 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221946, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221946 BINDING SITE, designated SEQ ID:15948, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29730] Another function of GAM189 is therefore inhibition of LOC221946 (Accession XP_168340.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221946.

[29731] LOC221960 (Accession XP_165859.1) is another GAM189 target gene, herein designated TARGET GENE. LOC221960 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221960, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221960 BINDING SITE, designated SEQ ID:14860, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29732] Another function of GAM189 is therefore inhibition of LOC221960 (Accession XP_165859.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221960.

[29733] LOC221964 (Accession XP_168342.1) is another GAM189

target gene, herein designated TARGET GENE. LOC221964 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221964, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221964 BINDING SITE, designated SEQ ID:17029, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29734] Another function of GAM189 is therefore inhibition of LOC221964 (Accession XP_168342.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221964.

[29735] LOC222057 (Accession XP_166594.2) is another GAM189 target gene, herein designated TARGET GENE. LOC222057 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222057, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222057 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29736] Another function of GAM189 is therefore inhibition of LOC222057 (Accession XP_166594.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222057.

[29737] LOC222068 (Accession XP_166556.1) is another GAM189 target gene, herein designated TARGET GENE. LOC222068 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC222068, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222068 BINDING SITE, designated SEQ ID:3232, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29738] Another function of GAM189 is therefore inhibition of LOC222068 (Accession XP_166556.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222068.

[29739] LOC222159 (Accession XP_212100.1) is another GAM189 target gene, herein designated TARGET GENE. LOC222159

BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC222159, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222159 BINDING SITE, designated SEQ ID:16228, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29740] Another function of GAM189 is therefore inhibition of LOC222159 (Accession XP_212100.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222159.

[29741] LOC252983 (Accession XP_170858.2) is another GAM189 target gene, herein designated TARGET GENE. LOC252983 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC252983, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC252983 BINDING SITE, designated SEQ ID:2959, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29742] Another function of GAM189 is therefore inhibition of LOC252983 (Accession XP_170858.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC252983.

[29743] LOC253612 (Accession XP_172985.2) is another GAM189 target gene, herein designated TARGET GENE. LOC253612 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253612, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253612 BINDING SITE, designated SEQ ID:5487, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29744] Another function of GAM189 is therefore inhibition of LOC253612 (Accession XP_172985.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253612.

[29745] LOC253805 (Accession XP_172854.1) is another GAM189 target gene, herein designated TARGET GENE. LOC253805

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC253805, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253805 BINDING SITE, designated SEQ ID:4532, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29746] Another function of GAM189 is therefore inhibition of LOC253805 (Accession XP_172854.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253805.

[29747] LOC254875 (Accession XP_171170.1) is another GAM189 target gene, herein designated TARGET GENE. LOC254875 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC254875, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254875 BINDING SITE, designated SEQ ID:6188, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29748] Another function of GAM189 is therefore inhibition of LOC254875 (Accession XP_171170.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254875.

[29749] LOC255031 (Accession XP_173187.1) is another GAM189 target gene, herein designated TARGET GENE. LOC255031 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC255031, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255031 BINDING SITE, designated SEQ ID:3261, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29750] Another function of GAM189 is therefore inhibition of LOC255031 (Accession XP_173187.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255031.

[29751] LOC255177 (Accession XP_172941.1) is another GAM189 target gene, herein designated TARGET GENE. LOC255177 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC255177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255177 BINDING SITE, designated SEQ ID:6294, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29752] Another function of GAM189 is therefore inhibition of LOC255177 (Accession XP_172941.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255177.

[29753] LOC255458 (Accession XP_173150.1) is another GAM189 target gene, herein designated TARGET GENE. LOC255458 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255458, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255458 BINDING SITE, designated SEQ ID:6365, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29754] Another function of GAM189 is therefore inhibition of

LOC255458 (Accession XP_173150.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255458.

[29755] LOC255488 (Accession XP_172581.2) is another GAM189 target gene, herein designated TARGET GENE. LOC255488 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC255488, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255488 BINDING SITE, designated SEQ ID:3150, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29756] Another function of GAM189 is therefore inhibition of LOC255488 (Accession XP_172581.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255488.

[29757] LOC255975 (Accession XP_171083.2) is another GAM189 target gene, herein designated TARGET GENE. LOC255975 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255975, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255975 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29758] Another function of GAM189 is therefore inhibition of LOC255975 (Accession XP_171083.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255975.

[29759] LOC256614 (Accession XP_172864.1) is another GAM189 target gene, herein designated TARGET GENE. LOC256614 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC256614, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256614 BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29760] Another function of GAM189 is therefore inhibition of LOC256614 (Accession XP_172864.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256614.

[29761] LOC282905 (Accession XP_212606.1) is another GAM189 target gene, herein designated TARGET GENE. LOC282905 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282905, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282905 BINDING SITE, designated SEQ ID:986, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29762] Another function of GAM189 is therefore inhibition of LOC282905 (Accession XP_212606.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282905.

[29763] LOC282943 (Accession XP_212647.1) is another GAM189 target gene, herein designated TARGET GENE. LOC282943 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282943, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282943 BINDING SITE, designated SEQ ID:986, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29764] Another function of GAM189 is therefore inhibition of LOC282943 (Accession XP_212647.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282943.

[29765] LOC282963 (Accession XP_210834.1) is another GAM189 target gene, herein designated TARGET GENE. LOC282963 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282963, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282963 BINDING SITE, designated SEQ ID:814, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29766] Another function of GAM189 is therefore inhibition of LOC282963 (Accession XP_210834.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC282963.

[29767] LOC282972 (Accession XP_210837.1) is another GAM189 target gene, herein designated TARGET GENE. LOC282972 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282972 BINDING SITE, designated SEQ ID:18172, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29768] Another function of GAM189 is therefore inhibition of LOC282972 (Accession XP_210837.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282972.

[29769] LOC282987 (Accession XP_210845.1) is another GAM189 target gene, herein designated TARGET GENE. LOC282987 BINDING SITE1 and LOC282987 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC282987, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282987 BINDING SITE1 and LOC282987 BINDING SITE2, designated SEQ ID:16541 and SEQ ID:12068 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29770] Another function of GAM189 is therefore inhibition of LOC282987 (Accession XP_210845.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282987.

[29771] LOC282997 (Accession XP_208473.1) is another GAM189 target gene, herein designated TARGET GENE. LOC282997 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282997, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282997 BINDING SITE, designated SEQ ID:11798, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29772] Another function of GAM189 is therefore inhibition of LOC282997 (Accession XP_208473.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282997.

[29773] LOC283047 (Accession XP_210870.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283047 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283047, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283047 BINDING SITE, designated SEQ ID:17587, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29774] Another function of GAM189 is therefore inhibition of LOC283047 (Accession XP_210870.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283047.

[29775] LOC283061 (Accession XP_210875.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283061, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283061 BINDING SITE, designated SEQ ID:7252, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29776] Another function of GAM189 is therefore inhibition of LOC283061 (Accession XP_210875.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283061.

[29777] LOC283087 (Accession XP_208509.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283087 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283087, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283087 BINDING SITE, designated SEQ ID:4176, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29778] Another function of GAM189 is therefore inhibition of LOC283087 (Accession XP_208509.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283087.

[29779] LOC283089 (Accession XP_210885.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283089 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283089, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283089 BINDING SITE, designated SEQ ID:2219, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29780] Another function of GAM189 is therefore inhibition of LOC283089 (Accession XP_210885.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283089.

[29781] LOC283119 (Accession XP_210895.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283119 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283119, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC283119 BINDING SITE, designated SEQ ID:16397, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29782] Another function of GAM189 is therefore inhibition of LOC283119 (Accession XP_210895.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283119.

[29783] LOC283130 (Accession XP_208525.3) is another GAM189 target gene, herein designated TARGET GENE. LOC283130 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283130, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283130 BINDING SITE, designated SEQ ID:5323, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29784] Another function of GAM189 is therefore inhibition of LOC283130 (Accession XP_208525.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283130.

[29785] LOC283140 (Accession XP_210911.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283140 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283140 BINDING SITE, designated SEQ ID:12544, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29786] Another function of GAM189 is therefore inhibition of LOC283140 (Accession XP_210911.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283140.

[29787] LOC283142 (Accession XP_210925.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283142 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC283142 BINDING SITE, designated SEQ ID:19977, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29788] Another function of GAM189 is therefore inhibition of LOC283142 (Accession XP_210925.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283142.

[29789] LOC283143 (Accession XP_210920.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283143 BINDING SITE, designated SEQ ID:2650, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29790] Another function of GAM189 is therefore inhibition of LOC283143 (Accession XP_210920.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283143.

[29791] LOC283152 (Accession XP_210917.2) is another GAM189 target gene, herein designated TARGET GENE. LOC283152 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283152, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283152 BINDING SITE, designated SEQ ID:19812, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29792] Another function of GAM189 is therefore inhibition of LOC283152 (Accession XP_210917.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283152.

[29793] LOC283170 (Accession XP_208535.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283170 BINDING SITE, designated SEQ ID:4979, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29794] Another function of GAM189 is therefore inhibition of LOC283170 (Accession XP_208535.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283170.

[29795] LOC283177 (Accession XP_210903.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283177 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283177 BINDING SITE, designated SEQ ID:15574, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29796] Another function of GAM189 is therefore inhibition of LOC283177 (Accession XP_210903.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283177.

[29797] LOC283215 (Accession XP_208555.2) is another GAM189

target gene, herein designated TARGET GENE. LOC283215 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283215, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283215 BINDING SITE, designated SEQ ID:10112, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29798] Another function of GAM189 is therefore inhibition of LOC283215 (Accession XP_208555.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283215.

[29799] LOC283241 (Accession NP_787089.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283241 BINDING SITE, designated SEQ ID:9525, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29800] Another function of GAM189 is therefore inhibition of LOC283241 (Accession NP_787089.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283241.

[29801] LOC283244 (Accession XP_208583.2) is another GAM189 target gene, herein designated TARGET GENE. LOC283244 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283244, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283244 BINDING SITE, designated SEQ ID:4496, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29802] Another function of GAM189 is therefore inhibition of LOC283244 (Accession XP_208583.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283244.

[29803] LOC283262 (Accession XP_210952.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283262

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283262 BINDING SITE, designated SEQ ID:8223, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29804] Another function of GAM189 is therefore inhibition of LOC283262 (Accession XP_210952.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283262.

[29805] LOC283278 (Accession XP_210961.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283278 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283278, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283278 BINDING SITE, designated SEQ ID:9036, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29806] Another function of GAM189 is therefore inhibition of LOC283278 (Accession XP_210961.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283278.

[29807] LOC283293 (Accession XP_210962.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283293 BINDING SITE, designated SEQ ID:17952, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29808] Another function of GAM189 is therefore inhibition of LOC283293 (Accession XP_210962.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283293.

[29809] LOC283299 (Accession XP_210965.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283299 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC283299, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283299 BINDING SITE, designated SEQ ID:9585, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29810] Another function of GAM189 is therefore inhibition of LOC283299 (Accession XP_210965.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283299.

[29811] LOC283329 (Accession XP_210978.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283329 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283329 BINDING SITE, designated SEQ ID:2201, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29812] Another function of GAM189 is therefore inhibition of

LOC283329 (Accession XP_210978.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283329.

[29813] LOC283335 (Accession XP_210981.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283335 BINDING SITE1 and LOC283335 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283335, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283335 BINDING SITE1 and LOC283335 BINDING SITE2, designated SEQ ID:2143 and SEQ ID:16144 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29814] Another function of GAM189 is therefore inhibition of LOC283335 (Accession XP_210981.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283335.

[29815] LOC283377 (Accession XP_208647.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283377

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283377, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283377 BINDING SITE, designated SEQ ID:8232, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29816] Another function of GAM189 is therefore inhibition of LOC283377 (Accession XP_208647.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283377.

[29817] LOC283387 (Accession XP_211007.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283387 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283387, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283387 BINDING SITE, designated SEQ ID:7265, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29818] Another function of GAM189 is therefore inhibition of LOC283387 (Accession XP_211007.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283387.

[29819] LOC283394 (Accession XP_211021.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283394 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283394, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283394 BINDING SITE, designated SEQ ID:1730, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29820] Another function of GAM189 is therefore inhibition of LOC283394 (Accession XP_211021.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283394.

[29821] LOC283395 (Accession XP_211020.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283395 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC283395, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283395 BINDING SITE, designated SEQ ID:9003, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29822] Another function of GAM189 is therefore inhibition of LOC283395 (Accession XP_211020.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283395.

[29823] LOC283400 (Accession XP_211024.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283400 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283400 BINDING SITE, designated SEQ ID:19206, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29824] Another function of GAM189 is therefore inhibition of

LOC283400 (Accession XP_211024.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283400.

[29825] LOC283432 (Accession XP_211032.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283432 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283432, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283432 BINDING SITE, designated SEQ ID:16658, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29826] Another function of GAM189 is therefore inhibition of LOC283432 (Accession XP_211032.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283432.

[29827] LOC283441 (Accession XP_211043.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283441 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283441, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283441 BINDING SITE, designated SEQ ID:2220, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29828] Another function of GAM189 is therefore inhibition of LOC283441 (Accession XP_211043.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283441.

[29829] LOC283442 (Accession XP_211037.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283442 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283442 BINDING SITE, designated SEQ ID:10032, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29830] Another function of GAM189 is therefore inhibition of LOC283442 (Accession XP_211037.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283442.

[29831] LOC283445 (Accession XP_211044.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283445 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283445 BINDING SITE, designated SEQ ID:5683, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29832] Another function of GAM189 is therefore inhibition of LOC283445 (Accession XP_211044.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283445.

[29833] LOC283452 (Accession XP_208679.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283452 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283452, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283452 BINDING SITE, designated SEQ ID:7397, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29834] Another function of GAM189 is therefore inhibition of LOC283452 (Accession XP_208679.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283452.

[29835] LOC283454 (Accession XP_211049.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283454 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283454, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283454 BINDING SITE, designated SEQ ID:14861, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29836] Another function of GAM189 is therefore inhibition of LOC283454 (Accession XP_211049.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283454.

[29837] LOC283467 (Accession XP_211050.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283467 BINDING SITE, designated SEQ ID:13967, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29838] Another function of GAM189 is therefore inhibition of LOC283467 (Accession XP_211050.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283467.

[29839] LOC283475 (Accession XP_211056.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283475 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC283475 BINDING SITE, designated SEQ ID:9892, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29840] Another function of GAM189 is therefore inhibition of LOC283475 (Accession XP_211056.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283475.

[29841] LOC283484 (Accession XP_211053.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283484 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283484, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283484 BINDING SITE, designated SEQ ID:17710, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29842] Another function of GAM189 is therefore inhibition of LOC283484 (Accession XP_211053.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283484.

[29843] LOC283487 (Accession XP_211062.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283487 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC283487, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283487 BINDING SITE, designated SEQ ID:7371, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29844] Another function of GAM189 is therefore inhibition of LOC283487 (Accession XP_211062.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283487.

[29845] LOC283507 (Accession XP_211075.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283507 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC283507 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29846] Another function of GAM189 is therefore inhibition of LOC283507 (Accession XP_211075.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283507.

[29847] LOC283534 (Accession XP_211083.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283534 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283534, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283534 BINDING SITE, designated SEQ ID:3199, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29848] Another function of GAM189 is therefore inhibition of LOC283534 (Accession XP_211083.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283534.

[29849] LOC283570 (Accession XP_211118.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283570 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283570, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283570 BINDING SITE, designated SEQ ID:13652, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29850] Another function of GAM189 is therefore inhibition of LOC283570 (Accession XP_211118.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283570.

[29851] LOC283575 (Accession XP_211095.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283575 BINDING SITE1 and LOC283575 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283575, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC283575 BINDING SITE1 and LOC283575 BINDING SITE2, designated SEQ ID:6183 and SEQ ID:10067 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29852] Another function of GAM189 is therefore inhibition of LOC283575 (Accession XP_211095.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283575.

[29853] LOC283585 (Accession XP_294741.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283585 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283585, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283585 BINDING SITE, designated SEQ ID:10466, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29854] Another function of GAM189 is therefore inhibition of LOC283585 (Accession XP_294741.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283585.

[29855] LOC283588 (Accession NP_787093.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283588 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283588, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283588 BINDING SITE, designated SEQ ID:10638, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29856] Another function of GAM189 is therefore inhibition of LOC283588 (Accession NP_787093.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283588.

[29857] LOC283624 (Accession XP_211126.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283624 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283624, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC283624 BINDING SITE, designated SEQ ID:4420, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29858] Another function of GAM189 is therefore inhibition of LOC283624 (Accession XP_211126.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283624.

[29859] LOC283637 (Accession XP_211134.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283637 BINDING SITE1 and LOC283637 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283637, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283637 BINDING SITE1 and LOC283637 BINDING SITE2, designated SEQ ID:14859 and SEQ ID:3581 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29860] Another function of GAM189 is therefore inhibition of LOC283637 (Accession XP_211134.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283637.

[29861] LOC283641 (Accession XP_208764.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283641 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283641, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283641 BINDING SITE, designated SEQ ID:17964, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29862] Another function of GAM189 is therefore inhibition of LOC283641 (Accession XP_208764.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283641.

[29863] LOC283663 (Accession XP_211147.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283663 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283663, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283663 BINDING SITE, designated SEQ ID:16674, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29864] Another function of GAM189 is therefore inhibition of LOC283663 (Accession XP_211147.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283663.

[29865] LOC283664 (Accession XP_208773.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283664 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283664, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283664 BINDING SITE, designated SEQ ID:8450, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29866] Another function of GAM189 is therefore inhibition of LOC283664 (Accession XP_208773.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283664.

[29867] LOC283672 (Accession XP_211152.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283672 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283672, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283672 BINDING SITE, designated SEQ ID:1730, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29868] Another function of GAM189 is therefore inhibition of LOC283672 (Accession XP_211152.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283672.

[29869] LOC283687 (Accession NP_787094.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC283687 BINDING SITE, designated SEQ ID:11904, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29870] Another function of GAM189 is therefore inhibition of LOC283687 (Accession NP_787094.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283687.

[29871] LOC283693 (Accession XP_208788.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283693 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283693, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283693 BINDING SITE, designated SEQ ID:5305, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29872] Another function of GAM189 is therefore inhibition of LOC283693 (Accession XP_208788.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283693.

[29873] LOC283701 (Accession XP_211170.3) is another GAM189 target gene, herein designated TARGET GENE. LOC283701 BINDING SITE1 and LOC283701 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283701, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283701 BINDING SITE1 and LOC283701 BINDING SITE2, designated SEQ ID:13716 and SEQ ID:14381 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29874] Another function of GAM189 is therefore inhibition of LOC283701 (Accession XP_211170.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283701.

[29875] LOC283723 (Accession XP_211176.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283723 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283723, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283723 BINDING SITE, designated SEQ ID:9256, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29876] Another function of GAM189 is therefore inhibition of LOC283723 (Accession XP_211176.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283723.

[29877] LOC283741 (Accession XP_208115.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283741 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283741, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283741 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29878] Another function of GAM189 is therefore inhibition of LOC283741 (Accession XP_208115.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283741.

[29879] LOC283767 (Accession XP_208835.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283767 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283767, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283767 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29880] Another function of GAM189 is therefore inhibition of LOC283767 (Accession XP_208835.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283767.

[29881] LOC283778 (Accession XP_211199.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283778 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283778, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC283778 BINDING SITE, designated SEQ ID:4370, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29882] Another function of GAM189 is therefore inhibition of LOC283778 (Accession XP_211199.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283778.

[29883] LOC283779 (Accession XP_211198.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283779 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283779, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283779 BINDING SITE, designated SEQ ID:17644, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29884] Another function of GAM189 is therefore inhibition of LOC283779 (Accession XP_211198.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283779.

[29885] LOC283801 (Accession XP_208122.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283801 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283801, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283801 BINDING SITE, designated SEQ ID:6265, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29886] Another function of GAM189 is therefore inhibition of LOC283801 (Accession XP_208122.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283801.

[29887] LOC283802 (Accession XP_208850.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283802 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283802, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC283802 BINDING SITE, designated SEQ ID:16700, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29888] Another function of GAM189 is therefore inhibition of LOC283802 (Accession XP_208850.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283802.

[29889] LOC283818 (Accession XP_211218.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283818 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283818 BINDING SITE, designated SEQ ID:9546, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29890] Another function of GAM189 is therefore inhibition of LOC283818 (Accession XP_211218.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283818.

[29891] LOC283849 (Accession XP_208870.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283849 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC283849, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283849 BINDING SITE, designated SEQ ID:4308, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29892] Another function of GAM189 is therefore inhibition of LOC283849 (Accession XP_208870.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283849.

[29893] LOC283849 (Accession NP_848611.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283849 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC283849, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of LOC283849 BINDING SITE, designated SEQ ID:4308, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29894] Another function of GAM189 is therefore inhibition of LOC283849 (Accession NP_848611.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283849.

[29895] LOC283851 (Accession XP_211229.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283851 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283851, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283851 BINDING SITE, designated SEQ ID:4974, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29896] Another function of GAM189 is therefore inhibition of LOC283851 (Accession XP_211229.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283851.

[29897] LOC283856 (Accession XP_211233.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283856 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283856 BINDING SITE, designated SEQ ID:6184, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29898] Another function of GAM189 is therefore inhibition of LOC283856 (Accession XP_211233.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283856.

[29899] LOC283861 (Accession NP_787095.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283861 BINDING SITE1 and LOC283861 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283861, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC283861 BINDING SITE1 and LOC283861 BINDING SITE2, designated SEQ ID:1401 and SEQ ID:1635 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29900] Another function of GAM189 is therefore inhibition of LOC283861 (Accession NP_787095.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283861.

[29901] LOC283863 (Accession XP_208875.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283863 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283863, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283863 BINDING SITE, designated SEQ ID:13285, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29902] Another function of GAM189 is therefore inhibition of LOC283863 (Accession XP_208875.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283863.

[29903] LOC283887 (Accession XP_211248.2) is another GAM189 target gene, herein designated TARGET GENE. LOC283887 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283887, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283887 BINDING SITE, designated SEQ ID:18993, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29904] Another function of GAM189 is therefore inhibition of LOC283887 (Accession XP_211248.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283887.

[29905] LOC283888 (Accession XP_211249.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283888 BINDING SITE1 and LOC283888 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283888, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283888 BINDING SITE1 and LOC283888 BINDING SITE2, designated SEQ ID:14104 and SEQ ID:11072 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29906] Another function of GAM189 is therefore inhibition of LOC283888 (Accession XP_211249.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283888.

[29907] LOC283889 (Accession XP_208899.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283889 BINDING SITE1 and LOC283889 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283889, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283889 BINDING SITE1 and LOC283889 BINDING SITE2, designated SEQ ID:10739 and SEQ ID:3899 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29908] Another function of GAM189 is therefore inhibition of LOC283889 (Accession XP_208899.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283889.

[29909] LOC283928 (Accession XP_208909.1) is another GAM189 target gene, herein designated TARGET GENE. LOC283928 BINDING SITE1 and LOC283928 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283928, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283928 BINDING SITE1 and LOC283928 BINDING SITE2, designated SEQ ID:20101 and SEQ ID:4703 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29910] Another function of GAM189 is therefore inhibition of LOC283928 (Accession XP_208909.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283928.

[29911] LOC283929 (Accession XP_208905.2) is another GAM189

target gene, herein designated TARGET GENE. LOC283929 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283929, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283929 BINDING SITE, designated SEQ ID:15775, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29912] Another function of GAM189 is therefore inhibition of LOC283929 (Accession XP_208905.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283929.

[29913] LOC283964 (Accession XP_208145.2) is another GAM189 target gene, herein designated TARGET GENE. LOC283964 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283964, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283964 BINDING SITE, designated SEQ ID:19569, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29914] Another function of GAM189 is therefore inhibition of LOC283964 (Accession XP_208145.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283964.

[29915] LOC284001 (Accession XP_208958.2) is another GAM189 target gene, herein designated TARGET GENE. LOC284001 BINDING SITE1 and LOC284001 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284001, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284001 BINDING SITE1 and LOC284001 BINDING SITE2, designated SEQ ID:11764 and SEQ ID:18161 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29916] Another function of GAM189 is therefore inhibition of LOC284001 (Accession XP_208958.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284001.

[29917] LOC284016 (Accession XP_211298.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284016 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284016, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284016 BINDING SITE, designated SEQ ID:3244, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29918] Another function of GAM189 is therefore inhibition of LOC284016 (Accession XP_211298.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284016.

[29919] LOC284017 (Accession XP_208961.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284017 BINDING SITE, designated SEQ ID:18610, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29920] Another function of GAM189 is therefore inhibition of LOC284017 (Accession XP_208961.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284017.

[29921] LOC284019 (Accession XP_211302.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284019 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284019, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284019 BINDING SITE, designated SEQ ID:10124, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29922] Another function of GAM189 is therefore inhibition of LOC284019 (Accession XP_211302.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284019.

[29923] LOC284023 (Accession XP_208983.3) is another GAM189

target gene, herein designated TARGET GENE. LOC284023 BINDING SITE1 and LOC284023 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284023, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284023 BINDING SITE1 and LOC284023 BINDING SITE2, designated SEQ ID:17953 and SEQ ID:14597 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29924] Another function of GAM189 is therefore inhibition of LOC284023 (Accession XP_208983.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284023.

[29925] LOC284048 (Accession XP_208152.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284048 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284048, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC284048 BINDING SITE, designated SEQ ID:10847, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29926] Another function of GAM189 is therefore inhibition of LOC284048 (Accession XP_208152.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284048.

[29927] LOC284074 (Accession XP_211321.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284074 BINDING SITE1 and LOC284074 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284074, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284074 BINDING SITE1 and LOC284074 BINDING SITE2, designated SEQ ID:15531 and SEQ ID:1596 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29928] Another function of GAM189 is therefore inhibition of LOC284074 (Accession XP_211321.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284074.

[29929] LOC284082 (Accession XP_211323.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284082 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284082, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284082 BINDING SITE, designated SEQ ID:18527, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29930] Another function of GAM189 is therefore inhibition of LOC284082 (Accession XP_211323.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284082.

[29931] LOC284095 (Accession XP_211324.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284095 BINDING SITE1 through LOC284095 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284095, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284095 BINDING SITE1 through LOC284095 BINDING SITE3, designated SEQ ID:15513, SEQ ID:11799 and SEQ ID:7333 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29932] Another function of GAM189 is therefore inhibition of LOC284095 (Accession XP_211324.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284095.

[29933] LOC284098 (Accession XP_209008.3) is another GAM189 target gene, herein designated TARGET GENE. LOC284098 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284098, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284098 BINDING SITE, designated SEQ ID:8582, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29934] Another function of GAM189 is therefore inhibition of LOC284098 (Accession XP_209008.3) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284098.

[29935] LOC284100 (Accession XP_209015.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284100 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284100, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284100 BINDING SITE, designated SEQ ID:1777, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29936] Another function of GAM189 is therefore inhibition of LOC284100 (Accession XP_209015.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284100.

[29937] LOC284101 (Accession XP_209019.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284101 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284101, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284101 BINDING SITE, designated SEQ ID:19537, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29938] Another function of GAM189 is therefore inhibition of LOC284101 (Accession XP_209019.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284101.

[29939] LOC284102 (Accession XP_211327.3) is another GAM189 target gene, herein designated TARGET GENE. LOC284102 BINDING SITE1 through LOC284102 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284102, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284102 BINDING SITE1 through LOC284102 BINDING SITE3, designated SEQ ID:7745, SEQ ID:18149 and SEQ ID:3233 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29940] Another function of GAM189 is therefore inhibition of

LOC284102 (Accession XP_211327.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284102.

[29941] LOC284128 (Accession XP_211342.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284128 BINDING SITE1 and LOC284128 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284128, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284128 BINDING SITE1 and LOC284128 BINDING SITE2, designated SEQ ID:17271 and SEQ ID:1966 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29942] Another function of GAM189 is therefore inhibition of LOC284128 (Accession XP_211342.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284128.

[29943] LOC284135 (Accession XP_209032.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284135

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284135 BINDING SITE, designated SEQ ID:12779, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29944] Another function of GAM189 is therefore inhibition of LOC284135 (Accession XP_209032.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284135.

[29945] LOC284145 (Accession XP_211353.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284145 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284145, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284145 BINDING SITE, designated SEQ ID:4102, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29946] Another function of GAM189 is therefore inhibition of LOC284145 (Accession XP_211353.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284145.

[29947] LOC284171 (Accession XP_209051.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284171 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284171, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284171 BINDING SITE, designated SEQ ID:11530, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29948] Another function of GAM189 is therefore inhibition of LOC284171 (Accession XP_209051.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284171.

[29949] LOC284183 (Accession XP_209059.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284183 BINDING SITE1 and LOC284183 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by LOC284183, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284183 BINDING SITE1 and LOC284183 BINDING SITE2, designated SEQ ID:1111 and SEQ ID:9456 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29950] Another function of GAM189 is therefore inhibition of LOC284183 (Accession XP_209059.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284183.

[29951] LOC284186 (Accession XP_209060.2) is another GAM189 target gene, herein designated TARGET GENE. LOC284186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284186 BINDING SITE, designated SEQ ID:14861, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29952] Another function of GAM189 is therefore inhibition of LOC284186 (Accession XP_209060.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284186.

[29953] LOC284191 (Accession XP_211377.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284191 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284191, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284191 BINDING SITE, designated SEQ ID:4421, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29954] Another function of GAM189 is therefore inhibition of LOC284191 (Accession XP_211377.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284191.

[29955] LOC284202 (Accession XP_208174.2) is another GAM189 target gene, herein designated TARGET GENE. LOC284202

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284202, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284202 BINDING SITE, designated SEQ ID:3800, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29956] Another function of GAM189 is therefore inhibition of LOC284202 (Accession XP_208174.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284202.

[29957] LOC284267 (Accession XP_211411.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284267 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284267, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284267 BINDING SITE, designated SEQ ID:8494, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29958] Another function of GAM189 is therefore inhibition of LOC284267 (Accession XP_211411.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284267.

[29959] LOC284276 (Accession XP_211412.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284276 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284276, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284276 BINDING SITE, designated SEQ ID:1026, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29960] Another function of GAM189 is therefore inhibition of LOC284276 (Accession XP_211412.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284276.

[29961] LOC284286 (Accession XP_211419.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284286 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC284286, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284286 BINDING SITE, designated SEQ ID:19875, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29962] Another function of GAM189 is therefore inhibition of LOC284286 (Accession XP_211419.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284286.

[29963] LOC284289 (Accession XP_209105.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284289 BINDING SITE1 and LOC284289 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284289, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284289 BINDING SITE1 and LOC284289 BINDING SITE2, designated SEQ ID:16648 and SEQ ID:1885 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:246.

[29964] Another function of GAM189 is therefore inhibition of LOC284289 (Accession XP_209105.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284289.

[29965] LOC284297 (Accession XP_209112.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284297 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284297, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284297 BINDING SITE, designated SEQ ID:1751, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29966] Another function of GAM189 is therefore inhibition of LOC284297 (Accession XP_209112.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284297.

[29967] LOC284304 (Accession XP_211426.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284304

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284304, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284304 BINDING SITE, designated SEQ ID:4849, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29968] Another function of GAM189 is therefore inhibition of LOC284304 (Accession XP_211426.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284304.

[29969] LOC284317 (Accession XP_209162.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284317 BINDING SITE1 and LOC284317 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284317, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284317 BINDING SITE1 and LOC284317 BINDING SITE2, designated SEQ ID:7077 and SEQ ID:3386 respectively, to the nucleotide sequence

of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29970] Another function of GAM189 is therefore inhibition of LOC284317 (Accession XP_209162.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284317.

[29971] LOC284325 (Accession XP_209143.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284325 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284325, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284325 BINDING SITE, designated SEQ ID:1731, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29972] Another function of GAM189 is therefore inhibition of LOC284325 (Accession XP_209143.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284325.

[29973] LOC284356 (Accession XP_211437.1) is another GAM189

target gene, herein designated TARGET GENE. LOC284356 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284356 BINDING SITE, designated SEQ ID:11986, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29974] Another function of GAM189 is therefore inhibition of LOC284356 (Accession XP_211437.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284356.

[29975] LOC284362 (Accession XP_211435.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284362 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284362, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284362 BINDING SITE, designated SEQ ID:18898, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[29976] Another function of GAM189 is therefore inhibition of LOC284362 (Accession XP_211435.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284362.

[29977] LOC284375 (Accession XP_209154.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284375 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284375, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284375 BINDING SITE, designated SEQ ID:16701, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29978] Another function of GAM189 is therefore inhibition of LOC284375 (Accession XP_209154.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284375.

[29979] LOC284376 (Accession XP_209157.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284376

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284376, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284376 BINDING SITE, designated SEQ ID:19718, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29980] Another function of GAM189 is therefore inhibition of LOC284376 (Accession XP_209157.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284376.

[29981] LOC284379 (Accession XP_209163.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284379 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284379, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284379 BINDING SITE, designated SEQ ID:9312, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29982] Another function of GAM189 is therefore inhibition of LOC284379 (Accession XP_209163.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284379.

[29983] LOC284395 (Accession XP_211454.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284395 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284395, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284395 BINDING SITE, designated SEQ ID:16459, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29984] Another function of GAM189 is therefore inhibition of LOC284395 (Accession XP_211454.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284395.

[29985] LOC284396 (Accession XP_211452.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284396 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC284396, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284396 BINDING SITE, designated SEQ ID:10399, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29986] Another function of GAM189 is therefore inhibition of LOC284396 (Accession XP_211452.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284396.

[29987] LOC284405 (Accession XP_209183.2) is another GAM189 target gene, herein designated TARGET GENE. LOC284405 BINDING SITE1 and LOC284405 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284405, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284405 BINDING SITE1 and LOC284405 BINDING SITE2, designated SEQ ID:19462 and SEQ ID:2645 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:246.

[29988] Another function of GAM189 is therefore inhibition of LOC284405 (Accession XP_209183.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284405.

[29989] LOC284408 (Accession XP_211443.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284408 BINDING SITE, designated SEQ ID:14364, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29990] Another function of GAM189 is therefore inhibition of LOC284408 (Accession XP_211443.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284408.

[29991] LOC284410 (Accession XP_211449.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284410

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284410, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284410 BINDING SITE, designated SEQ ID:17304, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29992] Another function of GAM189 is therefore inhibition of LOC284410 (Accession XP_211449.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284410.

[29993] LOC284421 (Accession XP_209200.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284421 BINDING SITE1 and LOC284421 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284421, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284421 BINDING SITE1 and LOC284421 BINDING SITE2, designated SEQ ID:4533 and SEQ ID:15844 respectively, to the nucleotide se-

quence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29994] Another function of GAM189 is therefore inhibition of LOC284421 (Accession XP_209200.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284421.

[29995] LOC284421 (Accession XP_209200.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284421 BINDING SITE1 and LOC284421 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284421, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284421 BINDING SITE1 and LOC284421 BINDING SITE2, designated SEQ ID:15844 and SEQ ID:4975 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29996] Another function of GAM189 is therefore inhibition of LOC284421 (Accession XP_209200.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284421.

[29997] LOC284426 (Accession XP_209198.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284426 BINDING SITE1 through LOC284426 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284426, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284426 BINDING SITE1 through LOC284426 BINDING SITE3, designated SEQ ID:5357, SEQ ID:13177 and SEQ ID:8752 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[29998] Another function of GAM189 is therefore inhibition of LOC284426 (Accession XP_209198.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284426.

[29999] LOC284454 (Accession XP_209216.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284454 BINDING SITE1 through LOC284454 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284454, corresponding to target

binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284454 BINDING SITE1 through LOC284454 BINDING SITE3, designated SEQ ID:3999, SEQ ID:19117 and SEQ ID:16031 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30000] Another function of GAM189 is therefore inhibition of LOC284454 (Accession XP_209216.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284454.

[30001] LOC284456 (Accession XP_211470.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284456 BINDING SITE, designated SEQ ID:18777, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30002] Another function of GAM189 is therefore inhibition of

LOC284456 (Accession XP_211470.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284456.

[30003] LOC284471 (Accession XP_209225.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284471 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284471, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284471 BINDING SITE, designated SEQ ID:19286, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30004] Another function of GAM189 is therefore inhibition of LOC284471 (Accession XP_209225.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284471.

[30005] LOC284512 (Accession XP_211500.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284512 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284512, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284512 BINDING SITE, designated SEQ ID:14119, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30006] Another function of GAM189 is therefore inhibition of LOC284512 (Accession XP_211500.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284512.

[30007] LOC284513 (Accession XP_211502.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284513 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284513, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284513 BINDING SITE, designated SEQ ID:18865, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30008] Another function of GAM189 is therefore inhibition of LOC284513 (Accession XP_211502.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284513.

[30009] LOC284549 (Accession XP_211514.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284549 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284549, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284549 BINDING SITE, designated SEQ ID:19112, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30010] Another function of GAM189 is therefore inhibition of LOC284549 (Accession XP_211514.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284549.

[30011] LOC284551 (Accession XP_211515.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284551 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284551, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284551 BINDING SITE, designated SEQ ID:9493, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30012] Another function of GAM189 is therefore inhibition of LOC284551 (Accession XP_211515.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284551.

[30013] LOC284577 (Accession XP_211522.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284577 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284577, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284577 BINDING SITE, designated SEQ ID:19533, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30014] Another function of GAM189 is therefore inhibition of LOC284577 (Accession XP_211522.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284577.

[30015] LOC284587 (Accession XP_209278.3) is another GAM189 target gene, herein designated TARGET GENE. LOC284587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284587 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30016] Another function of GAM189 is therefore inhibition of LOC284587 (Accession XP_209278.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284587.

[30017] LOC284611 (Accession XP_211552.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284611 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284611, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC284611 BINDING SITE, designated SEQ ID:12497, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30018] Another function of GAM189 is therefore inhibition of LOC284611 (Accession XP_211552.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284611.

[30019] LOC284628 (Accession XP_211561.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284628 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284628, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284628 BINDING SITE, designated SEQ ID:18882, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30020] Another function of GAM189 is therefore inhibition of LOC284628 (Accession XP_211561.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284628.

[30021] LOC284675 (Accession XP_209319.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284675 BINDING SITE1 and LOC284675 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284675, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284675 BINDING SITE1 and LOC284675 BINDING SITE2, designated SEQ ID:2389 and SEQ ID:501 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30022] Another function of GAM189 is therefore inhibition of LOC284675 (Accession XP_209319.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284675.

[30023] LOC284683 (Accession XP_208236.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284683 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284683, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284683 BINDING SITE, designated SEQ ID:5926, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30024] Another function of GAM189 is therefore inhibition of LOC284683 (Accession XP_208236.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284683.

[30025] LOC284701 (Accession XP_294994.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284701 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284701, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284701 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30026] Another function of GAM189 is therefore inhibition of LOC284701 (Accession XP_294994.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284701.

[30027] LOC284708 (Accession XP_209332.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284708 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284708 BINDING SITE, designated SEQ ID:5153, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30028] Another function of GAM189 is therefore inhibition of LOC284708 (Accession XP_209332.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284708.

[30029] LOC284723 (Accession XP_211602.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284723 BINDING SITE1 through LOC284723 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284723, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284723 BINDING SITE1 through LOC284723 BINDING SITE3, designated SEQ ID:6498, SEQ ID:3182 and SEQ ID:2215 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30030] Another function of GAM189 is therefore inhibition of LOC284723 (Accession XP_211602.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284723.

[30031] LOC284805 (Accession XP_209371.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284805 BINDING SITE1 through LOC284805 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284805, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284805 BINDING SITE1 through LOC284805 BINDING SITE3, designated SEQ ID:8046, SEQ ID:853 and SEQ ID:1544 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30032] Another function of GAM189 is therefore inhibition of LOC284805 (Accession XP_209371.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284805.

[30033] LOC284839 (Accession XP_211661.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284839 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284839, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284839 BINDING SITE, designated SEQ ID:19401, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30034] Another function of GAM189 is therefore inhibition of LOC284839 (Accession XP_211661.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284839.

[30035] LOC284853 (Accession XP_209383.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284853 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC284853, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284853 BINDING SITE, designated SEQ ID:3582, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30036] Another function of GAM189 is therefore inhibition of LOC284853 (Accession XP_209383.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284853.

[30037] LOC284856 (Accession XP_302835.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284856 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC284856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284856 BINDING SITE, designated SEQ ID:12736, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30038] Another function of GAM189 is therefore inhibition of LOC284856 (Accession XP_302835.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284856.

[30039] LOC284856 (Accession XP_211668.2) is another GAM189 target gene, herein designated TARGET GENE. LOC284856 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC284856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284856 BINDING SITE, designated SEQ ID:12736, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30040] Another function of GAM189 is therefore inhibition of LOC284856 (Accession XP_211668.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284856.

[30041] LOC284859 (Accession XP_209384.2) is another GAM189 target gene, herein designated TARGET GENE. LOC284859

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284859, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284859 BINDING SITE, designated SEQ ID:16785, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30042] Another function of GAM189 is therefore inhibition of LOC284859 (Accession XP_209384.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284859.

[30043] LOC284861 (Accession XP_211670.2) is another GAM189 target gene, herein designated TARGET GENE. LOC284861 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284861, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284861 BINDING SITE, designated SEQ ID:16785, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30044] Another function of GAM189 is therefore inhibition of LOC284861 (Accession XP_211670.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284861.

[30045] LOC284865 (Accession XP_211672.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284865 BINDING SITE, designated SEQ ID:1645, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30046] Another function of GAM189 is therefore inhibition of LOC284865 (Accession XP_211672.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284865.

[30047] LOC284873 (Accession XP_209412.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284873 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC284873, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284873 BINDING SITE, designated SEQ ID:16785, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30048] Another function of GAM189 is therefore inhibition of LOC284873 (Accession XP_209412.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284873.

[30049] LOC284874 (Accession XP_209394.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284874 BINDING SITE1 and LOC284874 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284874, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284874 BINDING SITE1 and LOC284874 BINDING SITE2, designated SEQ ID:3846 and SEQ ID:16244 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA,

also designated SEQ ID:246.

[30050] Another function of GAM189 is therefore inhibition of LOC284874 (Accession XP_209394.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284874.

[30051] LOC284934 (Accession XP_211696.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284934 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284934, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284934 BINDING SITE, designated SEQ ID:14894, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30052] Another function of GAM189 is therefore inhibition of LOC284934 (Accession XP_211696.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284934.

[30053] LOC284947 (Accession XP_211705.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284947

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284947, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284947 BINDING SITE, designated SEQ ID:5465, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30054] Another function of GAM189 is therefore inhibition of LOC284947 (Accession XP_211705.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284947.

[30055] LOC284950 (Accession XP_211703.1) is another GAM189 target gene, herein designated TARGET GENE. LOC284950 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284950, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284950 BINDING SITE, designated SEQ ID:4025, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30056] Another function of GAM189 is therefore inhibition of LOC284950 (Accession XP_211703.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284950.

[30057] LOC285002 (Accession XP_211731.2) is another GAM189 target gene, herein designated TARGET GENE. LOC285002 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285002, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285002 BINDING SITE, designated SEQ ID:3500, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30058] Another function of GAM189 is therefore inhibition of LOC285002 (Accession XP_211731.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285002.

[30059] LOC285026 (Accession XP_209440.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285026 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC285026, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285026 BINDING SITE, designated SEQ ID:17523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30060] Another function of GAM189 is therefore inhibition of LOC285026 (Accession XP_209440.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285026.

[30061] LOC285052 (Accession XP_211751.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285052 BINDING SITE, designated SEQ ID:2174, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30062] Another function of GAM189 is therefore inhibition of

LOC285052 (Accession XP_211751.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285052.

[30063] LOC285058 (Accession XP_211753.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285058 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285058 BINDING SITE, designated SEQ ID:20023, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30064] Another function of GAM189 is therefore inhibition of LOC285058 (Accession XP_211753.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285058.

[30065] LOC285083 (Accession XP_209464.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285083 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285083, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285083 BINDING SITE, designated SEQ ID:5667, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30066] Another function of GAM189 is therefore inhibition of LOC285083 (Accession XP_209464.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285083.

[30067] LOC285088 (Accession XP_209465.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285088 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285088, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285088 BINDING SITE, designated SEQ ID:6092, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30068] Another function of GAM189 is therefore inhibition of LOC285088 (Accession XP_209465.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285088.

[30069] LOC285123 (Accession XP_211773.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285123 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285123 BINDING SITE, designated SEQ ID:17113, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30070] Another function of GAM189 is therefore inhibition of LOC285123 (Accession XP_211773.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285123.

[30071] LOC285127 (Accession XP_211771.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285127 BINDING SITE1 and LOC285127 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285127, corresponding to target binding

sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285127 BINDING SITE1 and LOC285127 BINDING SITE2, designated SEQ ID:11528 and SEQ ID:5921 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30072] Another function of GAM189 is therefore inhibition of LOC285127 (Accession XP_211771.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285127.

[30073] LOC285166 (Accession XP_211791.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285166 BINDING SITE, designated SEQ ID:4283, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30074] Another function of GAM189 is therefore inhibition of

LOC285166 (Accession XP_211791.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285166.

[30075] LOC285176 (Accession XP_209500.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285176 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285176, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285176 BINDING SITE, designated SEQ ID:7860, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30076] Another function of GAM189 is therefore inhibition of LOC285176 (Accession XP_209500.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285176.

[30077] LOC285193 (Accession XP_209509.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285193, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285193 BINDING SITE, designated SEQ ID:1745, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30078] Another function of GAM189 is therefore inhibition of LOC285193 (Accession XP_209509.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285193.

[30079] LOC285221 (Accession XP_209521.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285221 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285221, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285221 BINDING SITE, designated SEQ ID:13597, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30080] Another function of GAM189 is therefore inhibition of LOC285221 (Accession XP_209521.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285221.

[30081] LOC285231 (Accession XP_211813.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285231 BINDING SITE1 through LOC285231 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC285231, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285231 BINDING SITE1 through LOC285231 BINDING SITE3, designated SEQ ID:8001, SEQ ID:8001 and SEQ ID:15366 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30082] Another function of GAM189 is therefore inhibition of LOC285231 (Accession XP_211813.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285231.

[30083] LOC285231 (Accession XP_211813.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285231 BINDING SITE1 through LOC285231 BINDING SITE3 are

target binding sites found in untranslated regions of mRNA encoded by LOC285231, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285231 BINDING SITE1 through LOC285231 BINDING SITE3, designated SEQ ID:9352, SEQ ID:15575 and SEQ ID:9374 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30084] Another function of GAM189 is therefore inhibition of LOC285231 (Accession XP_211813.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285231.

[30085] LOC285334 (Accession XP_211844.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285334 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285334 BINDING SITE, designated SEQ ID:1027, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[30086] Another function of GAM189 is therefore inhibition of LOC285334 (Accession XP_211844.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285334.

[30087] LOC285345 (Accession XP_211854.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285345 BINDING SITE1 and LOC285345 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285345, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285345 BINDING SITE1 and LOC285345 BINDING SITE2, designated SEQ ID:556 and SEQ ID:18883 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30088] Another function of GAM189 is therefore inhibition of LOC285345 (Accession XP_211854.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285345.

[30089] LOC285366 (Accession XP_209581.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285366 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285366, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285366 BINDING SITE, designated SEQ ID:6117, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30090] Another function of GAM189 is therefore inhibition of LOC285366 (Accession XP_209581.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285366.

[30091] LOC285369 (Accession XP_211861.3) is another GAM189 target gene, herein designated TARGET GENE. LOC285369 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285369, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285369 BINDING SITE, designated SEQ ID:10352, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30092] Another function of GAM189 is therefore inhibition of LOC285369 (Accession XP_211861.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285369.

[30093] LOC285389 (Accession XP_211873.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285389 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285389, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285389 BINDING SITE, designated SEQ ID:19692, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30094] Another function of GAM189 is therefore inhibition of LOC285389 (Accession XP_211873.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285389.

[30095] LOC285392 (Accession XP_211879.1) is another GAM189

target gene, herein designated TARGET GENE. LOC285392 BINDING SITE1 and LOC285392 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285392, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285392 BINDING SITE1 and LOC285392 BINDING SITE2, designated SEQ ID:9688 and SEQ ID:17969 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30096] Another function of GAM189 is therefore inhibition of LOC285392 (Accession XP_211879.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285392.

[30097] LOC285398 (Accession XP_209593.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285398 BINDING SITE1 and LOC285398 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285398, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC285398 BINDING SITE1 and LOC285398 BINDING SITE2, designated SEQ ID:4655 and SEQ ID:13286 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30098] Another function of GAM189 is therefore inhibition of LOC285398 (Accession XP_209593.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285398.

[30099] LOC285429 (Accession XP_209607.3) is another GAM189 target gene, herein designated TARGET GENE. LOC285429 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285429, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285429 BINDING SITE, designated SEQ ID:4171, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30100] Another function of GAM189 is therefore inhibition of LOC285429 (Accession XP_209607.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285429.

[30101] LOC285488 (Accession XP_211914.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285488 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285488, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285488 BINDING SITE, designated SEQ ID:13804, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30102] Another function of GAM189 is therefore inhibition of LOC285488 (Accession XP_211914.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285488.

[30103] LOC285491 (Accession XP_211917.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285491 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285491, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC285491 BINDING SITE, designated SEQ ID:11239, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30104] Another function of GAM189 is therefore inhibition of LOC285491 (Accession XP_211917.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285491.

[30105] LOC285509 (Accession XP_211923.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285509 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285509, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285509 BINDING SITE, designated SEQ ID:3519, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30106] Another function of GAM189 is therefore inhibition of LOC285509 (Accession XP_211923.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285509.

[30107] LOC285510 (Accession XP_209643.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285510 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285510, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285510 BINDING SITE, designated SEQ ID:14552, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30108] Another function of GAM189 is therefore inhibition of LOC285510 (Accession XP_209643.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285510.

[30109] LOC285540 (Accession XP_209654.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285540 BINDING SITE1 and LOC285540 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285540, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC285540 BINDING SITE1 and LOC285540 BINDING SITE2, designated SEQ ID:6961 and SEQ ID:9543 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30110] Another function of GAM189 is therefore inhibition of LOC285540 (Accession XP_209654.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285540.

[30111] LOC285560 (Accession XP_209660.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285560 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285560, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285560 BINDING SITE, designated SEQ ID:8718, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30112] Another function of GAM189 is therefore inhibition of LOC285560 (Accession XP_209660.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285560.

[30113] LOC285589 (Accession XP_209671.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285589 BINDING SITE1 and LOC285589 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285589, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285589 BINDING SITE1 and LOC285589 BINDING SITE2, designated SEQ ID:17087 and SEQ ID:12804 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30114] Another function of GAM189 is therefore inhibition of LOC285589 (Accession XP_209671.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285589.

[30115] LOC285626 (Accession XP_211959.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285626 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285626, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285626 BINDING SITE, designated SEQ ID:13843, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30116] Another function of GAM189 is therefore inhibition of LOC285626 (Accession XP_211959.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285626.

[30117] LOC285638 (Accession XP_209693.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285638 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285638, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285638 BINDING SITE, designated SEQ ID:4949, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30118] Another function of GAM189 is therefore inhibition of LOC285638 (Accession XP_209693.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285638.

[30119] LOC285679 (Accession XP_209719.2) is another GAM189 target gene, herein designated TARGET GENE. LOC285679 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285679, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285679 BINDING SITE, designated SEQ ID:19299, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30120] Another function of GAM189 is therefore inhibition of LOC285679 (Accession XP_209719.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285679.

[30121] LOC285689 (Accession XP_209724.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285689 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285689, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285689 BINDING SITE, designated SEQ ID:17726, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30122] Another function of GAM189 is therefore inhibition of LOC285689 (Accession XP_209724.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285689.

[30123] LOC285693 (Accession XP_211981.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285693 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285693, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285693 BINDING SITE, designated SEQ ID:16940, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30124] Another function of GAM189 is therefore inhibition of LOC285693 (Accession XP_211981.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285693.

[30125] LOC285722 (Accession XP_211997.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285722 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285722, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285722 BINDING SITE, designated SEQ ID:18012, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30126] Another function of GAM189 is therefore inhibition of LOC285722 (Accession XP_211997.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285722.

[30127] LOC285744 (Accession XP_209743.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285744 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285744, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC285744 BINDING SITE, designated SEQ ID:11141, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30128] Another function of GAM189 is therefore inhibition of LOC285744 (Accession XP_209743.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285744.

[30129] LOC285747 (Accession XP_209742.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285747 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285747, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285747 BINDING SITE, designated SEQ ID:11528, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30130] Another function of GAM189 is therefore inhibition of LOC285747 (Accession XP_209742.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285747.

[30131] LOC285760 (Accession XP_209750.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285760 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285760, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285760 BINDING SITE, designated SEQ ID:13412, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30132] Another function of GAM189 is therefore inhibition of LOC285760 (Accession XP_209750.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285760.

[30133] LOC285777 (Accession XP_212013.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285777 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285777, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC285777 BINDING SITE, designated SEQ ID:16810, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30134] Another function of GAM189 is therefore inhibition of LOC285777 (Accession XP_212013.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285777.

[30135] LOC285812 (Accession XP_212055.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285812 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285812 BINDING SITE, designated SEQ ID:559, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30136] Another function of GAM189 is therefore inhibition of LOC285812 (Accession XP_212055.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285812.

[30137] LOC285813 (Accession XP_212036.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285813 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285813 BINDING SITE, designated SEQ ID:12389, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30138] Another function of GAM189 is therefore inhibition of LOC285813 (Accession XP_212036.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285813.

[30139] LOC285822 (Accession XP_209777.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285822 BINDING SITE1 and LOC285822 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285822, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285822 BINDING SITE1

and LOC285822 BINDING SITE2, designated SEQ ID:1847 and SEQ ID:9753 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30140] Another function of GAM189 is therefore inhibition of LOC285822 (Accession XP_209777.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285822.

[30141] LOC285830 (Accession XP_212043.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285830 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285830, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285830 BINDING SITE, designated SEQ ID:986, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30142] Another function of GAM189 is therefore inhibition of LOC285830 (Accession XP_212043.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285830.

[30143] LOC285843 (Accession XP_212034.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285843 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285843, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285843 BINDING SITE, designated SEQ ID:17964, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30144] Another function of GAM189 is therefore inhibition of LOC285843 (Accession XP_212034.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285843.

[30145] LOC285847 (Accession XP_212045.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285847 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285847, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC285847 BINDING SITE, designated SEQ ID:18945, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30146] Another function of GAM189 is therefore inhibition of LOC285847 (Accession XP_212045.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285847.

[30147] LOC285872 (Accession XP_212061.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285872 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285872, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285872 BINDING SITE, designated SEQ ID:10885, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30148] Another function of GAM189 is therefore inhibition of LOC285872 (Accession XP_212061.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285872.

[30149] LOC285914 (Accession XP_209810.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285914 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285914, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285914 BINDING SITE, designated SEQ ID:6188, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30150] Another function of GAM189 is therefore inhibition of LOC285914 (Accession XP_209810.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285914.

[30151] LOC285923 (Accession XP_212104.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285923 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285923, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285923 BINDING SITE, designated SEQ ID:19536, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30152] Another function of GAM189 is therefore inhibition of LOC285923 (Accession XP_212104.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285923.

[30153] LOC285924 (Accession XP_209816.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285924 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285924, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285924 BINDING SITE, designated SEQ ID:17126, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30154] Another function of GAM189 is therefore inhibition of LOC285924 (Accession XP_209816.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285924.

[30155] LOC285945 (Accession XP_212092.1) is another GAM189

target gene, herein designated TARGET GENE. LOC285945 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285945, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285945 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30156] Another function of GAM189 is therefore inhibition of LOC285945 (Accession XP_212092.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285945.

[30157] LOC285952 (Accession XP_209821.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285952 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285952, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285952 BINDING SITE, designated SEQ ID:15323, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[30158] Another function of GAM189 is therefore inhibition of LOC285952 (Accession XP_209821.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285952.

[30159] LOC285961 (Accession XP_209833.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285961 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285961, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285961 BINDING SITE, designated SEQ ID:2604, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30160] Another function of GAM189 is therefore inhibition of LOC285961 (Accession XP_209833.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285961.

[30161] LOC285972 (Accession XP_212105.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285972

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285972 BINDING SITE, designated SEQ ID:5318, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30162] Another function of GAM189 is therefore inhibition of LOC285972 (Accession XP_212105.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285972.

[30163] LOC285979 (Accession XP_212117.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285979 BINDING SITE1 and LOC285979 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285979, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285979 BINDING SITE1 and LOC285979 BINDING SITE2, designated SEQ ID:1397 and SEQ ID:6388 respectively, to the nucleotide sequence

of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30164] Another function of GAM189 is therefore inhibition of LOC285979 (Accession XP_212117.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285979.

[30165] LOC285989 (Accession XP_212111.1) is another GAM189 target gene, herein designated TARGET GENE. LOC285989 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285989, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285989 BINDING SITE, designated SEQ ID:11742, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30166] Another function of GAM189 is therefore inhibition of LOC285989 (Accession XP_212111.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285989.

[30167] LOC285999 (Accession XP_212120.1) is another GAM189

target gene, herein designated TARGET GENE. LOC285999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285999 BINDING SITE, designated SEQ ID:3647, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30168] Another function of GAM189 is therefore inhibition of LOC285999 (Accession XP_212120.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285999.

[30169] LOC286029 (Accession XP_209866.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286029 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286029, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286029 BINDING SITE, designated SEQ ID:15231, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[30170] Another function of GAM189 is therefore inhibition of LOC286029 (Accession XP_209866.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286029.

[30171] LOC286030 (Accession XP_209868.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286030 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286030, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286030 BINDING SITE, designated SEQ ID:2244, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30172] Another function of GAM189 is therefore inhibition of LOC286030 (Accession XP_209868.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286030.

[30173] LOC286039 (Accession XP_209873.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286039

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286039, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286039 BINDING SITE, designated SEQ ID:11035, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30174] Another function of GAM189 is therefore inhibition of LOC286039 (Accession XP_209873.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286039.

[30175] LOC286052 (Accession XP_212152.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286052 BINDING SITE, designated SEQ ID:9367, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30176] Another function of GAM189 is therefore inhibition of LOC286052 (Accession XP_212152.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286052.

[30177] LOC286075 (Accession NP_776192.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286075 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286075, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286075 BINDING SITE, designated SEQ ID:17965, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30178] Another function of GAM189 is therefore inhibition of LOC286075 (Accession NP_776192.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286075.

[30179] LOC286078 (Accession XP_212163.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286078 BINDING SITE1 through LOC286078 BINDING SITE5 are

target binding sites found in untranslated regions of mRNA encoded by LOC286078, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286078 BINDING SITE1 through LOC286078 BINDING SITE5, designated SEQ ID:15589, SEQ ID:16716, SEQ ID:15083, SEQ ID:3810 and SEQ ID:13100 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30180] Another function of GAM189 is therefore inhibition of LOC286078 (Accession XP_212163.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286078.

[30181] LOC286090 (Accession XP_212166.3) is another GAM189 target gene, herein designated TARGET GENE. LOC286090 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286090, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286090 BINDING SITE, designated SEQ ID:16409, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30182] Another function of GAM189 is therefore inhibition of LOC286090 (Accession XP_212166.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286090.

[30183] LOC286126 (Accession XP_212185.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286126 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286126, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286126 BINDING SITE, designated SEQ ID:7847, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30184] Another function of GAM189 is therefore inhibition of LOC286126 (Accession XP_212185.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286126.

[30185] LOC286132 (Accession XP_212194.1) is another GAM189

target gene, herein designated TARGET GENE. LOC286132 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286132 BINDING SITE, designated SEQ ID:7113, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30186] Another function of GAM189 is therefore inhibition of LOC286132 (Accession XP_212194.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286132.

[30187] LOC286135 (Accession XP_212196.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286135 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286135 BINDING SITE, designated SEQ ID:9746, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[30188] Another function of GAM189 is therefore inhibition of LOC286135 (Accession XP_212196.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286135.

[30189] LOC286166 (Accession XP_209925.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286166 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286166 BINDING SITE, designated SEQ ID:3927, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30190] Another function of GAM189 is therefore inhibition of LOC286166 (Accession XP_209925.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286166.

[30191] LOC286170 (Accession XP_212211.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286170

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286170 BINDING SITE, designated SEQ ID:8426, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30192] Another function of GAM189 is therefore inhibition of LOC286170 (Accession XP_212211.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286170.

[30193] LOC286186 (Accession XP_212219.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286186 BINDING SITE1 and LOC286186 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC286186, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286186 BINDING SITE1 and LOC286186 BINDING SITE2, designated SEQ ID:18020 and SEQ ID:3430 respectively, to the nucleotide sequence

of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30194] Another function of GAM189 is therefore inhibition of LOC286186 (Accession XP_212219.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286186.

[30195] LOC286206 (Accession XP_209953.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286206 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286206, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286206 BINDING SITE, designated SEQ ID:2600, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30196] Another function of GAM189 is therefore inhibition of LOC286206 (Accession XP_209953.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286206.

[30197] LOC286207 (Accession XP_209941.1) is another GAM189

target gene, herein designated TARGET GENE. LOC286207 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286207, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286207 BINDING SITE, designated SEQ ID:19893, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30198] Another function of GAM189 is therefore inhibition of LOC286207 (Accession XP_209941.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286207.

[30199] LOC286208 (Accession XP_212230.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286208 BINDING SITE1 through LOC286208 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC286208, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286208 BINDING SITE1 through LOC286208 BINDING SITE3, des-

ignated SEQ ID:2849, SEQ ID:4372 and SEQ ID:9724 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30200] Another function of GAM189 is therefore inhibition of LOC286208 (Accession XP_212230.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286208.

[30201] LOC286215 (Accession XP_212228.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286215 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286215, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286215 BINDING SITE, designated SEQ ID:19240, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30202] Another function of GAM189 is therefore inhibition of LOC286215 (Accession XP_212228.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286215.

[30203] LOC286221 (Accession XP_212233.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286221 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286221, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286221 BINDING SITE, designated SEQ ID:7774, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30204] Another function of GAM189 is therefore inhibition of LOC286221 (Accession XP_212233.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286221.

[30205] LOC286223 (Accession XP_209956.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286223 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286223, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286223 BINDING SITE, designated SEQ ID:6118, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30206] Another function of GAM189 is therefore inhibition of LOC286223 (Accession XP_209956.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286223.

[30207] LOC286245 (Accession XP_212244.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286245 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286245, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286245 BINDING SITE, designated SEQ ID:6868, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30208] Another function of GAM189 is therefore inhibition of LOC286245 (Accession XP_212244.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286245.

[30209] LOC286341 (Accession XP_212278.1) is another GAM189

target gene, herein designated TARGET GENE. LOC286341 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286341, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286341 BINDING SITE, designated SEQ ID:15975, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30210] Another function of GAM189 is therefore inhibition of LOC286341 (Accession XP_212278.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286341.

[30211] LOC286347 (Accession XP_208408.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286347 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286347, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286347 BINDING SITE, designated SEQ ID:522, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[30212] Another function of GAM189 is therefore inhibition of LOC286347 (Accession XP_208408.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286347.

[30213] LOC286354 (Accession XP_212286.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286354 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286354, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286354 BINDING SITE, designated SEQ ID:15730, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30214] Another function of GAM189 is therefore inhibition of LOC286354 (Accession XP_212286.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286354.

[30215] LOC286356 (Accession XP_212290.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286356

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286356 BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30216] Another function of GAM189 is therefore inhibition of LOC286356 (Accession XP_212290.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286356.

[30217] LOC286357 (Accession XP_212285.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286357 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286357, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286357 BINDING SITE, designated SEQ ID:14974, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30218] Another function of GAM189 is therefore inhibition of LOC286357 (Accession XP_212285.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286357.

[30219] LOC286371 (Accession XP_212291.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286371 BINDING SITE, designated SEQ ID:3785, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30220] Another function of GAM189 is therefore inhibition of LOC286371 (Accession XP_212291.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286371.

[30221] LOC286395 (Accession XP_212308.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286395 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC286395, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286395 BINDING SITE, designated SEQ ID:2722, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30222] Another function of GAM189 is therefore inhibition of LOC286395 (Accession XP_212308.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286395.

[30223] LOC286401 (Accession XP_212310.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286401 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286401, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286401 BINDING SITE, designated SEQ ID:1038, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30224] Another function of GAM189 is therefore inhibition of

LOC286401 (Accession XP_212310.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286401.

[30225] LOC286441 (Accession XP_212319.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286441 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286441, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286441 BINDING SITE, designated SEQ ID:2754, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30226] Another function of GAM189 is therefore inhibition of LOC286441 (Accession XP_212319.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286441.

[30227] LOC286467 (Accession XP_210063.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286467, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286467 BINDING SITE, designated SEQ ID:9580, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30228] Another function of GAM189 is therefore inhibition of LOC286467 (Accession XP_210063.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286467.

[30229] LOC286553 (Accession XP_212340.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286553 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286553, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286553 BINDING SITE, designated SEQ ID:3183, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30230] Another function of GAM189 is therefore inhibition of LOC286553 (Accession XP_212340.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286553.

[30231] LOC286558 (Accession XP_210106.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286558 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286558, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286558 BINDING SITE, designated SEQ ID:9264, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30232] Another function of GAM189 is therefore inhibition of LOC286558 (Accession XP_210106.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286558.

[30233] LOC286564 (Accession XP_210108.1) is another GAM189 target gene, herein designated TARGET GENE. LOC286564 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286564, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286564 BINDING SITE, designated SEQ ID:9264, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30234] Another function of GAM189 is therefore inhibition of LOC286564 (Accession XP_210108.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286564.

[30235] LOC338562 (Accession XP_294654.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338562 BINDING SITE, designated SEQ ID:13760, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30236] Another function of GAM189 is therefore inhibition of LOC338562 (Accession XP_294654.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC338562.

[30237] LOC338565 (Accession XP_294653.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338565 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338565, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338565 BINDING SITE, designated SEQ ID:12867, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30238] Another function of GAM189 is therefore inhibition of LOC338565 (Accession XP_294653.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338565.

[30239] LOC338575 (Accession XP_290473.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338575 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338575, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC338575 BINDING SITE, designated SEQ ID:14074, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30240] Another function of GAM189 is therefore inhibition of LOC338575 (Accession XP_290473.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338575.

[30241] LOC338579 (Accession XP_290472.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338579 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338579, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338579 BINDING SITE, designated SEQ ID:4528, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30242] Another function of GAM189 is therefore inhibition of LOC338579 (Accession XP_290472.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC338579.

[30243] LOC338585 (Accession XP_294658.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338585 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338585, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338585 BINDING SITE, designated SEQ ID:7523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30244] Another function of GAM189 is therefore inhibition of LOC338585 (Accession XP_294658.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338585.

[30245] LOC338645 (Accession XP_290494.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338645 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338645, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC338645 BINDING SITE, designated SEQ ID:6626, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30246] Another function of GAM189 is therefore inhibition of LOC338645 (Accession XP_290494.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338645.

[30247] LOC338709 (Accession XP_211595.2) is another GAM189 target gene, herein designated TARGET GENE. LOC338709 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338709, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338709 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30248] Another function of GAM189 is therefore inhibition of LOC338709 (Accession XP_211595.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338709.

[30249] LOC338731 (Accession XP_294688.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338731 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338731, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338731 BINDING SITE, designated SEQ ID:6518, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30250] Another function of GAM189 is therefore inhibition of LOC338731 (Accession XP_294688.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338731.

[30251] LOC338739 (Accession XP_294690.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338739 BINDING SITE1 and LOC338739 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC338739, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338739 BINDING SITE1

and LOC338739 BINDING SITE2, designated SEQ ID:15044 and SEQ ID:14732 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30252] Another function of GAM189 is therefore inhibition of LOC338739 (Accession XP_294690.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338739.

[30253] LOC338773 (Accession XP_290570.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338773 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338773, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338773 BINDING SITE, designated SEQ ID:16493, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30254] Another function of GAM189 is therefore inhibition of LOC338773 (Accession XP_290570.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC338773.

[30255] LOC338819 (Accession XP_290216.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338819 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338819, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338819 BINDING SITE, designated SEQ ID:11507, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30256] Another function of GAM189 is therefore inhibition of LOC338819 (Accession XP_290216.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338819.

[30257] LOC338899 (Accession XP_294740.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338899 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC338899 BINDING SITE, designated SEQ ID:12341, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30258] Another function of GAM189 is therefore inhibition of LOC338899 (Accession XP_294740.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338899.

[30259] LOC338923 (Accession XP_294742.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338923 BINDING SITE1 and LOC338923 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC338923, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338923 BINDING SITE1 and LOC338923 BINDING SITE2, designated SEQ ID:8559 and SEQ ID:4298 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30260] Another function of GAM189 is therefore inhibition of LOC338923 (Accession XP_294742.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC338923.

[30261] LOC338963 (Accession XP_294757.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338963 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338963, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338963 BINDING SITE, designated SEQ ID:3348, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30262] Another function of GAM189 is therefore inhibition of LOC338963 (Accession XP_294757.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338963.

[30263] LOC338991 (Accession XP_290663.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338991 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338991, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC338991 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30264] Another function of GAM189 is therefore inhibition of LOC338991 (Accession XP_290663.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338991.

[30265] LOC338999 (Accession XP_290659.1) is another GAM189 target gene, herein designated TARGET GENE. LOC338999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338999 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30266] Another function of GAM189 is therefore inhibition of LOC338999 (Accession XP_290659.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC338999.

[30267] LOC339077 (Accession XP_294802.2) is another GAM189 target gene, herein designated TARGET GENE. LOC339077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339077 BINDING SITE, designated SEQ ID:17484, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30268] Another function of GAM189 is therefore inhibition of LOC339077 (Accession XP_294802.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339077.

[30269] LOC339078 (Accession XP_290692.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339078 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC339078 BINDING SITE, designated SEQ ID:9543, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30270] Another function of GAM189 is therefore inhibition of LOC339078 (Accession XP_290692.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339078.

[30271] LOC339083 (Accession XP_290697.2) is another GAM189 target gene, herein designated TARGET GENE. LOC339083 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339083, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339083 BINDING SITE, designated SEQ ID:1843, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30272] Another function of GAM189 is therefore inhibition of LOC339083 (Accession XP_290697.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339083.

[30273] LOC339108 (Accession XP_290711.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339108 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339108, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339108 BINDING SITE, designated SEQ ID:14266, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30274] Another function of GAM189 is therefore inhibition of LOC339108 (Accession XP_290711.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339108.

[30275] LOC339146 (Accession XP_294825.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339146 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339146 BINDING SITE, designated SEQ ID:15614, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30276] Another function of GAM189 is therefore inhibition of LOC339146 (Accession XP_294825.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339146.

[30277] LOC339178 (Accession XP_290742.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339178 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339178, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339178 BINDING SITE, designated SEQ ID:16261, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30278] Another function of GAM189 is therefore inhibition of LOC339178 (Accession XP_290742.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339178.

[30279] LOC339201 (Accession XP_290756.1) is another GAM189

target gene, herein designated TARGET GENE. LOC339201 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339201 BINDING SITE, designated SEQ ID:4056, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30280] Another function of GAM189 is therefore inhibition of LOC339201 (Accession XP_290756.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339201.

[30281] LOC339216 (Accession XP_290762.2) is another GAM189 target gene, herein designated TARGET GENE. LOC339216 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339216, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339216 BINDING SITE, designated SEQ ID:19537, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[30282] Another function of GAM189 is therefore inhibition of LOC339216 (Accession XP_290762.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339216.

[30283] LOC339248 (Accession XP_294879.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339248 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339248 BINDING SITE, designated SEQ ID:19597, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30284] Another function of GAM189 is therefore inhibition of LOC339248 (Accession XP_294879.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339248.

[30285] LOC339250 (Accession XP_294883.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339250

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339250, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339250 BINDING SITE, designated SEQ ID:19597, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30286] Another function of GAM189 is therefore inhibition of LOC339250 (Accession XP_294883.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339250.

[30287] LOC339282 (Accession XP_294900.2) is another GAM189 target gene, herein designated TARGET GENE. LOC339282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339282 BINDING SITE, designated SEQ ID:19537, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30288] Another function of GAM189 is therefore inhibition of LOC339282 (Accession XP_294900.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339282.

[30289] LOC339283 (Accession XP_294899.2) is another GAM189 target gene, herein designated TARGET GENE. LOC339283 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339283, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339283 BINDING SITE, designated SEQ ID:11314, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30290] Another function of GAM189 is therefore inhibition of LOC339283 (Accession XP_294899.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339283.

[30291] LOC339324 (Accession XP_290838.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339324 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC339324, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339324 BINDING SITE, designated SEQ ID:9544, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30292] Another function of GAM189 is therefore inhibition of LOC339324 (Accession XP_290838.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339324.

[30293] LOC339325 (Accession XP_290830.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339325 BINDING SITE1 and LOC339325 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339325, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339325 BINDING SITE1 and LOC339325 BINDING SITE2, designated SEQ ID:17114 and SEQ ID:16940 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA,

also designated SEQ ID:246.

[30294] Another function of GAM189 is therefore inhibition of LOC339325 (Accession XP_290830.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339325.

[30295] LOC339417 (Accession XP_294944.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339417 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339417, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339417 BINDING SITE, designated SEQ ID:2027, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30296] Another function of GAM189 is therefore inhibition of LOC339417 (Accession XP_294944.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339417.

[30297] LOC339448 (Accession XP_290902.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339448

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339448, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339448 BINDING SITE, designated SEQ ID:10679, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30298] Another function of GAM189 is therefore inhibition of LOC339448 (Accession XP_290902.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339448.

[30299] LOC339458 (Accession XP_290911.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339458 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339458, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339458 BINDING SITE, designated SEQ ID:5488, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30300] Another function of GAM189 is therefore inhibition of LOC339458 (Accession XP_290911.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339458.

[30301] LOC339459 (Accession XP_290907.2) is another GAM189 target gene, herein designated TARGET GENE. LOC339459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339459 BINDING SITE, designated SEQ ID:13513, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30302] Another function of GAM189 is therefore inhibition of LOC339459 (Accession XP_290907.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339459.

[30303] LOC339492 (Accession XP_290919.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339492 BINDING SITE1 through LOC339492 BINDING SITE3 are

target binding sites found in untranslated regions of mRNA encoded by LOC339492, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339492 BINDING SITE1 through LOC339492 BINDING SITE3, designated SEQ ID:7386, SEQ ID:8590 and SEQ ID:695 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30304] Another function of GAM189 is therefore inhibition of LOC339492 (Accession XP_290919.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339492.

[30305] LOC339577 (Accession XP_295005.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339577 BINDING SITE1 and LOC339577 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339577, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339577 BINDING SITE1 and LOC339577 BINDING SITE2, designated SEQ ID:14733

and SEQ ID:12075 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30306] Another function of GAM189 is therefore inhibition of LOC339577 (Accession XP_295005.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339577.

[30307] LOC339600 (Accession XP_295014.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339600 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339600, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339600 BINDING SITE, designated SEQ ID:15295, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30308] Another function of GAM189 is therefore inhibition of LOC339600 (Accession XP_295014.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339600.

[30309] LOC339659 (Accession XP_290981.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339659 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339659, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339659 BINDING SITE, designated SEQ ID:17076, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30310] Another function of GAM189 is therefore inhibition of LOC339659 (Accession XP_290981.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339659.

[30311] LOC339685 (Accession XP_295032.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339685 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339685, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339685 BINDING SITE, designated SEQ ID:1982, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30312] Another function of GAM189 is therefore inhibition of LOC339685 (Accession XP_295032.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339685.

[30313] LOC339694 (Accession XP_295035.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339694 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339694, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339694 BINDING SITE, designated SEQ ID:15954, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30314] Another function of GAM189 is therefore inhibition of LOC339694 (Accession XP_295035.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339694.

[30315] LOC339711 (Accession XP_295038.1) is another GAM189

target gene, herein designated TARGET GENE. LOC339711 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339711, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339711 BINDING SITE, designated SEQ ID:11528, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30316] Another function of GAM189 is therefore inhibition of LOC339711 (Accession XP_295038.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339711.

[30317] LOC339720 (Accession XP_295041.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339720 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339720, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339720 BINDING SITE, designated SEQ ID:16942, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[30318] Another function of GAM189 is therefore inhibition of LOC339720 (Accession XP_295041.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339720.

[30319] LOC339803 (Accession XP_295072.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339803 BINDING SITE, designated SEQ ID:13337, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30320] Another function of GAM189 is therefore inhibition of LOC339803 (Accession XP_295072.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339803.

[30321] LOC339808 (Accession XP_295071.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339808

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339808, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339808 BINDING SITE, designated SEQ ID:6146, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30322] Another function of GAM189 is therefore inhibition of LOC339808 (Accession XP_295071.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339808.

[30323] LOC339809 (Accession XP_291020.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339809 BINDING SITE1 and LOC339809 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339809, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339809 BINDING SITE1 and LOC339809 BINDING SITE2, designated SEQ ID:1744 and SEQ ID:17750 respectively, to the nucleotide se-

quence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30324] Another function of GAM189 is therefore inhibition of LOC339809 (Accession XP_291020.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339809.

[30325] LOC339833 (Accession XP_291031.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339833 BINDING SITE1 and LOC339833 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339833, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339833 BINDING SITE1 and LOC339833 BINDING SITE2, designated SEQ ID:7633 and SEQ ID:10421 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30326] Another function of GAM189 is therefore inhibition of LOC339833 (Accession XP_291031.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC339833.

[30327] LOC339834 (Accession XP_291033.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339834 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC339834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339834 BINDING SITE, designated SEQ ID:14645, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30328] Another function of GAM189 is therefore inhibition of LOC339834 (Accession XP_291033.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339834.

[30329] LOC339834 (Accession NP_835467.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339834 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC339834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339834 BINDING SITE, designated SEQ ID:14645, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30330] Another function of GAM189 is therefore inhibition of LOC339834 (Accession NP_835467.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339834.

[30331] LOC339872 (Accession XP_291050.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339872 BINDING SITE1 through LOC339872 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC339872, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339872 BINDING SITE1 through LOC339872 BINDING SITE3, designated SEQ ID:5858, SEQ ID:9299 and SEQ ID:4026 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30332] Another function of GAM189 is therefore inhibition of

LOC339872 (Accession XP_291050.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339872.

[30333] LOC339894 (Accession XP_295095.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339894 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339894 BINDING SITE, designated SEQ ID:1081, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30334] Another function of GAM189 is therefore inhibition of LOC339894 (Accession XP_295095.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339894.

[30335] LOC339907 (Accession XP_291065.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339907 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339907, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339907 BINDING SITE, designated SEQ ID:3425, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30336] Another function of GAM189 is therefore inhibition of LOC339907 (Accession XP_291065.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339907.

[30337] LOC339909 (Accession XP_291069.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339909 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339909, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339909 BINDING SITE, designated SEQ ID:10709, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30338] Another function of GAM189 is therefore inhibition of LOC339909 (Accession XP_291069.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339909.

[30339] LOC339914 (Accession XP_295099.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339914 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339914, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339914 BINDING SITE, designated SEQ ID:714, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30340] Another function of GAM189 is therefore inhibition of LOC339914 (Accession XP_295099.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339914.

[30341] LOC339970 (Accession XP_291095.1) is another GAM189 target gene, herein designated TARGET GENE. LOC339970 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339970, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339970 BINDING SITE, designated SEQ ID:16942, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30342] Another function of GAM189 is therefore inhibition of LOC339970 (Accession XP_291095.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339970.

[30343] LOC340037 (Accession XP_295137.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340037 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340037, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340037 BINDING SITE, designated SEQ ID:12244, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30344] Another function of GAM189 is therefore inhibition of LOC340037 (Accession XP_295137.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC340037.

[30345] LOC340125 (Accession XP_291150.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340125 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340125, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340125 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30346] Another function of GAM189 is therefore inhibition of LOC340125 (Accession XP_291150.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340125.

[30347] LOC340138 (Accession XP_291153.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340138 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC340138 BINDING SITE, designated SEQ ID:11753, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30348] Another function of GAM189 is therefore inhibition of LOC340138 (Accession XP_291153.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340138.

[30349] LOC340156 (Accession XP_291158.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340156 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340156, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340156 BINDING SITE, designated SEQ ID:10096, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30350] Another function of GAM189 is therefore inhibition of LOC340156 (Accession XP_291158.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC340156.

[30351] LOC340227 (Accession XP_291203.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340227 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340227, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340227 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30352] Another function of GAM189 is therefore inhibition of LOC340227 (Accession XP_291203.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340227.

[30353] LOC340238 (Accession XP_295188.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340238 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340238, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC340238 BINDING SITE, designated SEQ ID:2179, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30354] Another function of GAM189 is therefore inhibition of LOC340238 (Accession XP_295188.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340238.

[30355] LOC340259 (Accession XP_295190.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340259 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340259, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340259 BINDING SITE, designated SEQ ID:18147, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30356] Another function of GAM189 is therefore inhibition of LOC340259 (Accession XP_295190.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340259.

[30357] LOC340290 (Accession XP_291214.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340290 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340290, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340290 BINDING SITE, designated SEQ ID:15740, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30358] Another function of GAM189 is therefore inhibition of LOC340290 (Accession XP_291214.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340290.

[30359] LOC340390 (Accession XP_291269.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340390 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340390, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340390 BINDING SITE, designated SEQ ID:18868, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30360] Another function of GAM189 is therefore inhibition of LOC340390 (Accession XP_291269.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340390.

[30361] LOC340408 (Accession XP_291274.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340408 BINDING SITE, designated SEQ ID:1309, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30362] Another function of GAM189 is therefore inhibition of LOC340408 (Accession XP_291274.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340408.

[30363] LOC340414 (Accession XP_295240.1) is another GAM189

target gene, herein designated TARGET GENE. LOC340414 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340414, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340414 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30364] Another function of GAM189 is therefore inhibition of LOC340414 (Accession XP_295240.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340414.

[30365] LOC340450 (Accession XP_295252.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340450 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340450, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340450 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[30366] Another function of GAM189 is therefore inhibition of LOC340450 (Accession XP_295252.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340450.

[30367] LOC340528 (Accession XP_295268.1) is another GAM189 target gene, herein designated TARGET GENE. LOC340528 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340528, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340528 BINDING SITE, designated SEQ ID:13053, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30368] Another function of GAM189 is therefore inhibition of LOC340528 (Accession XP_295268.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340528.

[30369] LOC342926 (Accession XP_292790.2) is another GAM189 target gene, herein designated TARGET GENE. LOC342926

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC342926, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC342926 BINDING SITE, designated SEQ ID:13464, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30370] Another function of GAM189 is therefore inhibition of LOC342926 (Accession XP_292790.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC342926.

[30371] LOC343435 (Accession XP_295563.1) is another GAM189 target gene, herein designated TARGET GENE. LOC343435 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC343435, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC343435 BINDING SITE, designated SEQ ID:439, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30372] Another function of GAM189 is therefore inhibition of LOC343435 (Accession XP_295563.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC343435.

[30373] LOC345275 (Accession NP_835236.1) is another GAM189 target gene, herein designated TARGET GENE. LOC345275 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC345275, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC345275 BINDING SITE, designated SEQ ID:523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30374] Another function of GAM189 is therefore inhibition of LOC345275 (Accession NP_835236.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC345275.

[30375] LOC345878 (Accession XP_293993.2) is another GAM189 target gene, herein designated TARGET GENE. LOC345878

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC345878, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC345878 BINDING SITE, designated SEQ ID:12611, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30376] Another function of GAM189 is therefore inhibition of LOC345878 (Accession XP_293993.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC345878.

[30377] LOC346653 (Accession XP_294357.2) is another GAM189 target gene, herein designated TARGET GENE. LOC346653 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC346653, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC346653 BINDING SITE, designated SEQ ID:17927, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30378] Another function of GAM189 is therefore inhibition of LOC346653 (Accession XP_294357.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC346653.

[30379] LOC347648 (Accession XP_300226.1) is another GAM189 target gene, herein designated TARGET GENE. LOC347648 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC347648, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347648 BINDING SITE, designated SEQ ID:9837, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30380] Another function of GAM189 is therefore inhibition of LOC347648 (Accession XP_300226.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347648.

[30381] LOC347764 (Accession XP_300530.1) is another GAM189 target gene, herein designated TARGET GENE. LOC347764 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC347764, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347764 BINDING SITE, designated SEQ ID:11420, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30382] Another function of GAM189 is therefore inhibition of LOC347764 (Accession XP_300530.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347764.

[30383] LOC347905 (Accession XP_302624.1) is another GAM189 target gene, herein designated TARGET GENE. LOC347905 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347905, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347905 BINDING SITE, designated SEQ ID:9505, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30384] Another function of GAM189 is therefore inhibition of

LOC347905 (Accession XP_302624.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347905.

[30385] LOC347918 (Accession XP_300565.1) is another GAM189 target gene, herein designated TARGET GENE. LOC347918 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347918, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347918 BINDING SITE, designated SEQ ID:17689, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30386] Another function of GAM189 is therefore inhibition of LOC347918 (Accession XP_300565.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347918.

[30387] LOC348075 (Accession XP_302653.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348075 BINDING SITE1 and LOC348075 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by LOC348075, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348075 BINDING SITE1 and LOC348075 BINDING SITE2, designated SEQ ID:13716 and SEQ ID:14381 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30388] Another function of GAM189 is therefore inhibition of LOC348075 (Accession XP_302653.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348075.

[30389] LOC348094 (Accession XP_300615.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348094 BINDING SITE1 and LOC348094 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348094, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348094 BINDING SITE1 and LOC348094 BINDING SITE2, designated SEQ ID:13332 and SEQ ID:16473 respectively, to the nucleotide se-

quence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30390] Another function of GAM189 is therefore inhibition of LOC348094 (Accession XP_300615.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348094.

[30391] LOC348113 (Accession XP_300623.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348113 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30392] Another function of GAM189 is therefore inhibition of LOC348113 (Accession XP_300623.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348113.

[30393] LOC348115 (Accession XP_300626.1) is another GAM189

target gene, herein designated TARGET GENE. LOC348115 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348115, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348115 BINDING SITE, designated SEQ ID:13705, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30394] Another function of GAM189 is therefore inhibition of LOC348115 (Accession XP_300626.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348115.

[30395] LOC348137 (Accession XP_300635.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348137 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[30396] Another function of GAM189 is therefore inhibition of LOC348137 (Accession XP_300635.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348137.

[30397] LOC348142 (Accession XP_300636.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348142 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348142 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30398] Another function of GAM189 is therefore inhibition of LOC348142 (Accession XP_300636.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348142.

[30399] LOC348235 (Accession XP_300670.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348235

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348235 BINDING SITE, designated SEQ ID:15852, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30400] Another function of GAM189 is therefore inhibition of LOC348235 (Accession XP_300670.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348235.

[30401] LOC348262 (Accession XP_300683.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348262 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348262 BINDING SITE, designated SEQ ID:7306, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30402] Another function of GAM189 is therefore inhibition of LOC348262 (Accession XP_300683.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348262.

[30403] LOC348314 (Accession XP_302716.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348314 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348314, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348314 BINDING SITE, designated SEQ ID:16669, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30404] Another function of GAM189 is therefore inhibition of LOC348314 (Accession XP_302716.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348314.

[30405] LOC348326 (Accession XP_300696.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348326 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC348326, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348326 BINDING SITE, designated SEQ ID:19778, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30406] Another function of GAM189 is therefore inhibition of LOC348326 (Accession XP_300696.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348326.

[30407] LOC348327 (Accession XP_030209.2) is another GAM189 target gene, herein designated TARGET GENE. LOC348327 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348327, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348327 BINDING SITE, designated SEQ ID:8820, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30408] Another function of GAM189 is therefore inhibition of

LOC348327 (Accession XP_030209.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348327.

[30409] LOC348393 (Accession XP_302741.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348393 BINDING SITE1 and LOC348393 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348393, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348393 BINDING SITE1 and LOC348393 BINDING SITE2, designated SEQ ID:872 and SEQ ID:11192 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30410] Another function of GAM189 is therefore inhibition of LOC348393 (Accession XP_302741.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348393.

[30411] LOC348396 (Accession XP_300729.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348396

BINDING SITE1 through LOC348396 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC348396, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348396 BINDING SITE1 through LOC348396 BINDING SITE3, designated SEQ ID:10270, SEQ ID:1569 and SEQ ID:9545 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30412] Another function of GAM189 is therefore inhibition of LOC348396 (Accession XP_300729.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348396.

[30413] LOC348402 (Accession XP_300730.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348402 BINDING SITE1 through LOC348402 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC348402, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348402

BINDING SITE1 through LOC348402 BINDING SITE3, designated SEQ ID:7386, SEQ ID:695 and SEQ ID:8590 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30414] Another function of GAM189 is therefore inhibition of LOC348402 (Accession XP_300730.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348402.

[30415] LOC348445 (Accession XP_300738.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348445 BINDING SITE, designated SEQ ID:19778, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30416] Another function of GAM189 is therefore inhibition of LOC348445 (Accession XP_300738.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC348445.

[30417] LOC348455 (Accession XP_302760.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348455 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348455, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348455 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30418] Another function of GAM189 is therefore inhibition of LOC348455 (Accession XP_302760.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348455.

[30419] LOC348460 (Accession XP_300743.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348460 BINDING SITE1 and LOC348460 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348460, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC348460 BINDING SITE1 and LOC348460 BINDING SITE2, designated SEQ ID:13465 and SEQ ID:4143 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30420] Another function of GAM189 is therefore inhibition of LOC348460 (Accession XP_300743.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348460.

[30421] LOC348474 (Accession XP_209299.2) is another GAM189 target gene, herein designated TARGET GENE. LOC348474 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348474, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348474 BINDING SITE, designated SEQ ID:17206, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30422] Another function of GAM189 is therefore inhibition of LOC348474 (Accession XP_209299.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348474.

[30423] LOC348494 (Accession XP_302789.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348494 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348494, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348494 BINDING SITE, designated SEQ ID:6119, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30424] Another function of GAM189 is therefore inhibition of LOC348494 (Accession XP_302789.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348494.

[30425] LOC348503 (Accession XP_300762.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348503 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348503, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC348503 BINDING SITE, designated SEQ ID:19361, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30426] Another function of GAM189 is therefore inhibition of LOC348503 (Accession XP_300762.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348503.

[30427] LOC348508 (Accession XP_302806.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348508 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348508, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348508 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30428] Another function of GAM189 is therefore inhibition of LOC348508 (Accession XP_302806.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC348508.

[30429] LOC348525 (Accession XP_300778.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348525 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348525, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348525 BINDING SITE, designated SEQ ID:5488, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30430] Another function of GAM189 is therefore inhibition of LOC348525 (Accession XP_300778.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348525.

[30431] LOC348532 (Accession XP_302818.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348532 BINDING SITE1 and LOC348532 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348532, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC348532 BINDING SITE1 and LOC348532 BINDING SITE2, designated SEQ ID:872 and SEQ ID:11192 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30432] Another function of GAM189 is therefore inhibition of LOC348532 (Accession XP_302818.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348532.

[30433] LOC348583 (Accession XP_302833.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348583 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348583, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348583 BINDING SITE, designated SEQ ID:8544, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30434] Another function of GAM189 is therefore inhibition of LOC348583 (Accession XP_302833.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348583.

[30435] LOC348594 (Accession XP_302834.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348594 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348594, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348594 BINDING SITE, designated SEQ ID:16785, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30436] Another function of GAM189 is therefore inhibition of LOC348594 (Accession XP_302834.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348594.

[30437] LOC348595 (Accession XP_302837.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348595 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348595, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC348595 BINDING SITE, designated SEQ ID:16785, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30438] Another function of GAM189 is therefore inhibition of LOC348595 (Accession XP_302837.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348595.

[30439] LOC348603 (Accession XP_302844.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348603 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348603 BINDING SITE, designated SEQ ID:16785, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30440] Another function of GAM189 is therefore inhibition of LOC348603 (Accession XP_302844.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC348603.

[30441] LOC348605 (Accession XP_300793.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348605 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348605, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348605 BINDING SITE, designated SEQ ID:16785, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30442] Another function of GAM189 is therefore inhibition of LOC348605 (Accession XP_300793.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348605.

[30443] LOC348702 (Accession XP_300808.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348702 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348702, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC348702 BINDING SITE, designated SEQ ID:7387, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30444] Another function of GAM189 is therefore inhibition of LOC348702 (Accession XP_300808.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348702.

[30445] LOC348790 (Accession XP_300843.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348790 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348790, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348790 BINDING SITE, designated SEQ ID:810, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30446] Another function of GAM189 is therefore inhibition of LOC348790 (Accession XP_300843.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348790.

[30447] LOC348797 (Accession XP_302888.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348797 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348797, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348797 BINDING SITE, designated SEQ ID:7741, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30448] Another function of GAM189 is therefore inhibition of LOC348797 (Accession XP_302888.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348797.

[30449] LOC348798 (Accession XP_300845.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348798 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348798, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348798 BINDING SITE, designated SEQ ID:19402, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30450] Another function of GAM189 is therefore inhibition of LOC348798 (Accession XP_300845.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348798.

[30451] LOC348825 (Accession XP_300853.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348825 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348825, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348825 BINDING SITE, designated SEQ ID:15126, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30452] Another function of GAM189 is therefore inhibition of LOC348825 (Accession XP_300853.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348825.

[30453] LOC348842 (Accession XP_300861.1) is another GAM189

target gene, herein designated TARGET GENE. LOC348842 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348842 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30454] Another function of GAM189 is therefore inhibition of LOC348842 (Accession XP_300861.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348842.

[30455] LOC348947 (Accession XP_302929.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348947 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348947, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348947 BINDING SITE, designated SEQ ID:8605, to the nucleotide sequence of GAM189 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:246.

[30456] Another function of GAM189 is therefore inhibition of LOC348947 (Accession XP_302929.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348947.

[30457] LOC348995 (Accession XP_300434.1) is another GAM189 target gene, herein designated TARGET GENE. LOC348995 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348995, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348995 BINDING SITE, designated SEQ ID:1900, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30458] Another function of GAM189 is therefore inhibition of LOC348995 (Accession XP_300434.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348995.

[30459] LOC349024 (Accession XP_300250.1) is another GAM189 target gene, herein designated TARGET GENE. LOC349024

BINDING SITE1 and LOC349024 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC349024, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349024 BINDING SITE1 and LOC349024 BINDING SITE2, designated SEQ ID:1746 and SEQ ID:4617 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30460] Another function of GAM189 is therefore inhibition of LOC349024 (Accession XP_300250.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349024.

[30461] LOC349075 (Accession XP_300932.1) is another GAM189 target gene, herein designated TARGET GENE. LOC349075 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349075, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349075 BINDING SITE, designated SEQ ID:16022, to

the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30462] Another function of GAM189 is therefore inhibition of LOC349075 (Accession XP_300932.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349075.

[30463] LOC349096 (Accession XP_300937.1) is another GAM189 target gene, herein designated TARGET GENE. LOC349096 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349096, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349096 BINDING SITE, designated SEQ ID:6188, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30464] Another function of GAM189 is therefore inhibition of LOC349096 (Accession XP_300937.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349096.

[30465] LOC349114 (Accession XP_302960.1) is another GAM189

target gene, herein designated TARGET GENE. LOC349114 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349114 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30466] Another function of GAM189 is therefore inhibition of LOC349114 (Accession XP_302960.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349114.

[30467] LOC349170 (Accession XP_300969.1) is another GAM189 target gene, herein designated TARGET GENE. LOC349170 BINDING SITE1 through LOC349170 BINDING SITE5 are target binding sites found in untranslated regions of mRNA encoded by LOC349170, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349170 BINDING SITE1 through LOC349170 BINDING SITE5, des-

ignated SEQ ID:9545, SEQ ID:11508, SEQ ID:18074, SEQ ID:3349 and SEQ ID:958 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30468] Another function of GAM189 is therefore inhibition of LOC349170 (Accession XP_300969.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349170.

[30469] LOC349251 (Accession XP_300251.1) is another GAM189 target gene, herein designated TARGET GENE. LOC349251 BINDING SITE1 and LOC349251 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC349251, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349251 BINDING SITE1 and LOC349251 BINDING SITE2, designated SEQ ID:4454 and SEQ ID:2323 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30470] Another function of GAM189 is therefore inhibition of LOC349251 (Accession XP_300251.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349251.

[30471] LOC349360 (Accession XP_088528.1) is another GAM189 target gene, herein designated TARGET GENE. LOC349360 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349360, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349360 BINDING SITE, designated SEQ ID:10639, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30472] Another function of GAM189 is therefore inhibition of LOC349360 (Accession XP_088528.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349360.

[30473] LOC349408 (Accession XP_303044.1) is another GAM189 target gene, herein designated TARGET GENE. LOC349408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349408, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349408 BINDING SITE, designated SEQ ID:13466, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30474] Another function of GAM189 is therefore inhibition of LOC349408 (Accession XP_303044.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349408.

[30475] LOC349440 (Accession XP_300513.1) is another GAM189 target gene, herein designated TARGET GENE. LOC349440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349440 BINDING SITE, designated SEQ ID:4112, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30476] Another function of GAM189 is therefore inhibition of LOC349440 (Accession XP_300513.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC349440.

[30477] LOC350106 (Accession XP_303810.1) is another GAM189 target gene, herein designated TARGET GENE. LOC350106 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC350106, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC350106 BINDING SITE, designated SEQ ID:18715, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30478] Another function of GAM189 is therefore inhibition of LOC350106 (Accession XP_303810.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC350106.

[30479] LOC350914 (Accession XP_304556.1) is another GAM189 target gene, herein designated TARGET GENE. LOC350914 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC350914, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC350914 BINDING SITE, designated SEQ ID:19860, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30480] Another function of GAM189 is therefore inhibition of LOC350914 (Accession XP_304556.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC350914.

[30481] LOC51058 (Accession NP_056995.1) is another GAM189 target gene, herein designated TARGET GENE. LOC51058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51058 BINDING SITE, designated SEQ ID:5678, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30482] Another function of GAM189 is therefore inhibition of LOC51058 (Accession NP_056995.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC51058.

[30483] LOC51193 (Accession NP_057415.1) is another GAM189 target gene, herein designated TARGET GENE. LOC51193 BINDING SITE1 and LOC51193 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC51193, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51193 BINDING SITE1 and LOC51193 BINDING SITE2, designated SEQ ID:3111 and SEQ ID:14721 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30484] Another function of GAM189 is therefore inhibition of LOC51193 (Accession NP_057415.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51193.

[30485] LOC51257 (Accession NP_057580.2) is another GAM189 target gene, herein designated TARGET GENE. LOC51257 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC51257, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51257 BINDING SITE, designated SEQ ID:14855, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30486] Another function of GAM189 is therefore inhibition of LOC51257 (Accession NP_057580.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51257.

[30487] LOC51334 (Accession NP_057728.1) is another GAM189 target gene, herein designated TARGET GENE. LOC51334 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC51334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51334 BINDING SITE, designated SEQ ID:8243, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30488] Another function of GAM189 is therefore inhibition of LOC51334 (Accession NP_057728.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC51334.

[30489] LOC51336 (Accession NP_057730.1) is another GAM189 target gene, herein designated TARGET GENE. LOC51336 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51336 BINDING SITE, designated SEQ ID:18703, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30490] Another function of GAM189 is therefore inhibition of LOC51336 (Accession NP_057730.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51336.

[30491] LOC55954 (Accession NP_061976.1) is another GAM189 target gene, herein designated TARGET GENE. LOC55954 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC55954, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of LOC55954 BINDING SITE, designated SEQ ID:17853, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30492] Another function of GAM189 is therefore inhibition of LOC55954 (Accession NP_061976.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC55954.

[30493] LOC56902 (Accession NP_064528.1) is another GAM189 target gene, herein designated TARGET GENE. LOC56902 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC56902, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC56902 BINDING SITE, designated SEQ ID:5945, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30494] Another function of GAM189 is therefore inhibition of LOC56902 (Accession NP_064528.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC56902.

[30495] LOC56926 (Accession NP_064555.1) is another GAM189 target gene, herein designated TARGET GENE. LOC56926 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC56926, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC56926 BINDING SITE, designated SEQ ID:8643, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30496] Another function of GAM189 is therefore inhibition of LOC56926 (Accession NP_064555.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56926.

[30497] LOC57107 (Accession NP_065114.2) is another GAM189 target gene, herein designated TARGET GENE. LOC57107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC57107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

LOC57107 BINDING SITE, designated SEQ ID:16916, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30498] Another function of GAM189 is therefore inhibition of LOC57107 (Accession NP_065114.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57107.

[30499] LOC57146 (Accession NP_065155.2) is another GAM189 target gene, herein designated TARGET GENE. LOC57146 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC57146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC57146 BINDING SITE, designated SEQ ID:11036, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30500] Another function of GAM189 is therefore inhibition of LOC57146 (Accession NP_065155.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57146.

[30501] LOC89894 (Accession NP_612350.1) is another GAM189 target gene, herein designated TARGET GENE. LOC89894 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC89894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC89894 BINDING SITE, designated SEQ ID:14184, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30502] Another function of GAM189 is therefore inhibition of LOC89894 (Accession NP_612350.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC89894.

[30503] LOC90408 (Accession XP_031517.1) is another GAM189 target gene, herein designated TARGET GENE. LOC90408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC90408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90408 BINDING SITE, designated SEQ ID:7704, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30504] Another function of GAM189 is therefore inhibition of LOC90408 (Accession XP_031517.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90408.

[30505] LOC90485 (Accession XP_032059.1) is another GAM189 target gene, herein designated TARGET GENE. LOC90485 BINDING SITE1 and LOC90485 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC90485, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90485 BINDING SITE1 and LOC90485 BINDING SITE2, designated SEQ ID:18698 and SEQ ID:6896 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30506] Another function of GAM189 is therefore inhibition of LOC90485 (Accession XP_032059.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC90485.

[30507] LOC90719 (Accession XP_033704.1) is another GAM189 target gene, herein designated TARGET GENE. LOC90719 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90719 BINDING SITE, designated SEQ ID:13994, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30508] Another function of GAM189 is therefore inhibition of LOC90719 (Accession XP_033704.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90719.

[30509] LOC90999 (Accession XP_035410.1) is another GAM189 target gene, herein designated TARGET GENE. LOC90999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

LOC90999 BINDING SITE, designated SEQ ID:15038, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30510] Another function of GAM189 is therefore inhibition of LOC90999 (Accession XP_035410.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90999.

[30511] LOC91115 (Accession XP_036218.1) is another GAM189 target gene, herein designated TARGET GENE. LOC91115 BINDING SITE1 through LOC91115 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC91115, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91115 BINDING SITE1 through LOC91115 BINDING SITE3, designated SEQ ID:19989, SEQ ID:12591 and SEQ ID:17831 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30512] Another function of GAM189 is therefore inhibition of LOC91115 (Accession XP_036218.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC91115.

[30513] LOC91170 (Accession XP_036612.1) is another GAM189 target gene, herein designated TARGET GENE. LOC91170 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91170 BINDING SITE, designated SEQ ID:16178, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30514] Another function of GAM189 is therefore inhibition of LOC91170 (Accession XP_036612.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91170.

[30515] LOC91250 (Accession XP_037135.1) is another GAM189 target gene, herein designated TARGET GENE. LOC91250 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91250, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of LOC91250 BINDING SITE, designated SEQ ID:8577, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30516] Another function of GAM189 is therefore inhibition of LOC91250 (Accession XP_037135.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91250.

[30517] LOC91266 (Accession XP_037268.1) is another GAM189 target gene, herein designated TARGET GENE. LOC91266 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91266, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91266 BINDING SITE, designated SEQ ID:18355, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30518] Another function of GAM189 is therefore inhibition of LOC91266 (Accession XP_037268.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC91266.

[30519] LOC91373 (Accession XP_038063.5) is another GAM189 target gene, herein designated TARGET GENE. LOC91373 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91373, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91373 BINDING SITE, designated SEQ ID:9077, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30520] Another function of GAM189 is therefore inhibition of LOC91373 (Accession XP_038063.5) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91373.

[30521] LOC91549 (Accession XP_039115.1) is another GAM189 target gene, herein designated TARGET GENE. LOC91549 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91549, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

LOC91549 BINDING SITE, designated SEQ ID:17238, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30522] Another function of GAM189 is therefore inhibition of LOC91549 (Accession XP_039115.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91549.

[30523] LOC91661 (Accession NP_612381.1) is another GAM189 target gene, herein designated TARGET GENE. LOC91661 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91661, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91661 BINDING SITE, designated SEQ ID:8303, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30524] Another function of GAM189 is therefore inhibition of LOC91661 (Accession NP_612381.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91661.

[30525] LOC91663 (Accession NP_612382.1) is another GAM189 target gene, herein designated TARGET GENE. LOC91663 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91663 BINDING SITE, designated SEQ ID:8075, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30526] Another function of GAM189 is therefore inhibition of LOC91663 (Accession NP_612382.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91663.

[30527] LOC91893 (Accession XP_041340.1) is another GAM189 target gene, herein designated TARGET GENE. LOC91893 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91893, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91893 BINDING SITE, designated SEQ ID:14589, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30528] Another function of GAM189 is therefore inhibition of LOC91893 (Accession XP_041340.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91893.

[30529] LOC92148 (Accession XP_043160.1) is another GAM189 target gene, herein designated TARGET GENE. LOC92148 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC92148, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92148 BINDING SITE, designated SEQ ID:4097, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30530] Another function of GAM189 is therefore inhibition of LOC92148 (Accession XP_043160.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92148.

[30531] LOC92597 (Accession NP_775739.1) is another GAM189

target gene, herein designated TARGET GENE. LOC92597 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92597, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92597 BINDING SITE, designated SEQ ID:19339, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30532] Another function of GAM189 is therefore inhibition of LOC92597 (Accession NP_775739.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92597.

[30533] LOC93132 (Accession XP_049396.1) is another GAM189 target gene, herein designated TARGET GENE. LOC93132 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC93132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC93132 BINDING SITE, designated SEQ ID:9953, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[30534] Another function of GAM189 is therefore inhibition of LOC93132 (Accession XP_049396.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93132.

[30535] Lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS, Accession NP_002331.2) is another GAM189 target gene, herein designated TARGET GENE. LSS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LSS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LSS BINDING SITE, designated SEQ ID:6091, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30536] Another function of GAM189 is therefore inhibition of Lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS, Accession NP_002331.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LSS.

[30537] Leukotriene b4 receptor (LTB4R, Accession NP_000743.1)

is another GAM189 target gene, herein designated TARGET GENE. LTB4R BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LTB4R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LTB4R BINDING SITE, designated SEQ ID:1022, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30538] Another function of GAM189 is therefore inhibition of Leukotriene b4 receptor (LTB4R, Accession NP_000743.1), a gene which may be the cardiac p2y receptor involved in the regulation of cardiac muscle contraction through modulation of l- type calcium currents. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LTB4R.

[30539] The function of LTB4R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Leukotriene b4 receptor 2 (LTB4R2, Accession NP_062813.1) is another GAM189 target gene, herein designated TARGET GENE. LTB4R2 BINDING SITE is a tar-

get binding site found in the 5` untranslated region of mRNA encoded by LTB4R2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LTB4R2 BINDING SITE, designated SEQ ID:15504, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30540] Another function of GAM189 is therefore inhibition of Leukotriene b4 receptor 2 (LTB4R2, Accession NP_062813.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LTB4R2.

[30541] Lymphocyte antigen 75 (LY75, Accession NP_002340.1) is another GAM189 target gene, herein designated TARGET GENE. LY75 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LY75, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LY75 BINDING SITE, designated SEQ ID:17724, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30542] Another function of GAM189 is therefore inhibition of Lymphocyte antigen 75 (LY75, Accession NP_002340.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LY75.

[30543] Lysozyme (renal amyloidosis) (LYZ, Accession NP_000230.1) is another GAM189 target gene, herein designated TARGET GENE. LYZ BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LYZ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LYZ BINDING SITE, designated SEQ ID:7382, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30544] Another function of GAM189 is therefore inhibition of Lysozyme (renal amyloidosis) (LYZ, Accession NP_000230.1), a gene which a bacteriolytic enzyme. and therefore may be associated with Renal amyloidosis. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Renal amyloidosis, and of other diseases and clinical conditions associated with LYZ.

[30545] The function of LYZ has been established by previous

studies. Lysozyme (EC 3.2.1.17) catalyzes the hydrolysis of certain mucopolysaccharides of bacterial cell walls. Specifically, it catalyzes the hydrolysis of the bacterial cell wall beta(1- 4) glycosidic linkages between N- acetylmuramic acid and N- acetylglucosamine. It is found in spleen, lung, kidney, white blood cells, plasma, saliva, milk and tears. Alexander Fleming (1881- 1955), of penicillin fame, discovered and named lysozyme. In a communication to the Royal Society, Fleming (1922) wrote: '.I wish to draw attention to a substance present in the tissues and secretions of the body, which is capable of rapidly dissolving certain bacteria. As this substance has properties akin to those of ferments I have called it a Lysozyme.' Fleming and Allison (1922) demonstrated an unusually high concentration in cartilage, indeed the highest of any tissue. Its role in cartilage is unknown. It resembles lactalbumin (OMIM Ref. No. 149750) in structure. Human lysozyme has a molecular mass of 14,602 Da. Neufeld (1972) suggested that a genetic defect of lysozyme might underlie a skeletal dysplasia. Spitznagel et al. (1972) observed a patient with selective deficiency of a particular type of neutrophil granule which resulted in about 50% reduction in lysozyme levels. The patient

showed increased susceptibility to infectionPrieur et al. (1974) described inherited lysozyme deficiency in rabbits. No abnormality of cartilage or bone was noted (Greenwald et al., 1975). Older mutant rabbits showed increased susceptibility to infections, especially subcutaneous abscesses (Prieur, 1975). Camara et al. (1990) identified 2 isozymes of rabbit lysozyme and showed that their distribution was tissue specific. Leukocytic and gastrointestinal isozymes were clearly distinguished, and a possible lymphoepithelial isozyme that resembled the gastrointestinal isozyme electrophoretically and chromatographically but not kinetically was demonstrated. Mutant, lysozyme- deficient rabbits completely lacked a detectable leukocytic isozyme but had gastrointestinal and lymphoepithelial isozymes indistinguishable from those of normal rabbits. By electrophoretic methods, the mutant rabbits were shown to lack a protein band corresponding to that of the leukocytic isozyme in normal rabbits Canet et al. (1999) studied the unfolding and refolding properties of human lysozyme and 2 of its amyloidogenic variants, ile56 to thr and asp67 to his, by stopped- flow fluorescence and hydrogen exchange pulse labeling coupled with mass spectrometry. Their results suggested that the amyloidogenic

nature of the lysozyme variants arises from a decrease in the stability of the native fold relative to partially folded intermediates. The origin of this instability was different in the 2 variants, being caused in one case primarily by a reduction in the folding rate and in the other by an increase in the unfolding rate. In both cases, this resulted in a low population of soluble partially folded species that can aggregate in a slow and controlled manner to form amyloid fibrils

[30546]

[30547] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30548] Canet, D.; Sunde, M.; Last, A. M.; Miranker, A.; Spencer, A.; Robinson, C. V.; Dobson, C. M. : Mechanistic studies of the folding of human lysozyme and the origin of amyloidogenic behavior in its disease- related variants. Biochemistry 38: 6419- 6427, 1999. ; and

[30549] Camara, V. M.; Harding, J. W.; Prieur, D. J. : Inherited lysozyme deficiency in rabbits: the absence of a primary isozyme of lysozyme as the cause of the condition. Lab. Invest. 63: 544- 55.

[30550] Further studies establishing the function and utilities of

LYZ are found in John Hopkins OMIM database record ID 153450, and in cited publications listed in Table 5, which are hereby incorporated by reference.Leucine zipper, putative tumor suppressor 1 (LZTS1, Accession NP_066300.1) is another GAM189 target gene, herein designated TARGET GENE. LZTS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LZTS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LZTS1 BINDING SITE, designated SEQ ID:4518, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30551] Another function of GAM189 is therefore inhibition of Leucine zipper, putative tumor suppressor 1 (LZTS1, Accession NP_066300.1), a gene which is an essential component of the nucleoskeleton. potential role in crosslinking filaments or anchoring other molecules. it is essential for growth. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTS1.

[30552] The function of LZTS1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM130.1.MAC30 (Accession XP_031536.2) is another GAM189 target gene, herein designated TARGET GENE. MAC30 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAC30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAC30 BINDING SITE, designated SEQ ID:5069, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30553] Another function of GAM189 is therefore inhibition of MAC30 (Accession XP_031536.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAC30.

[30554] MAIL (Accession NP_113607.1) is another GAM189 target gene, herein designated TARGET GENE. MAIL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAIL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAIL BINDING SITE, designated SEQ ID:2338, to the nucleotide sequence

of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30555] Another function of GAM189 is therefore inhibition of MAIL (Accession NP_113607.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAIL.

[30556] Male germ cell-associated kinase (MAK, Accession NP_005897.1) is another GAM189 target gene, herein designated TARGET GENE. MAK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAK BINDING SITE, designated SEQ ID:1989, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30557] Another function of GAM189 is therefore inhibition of Male germ cell-associated kinase (MAK, Accession NP_005897.1), a gene which plays an important role in spermatogenesis. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAK.

[30558] The function of MAK and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.MAPA (Accession NP_660299.1) is another GAM189 target gene, herein designated TARGET GENE. MAPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPA BINDING SITE, designated SEQ ID:5231, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30559] Another function of GAM189 is therefore inhibition of MAPA (Accession NP_660299.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPA.

[30560] Mitogen-activated protein kinase 8 interacting protein 3 (MAPK8IP3, Accession NP_203750.1) is another GAM189 target gene, herein designated TARGET GENE. MAPK8IP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK8IP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPK8IP3 BINDING SITE, designated SEQ ID:14298, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30561] Another function of GAM189 is therefore inhibition of Mitogen-activated protein kinase 8 interacting protein 3 (MAPK8IP3, Accession NP_203750.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK8IP3.

[30562] MCLC (Accession NP_055942.1) is another GAM189 target gene, herein designated TARGET GENE. MCLC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MCLC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCLC BINDING SITE, designated SEQ ID:7270, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30563] Another function of GAM189 is therefore inhibition of MCLC (Accession NP_055942.1) . Accordingly, utilities of

GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCLC.

[30564] Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006873.1) is another GAM189 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30565] Another function of GAM189 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006873.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas

and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[30566] The function of MDM2 has been established by previous studies. MDM2 acts as a major regulator of the tumor suppressor p53 (OMIM Ref. No. 191170) by targeting its destruction. Oliner et al. (1992) used MDM2 clones to localize the human gene to 12q13- q14 by analysis of human- hamster somatic cell hybrids. By fluorescence in situ hybridization onto simultaneously DAPI- banded metaphase chromosomes and interphase nuclei, Mitchell et al. (1995) mapped MDM2 to 12q14.3- q15 distal to CDK4 (OMIM Ref. No. 123829) and flanked by Genethon microsatellites D12S80 and D12S83. On both the physical and the genetic maps of chromosome 12, Bureau et al. (1995) mapped the IFG gene (OMIM Ref. No. 147570) close to the D12S335 and D12S313 microsatellites. They also physically mapped it close to the locus of the MDM2 oncogene on 12q15, a localization proximal to that arrived at earlier. They described the organization of the Ifg, Myf6 (OMIM Ref. No. 159991), Mdm1, and Mdm2 loci on mouse chromosome 10 in a region with homology of synteny to human 12q15. . Bueso- Ramos et al. (1993) found overexpression of the MDM2 oncogene in leukemias. In-

activation of tumor suppressor genes leads to deregulated cell proliferation and is a key factor in human tumorigenesis. Mutations in the p53 and retinoblastoma (OMIM Ref. No. 180200) genes are frequently associated with human cancers, and simultaneous inactivation of both RB and p53 is frequently observed in naturally occurring tumors. Additionally, 3 distinct DNA tumor virus groups (papovaviruses, adenoviruses, and human papillomaviruses) transform cells by targeting and inactivating certain functions of both the p53 and RB1 gene products. Xiao et al. (1995) showed that MDM2 interacts physically and functionally with the RB protein and can inhibit its growth regulatory capacity. They thus demonstrated that both RB and p53 can be subjected to negative regulation by the product of a single cellular protooncogene. Mdm2 acts as a major regulator of the tumor suppressor p53 by targeting its destruction. Ries et al. (2000) showed that the mdm2 gene is also regulated by the Ras- driven Raf/MEK/MAP kinase pathway, in a p53- independent manner. Mdm2 induced by activated Raf degrades p53 in the absence of the Mdm2 inhibitor p19(ARF) (OMIM Ref. No. 600160). This regulatory pathway accounts for the observation that cells transformed by oncogenic Ras are more

resistant to p53- dependent apoptosis following exposure to DNA damage. Activation of the Ras- induced Raf/MEK/MAP kinase may therefore play a key role in suppressing p53 during tumor development and treatment. In primary cells, Raf also activates the Mdm2 inhibitor p19(ARF). Levels of p53 are therefore determined by opposing effects of Raf- induced p19(ARF) and Mdm2. The MDM2 oncoprotein promotes cell survival and cell cycle progression by inhibiting the p53 tumor suppressor protein (OMIM Ref. No. 191170). To regulate p53, MDM2 must gain nuclear entry; Mayo and Donner (2001) identified the mechanism that induces this. Mitogen- induced activation of phosphatidylinositol 3- kinase (see OMIM Ref. No. PIK3CA; 171834) and its downstream target, the AKT/PKB serine- threonine kinase (OMIM Ref. No. 164730), results in phosphorylation of MDM2 on serine-166 and serine- 186. Phosphorylation on these sites is necessary for translocation of MDM2 from the cytoplasm into the nucleus. Pharmacologic blockade of PI3- kinase/AKT signaling or expression of dominant- negative PI3-kinase or AKT inhibits nuclear entry of MDM2, increases cellular levels of p53, and augments p53 transcriptional activity. Expression of constitutively active AKT promotes

nuclear entry of MDM2, diminishes cellular levels of p53, and decreases p53 transcriptional activity. Mutation of the AKT phosphorylation sites in MDM2 produces a mutant protein that is unable to enter the nucleus and increases p53 activity. The demonstration that PI3- kinase/AKT signaling affects MDM2 localization provided insight into how this pathway, which is inappropriately activated in many malignancies, affects the function of p53. Testa and Bellacosa (2001) reviewed the central role of AKT in tumorigenesis.

[30567]

[30568] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30569] Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.; Sasazuki, T.; McMahon, M.; Oren, M.; McCormick, F. : Opposing effects of Ras on p53: transcriptional activation of mdm2 and induction of p19(ARF). Cell 103: 321- 330, 2000. ; and

[30570] Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S. A.; Albitar, M. : The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82: 2617- 2623, 1993.

[30571] Further studies establishing the function and utilities of

MDM2 are found in John Hopkins OMIM database record ID 164785, and in cited publications listed in Table 5, which are hereby incorporated by reference.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006870.1) is another GAM189 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30572] Another function of GAM189 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006870.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas

and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[30573] The function of MDM2 has been established by previous studies. MDM2 acts as a major regulator of the tumor suppressor p53 (OMIM Ref. No. 191170) by targeting its destruction. Oliner et al. (1992) used MDM2 clones to localize the human gene to 12q13- q14 by analysis of human- hamster somatic cell hybrids. By fluorescence in situ hybridization onto simultaneously DAPI- banded metaphase chromosomes and interphase nuclei, Mitchell et al. (1995) mapped MDM2 to 12q14.3- q15 distal to CDK4 (OMIM Ref. No. 123829) and flanked by Genethon microsatellites D12S80 and D12S83. On both the physical and the genetic maps of chromosome 12, Bureau et al. (1995) mapped the IFG gene (OMIM Ref. No. 147570) close to the D12S335 and D12S313 microsatellites. They also physically mapped it close to the locus of the MDM2 oncogene on 12q15, a localization proximal to that arrived at earlier. They described the organization of the Ifg, Myf6 (OMIM Ref. No. 159991), Mdm1, and Mdm2 loci on mouse chromosome 10 in a region with homology of synteny to human 12q15. . Bueso- Ramos et al. (1993) found overexpression of the MDM2 oncogene in leukemias. In-

activation of tumor suppressor genes leads to deregulated cell proliferation and is a key factor in human tumorigenesis. Mutations in the p53 and retinoblastoma (OMIM Ref. No. 180200) genes are frequently associated with human cancers, and simultaneous inactivation of both RB and p53 is frequently observed in naturally occurring tumors. Additionally, 3 distinct DNA tumor virus groups (papovaviruses, adenoviruses, and human papillomaviruses) transform cells by targeting and inactivating certain functions of both the p53 and RB1 gene products. Xiao et al. (1995) showed that MDM2 interacts physically and functionally with the RB protein and can inhibit its growth regulatory capacity. They thus demonstrated that both RB and p53 can be subjected to negative regulation by the product of a single cellular protooncogene. Mdm2 acts as a major regulator of the tumor suppressor p53 by targeting its destruction. Ries et al. (2000) showed that the mdm2 gene is also regulated by the Ras- driven Raf/MEK/MAP kinase pathway, in a p53- independent manner. Mdm2 induced by activated Raf degrades p53 in the absence of the Mdm2 inhibitor p19(ARF) (OMIM Ref. No. 600160). This regulatory pathway accounts for the observation that cells transformed by oncogenic Ras are more

resistant to p53- dependent apoptosis following exposure to DNA damage. Activation of the Ras- induced Raf/MEK/MAP kinase may therefore play a key role in suppressing p53 during tumor development and treatment. In primary cells, Raf also activates the Mdm2 inhibitor p19(ARF). Levels of p53 are therefore determined by opposing effects of Raf- induced p19(ARF) and Mdm2. The MDM2 oncoprotein promotes cell survival and cell cycle progression by inhibiting the p53 tumor suppressor protein (OMIM Ref. No. 191170). To regulate p53, MDM2 must gain nuclear entry; Mayo and Donner (2001) identified the mechanism that induces this. Mitogen- induced activation of phosphatidylinositol 3- kinase (see OMIM Ref. No. PIK3CA; 171834) and its downstream target, the AKT/PKB serine- threonine kinase (OMIM Ref. No. 164730), results in phosphorylation of MDM2 on serine-166 and serine- 186. Phosphorylation on these sites is necessary for translocation of MDM2 from the cytoplasm into the nucleus. Pharmacologic blockade of PI3- kinase/AKT signaling or expression of dominant- negative PI3-kinase or AKT inhibits nuclear entry of MDM2, increases cellular levels of p53, and augments p53 transcriptional activity. Expression of constitutively active AKT promotes

nuclear entry of MDM2, diminishes cellular levels of p53, and decreases p53 transcriptional activity. Mutation of the AKT phosphorylation sites in MDM2 produces a mutant protein that is unable to enter the nucleus and increases p53 activity. The demonstration that PI3- kinase/AKT signaling affects MDM2 localization provided insight into how this pathway, which is inappropriately activated in many malignancies, affects the function of p53. Testa and Bellacosa (2001) reviewed the central role of AKT in tumorigenesis.

[30574]

[30575] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30576] Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.; Sasazuki, T.; McMahon, M.; Oren, M.; McCormick, F. : Opposing effects of Ras on p53: transcriptional activation of mdm2 and induction of p19(ARF). Cell 103: 321- 330, 2000. ; and

[30577] Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S. A.; Albitar, M. : The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82: 2617- 2623, 1993.

[30578] Further studies establishing the function and utilities of

MDM2 are found in John Hopkins OMIM database record ID 164785, and in cited publications listed in Table 5, which are hereby incorporated by reference.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006869.1) is another GAM189 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30579] Another function of GAM189 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006869.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas

and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[30580] The function of MDM2 has been established by previous studies. MDM2 acts as a major regulator of the tumor suppressor p53 (OMIM Ref. No. 191170) by targeting its destruction. Oliner et al. (1992) used MDM2 clones to localize the human gene to 12q13- q14 by analysis of human- hamster somatic cell hybrids. By fluorescence in situ hybridization onto simultaneously DAPI- banded metaphase chromosomes and interphase nuclei, Mitchell et al. (1995) mapped MDM2 to 12q14.3- q15 distal to CDK4 (OMIM Ref. No. 123829) and flanked by Genethon microsatellites D12S80 and D12S83. On both the physical and the genetic maps of chromosome 12, Bureau et al. (1995) mapped the IFG gene (OMIM Ref. No. 147570) close to the D12S335 and D12S313 microsatellites. They also physically mapped it close to the locus of the MDM2 oncogene on 12q15, a localization proximal to that arrived at earlier. They described the organization of the Ifg, Myf6 (OMIM Ref. No. 159991), Mdm1, and Mdm2 loci on mouse chromosome 10 in a region with homology of synteny to human 12q15. . Bueso- Ramos et al. (1993) found overexpression of the MDM2 oncogene in leukemias. In-

activation of tumor suppressor genes leads to deregulated cell proliferation and is a key factor in human tumorigenesis. Mutations in the p53 and retinoblastoma (OMIM Ref. No. 180200) genes are frequently associated with human cancers, and simultaneous inactivation of both RB and p53 is frequently observed in naturally occurring tumors. Additionally, 3 distinct DNA tumor virus groups (papovaviruses, adenoviruses, and human papillomaviruses) transform cells by targeting and inactivating certain functions of both the p53 and RB1 gene products. Xiao et al. (1995) showed that MDM2 interacts physically and functionally with the RB protein and can inhibit its growth regulatory capacity. They thus demonstrated that both RB and p53 can be subjected to negative regulation by the product of a single cellular protooncogene. Mdm2 acts as a major regulator of the tumor suppressor p53 by targeting its destruction. Ries et al. (2000) showed that the mdm2 gene is also regulated by the Ras- driven Raf/MEK/MAP kinase pathway, in a p53- independent manner. Mdm2 induced by activated Raf degrades p53 in the absence of the Mdm2 inhibitor p19(ARF) (OMIM Ref. No. 600160). This regulatory pathway accounts for the observation that cells transformed by oncogenic Ras are more

resistant to p53- dependent apoptosis following exposure to DNA damage. Activation of the Ras- induced Raf/MEK/MAP kinase may therefore play a key role in suppressing p53 during tumor development and treatment. In primary cells, Raf also activates the Mdm2 inhibitor p19(ARF). Levels of p53 are therefore determined by opposing effects of Raf- induced p19(ARF) and Mdm2. The MDM2 oncoprotein promotes cell survival and cell cycle progression by inhibiting the p53 tumor suppressor protein (OMIM Ref. No. 191170). To regulate p53, MDM2 must gain nuclear entry; Mayo and Donner (2001) identified the mechanism that induces this. Mitogen- induced activation of phosphatidylinositol 3- kinase (see OMIM Ref. No. PIK3CA; 171834) and its downstream target, the AKT/PKB serine- threonine kinase (OMIM Ref. No. 164730), results in phosphorylation of MDM2 on serine-166 and serine- 186. Phosphorylation on these sites is necessary for translocation of MDM2 from the cytoplasm into the nucleus. Pharmacologic blockade of PI3- kinase/AKT signaling or expression of dominant- negative PI3-kinase or AKT inhibits nuclear entry of MDM2, increases cellular levels of p53, and augments p53 transcriptional activity. Expression of constitutively active AKT promotes

nuclear entry of MDM2, diminishes cellular levels of p53, and decreases p53 transcriptional activity. Mutation of the AKT phosphorylation sites in MDM2 produces a mutant protein that is unable to enter the nucleus and increases p53 activity. The demonstration that PI3- kinase/AKT signaling affects MDM2 localization provided insight into how this pathway, which is inappropriately activated in many malignancies, affects the function of p53. Testa and Bellacosa (2001) reviewed the central role of AKT in tumorigenesis.

[30581]

[30582] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30583] Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.; Sasazuki, T.; McMahon, M.; Oren, M.; McCormick, F. : Opposing effects of Ras on p53: transcriptional activation of mdm2 and induction of p19(ARF). Cell 103: 321- 330, 2000. ; and

[30584] Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S. A.; Albitar, M. : The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82: 2617- 2623, 1993.

[30585] Further studies establishing the function and utilities of

MDM2 are found in John Hopkins OMIM database record ID 164785, and in cited publications listed in Table 5, which are hereby incorporated by reference.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006872.1) is another GAM189 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30586] Another function of GAM189 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006872.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas

and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[30587] The function of MDM2 has been established by previous studies. MDM2 acts as a major regulator of the tumor suppressor p53 (OMIM Ref. No. 191170) by targeting its destruction. Oliner et al. (1992) used MDM2 clones to localize the human gene to 12q13- q14 by analysis of human- hamster somatic cell hybrids. By fluorescence in situ hybridization onto simultaneously DAPI- banded metaphase chromosomes and interphase nuclei, Mitchell et al. (1995) mapped MDM2 to 12q14.3- q15 distal to CDK4 (OMIM Ref. No. 123829) and flanked by Genethon microsatellites D12S80 and D12S83. On both the physical and the genetic maps of chromosome 12, Bureau et al. (1995) mapped the IFG gene (OMIM Ref. No. 147570) close to the D12S335 and D12S313 microsatellites. They also physically mapped it close to the locus of the MDM2 oncogene on 12q15, a localization proximal to that arrived at earlier. They described the organization of the Ifg, Myf6 (OMIM Ref. No. 159991), Mdm1, and Mdm2 loci on mouse chromosome 10 in a region with homology of synteny to human 12q15. . Bueso- Ramos et al. (1993) found overexpression of the MDM2 oncogene in leukemias. In-

activation of tumor suppressor genes leads to deregulated cell proliferation and is a key factor in human tumorigenesis. Mutations in the p53 and retinoblastoma (OMIM Ref. No. 180200) genes are frequently associated with human cancers, and simultaneous inactivation of both RB and p53 is frequently observed in naturally occurring tumors. Additionally, 3 distinct DNA tumor virus groups (papovaviruses, adenoviruses, and human papillomaviruses) transform cells by targeting and inactivating certain functions of both the p53 and RB1 gene products. Xiao et al. (1995) showed that MDM2 interacts physically and functionally with the RB protein and can inhibit its growth regulatory capacity. They thus demonstrated that both RB and p53 can be subjected to negative regulation by the product of a single cellular protooncogene. Mdm2 acts as a major regulator of the tumor suppressor p53 by targeting its destruction. Ries et al. (2000) showed that the mdm2 gene is also regulated by the Ras- driven Raf/MEK/MAP kinase pathway, in a p53- independent manner. Mdm2 induced by activated Raf degrades p53 in the absence of the Mdm2 inhibitor p19(ARF) (OMIM Ref. No. 600160). This regulatory pathway accounts for the observation that cells transformed by oncogenic Ras are more

resistant to p53- dependent apoptosis following exposure to DNA damage. Activation of the Ras- induced Raf/MEK/MAP kinase may therefore play a key role in suppressing p53 during tumor development and treatment. In primary cells, Raf also activates the Mdm2 inhibitor p19(ARF). Levels of p53 are therefore determined by opposing effects of Raf- induced p19(ARF) and Mdm2. The MDM2 oncoprotein promotes cell survival and cell cycle progression by inhibiting the p53 tumor suppressor protein (OMIM Ref. No. 191170). To regulate p53, MDM2 must gain nuclear entry; Mayo and Donner (2001) identified the mechanism that induces this. Mitogen- induced activation of phosphatidylinositol 3- kinase (see OMIM Ref. No. PIK3CA; 171834) and its downstream target, the AKT/PKB serine- threonine kinase (OMIM Ref. No. 164730), results in phosphorylation of MDM2 on serine-166 and serine- 186. Phosphorylation on these sites is necessary for translocation of MDM2 from the cytoplasm into the nucleus. Pharmacologic blockade of PI3- kinase/AKT signaling or expression of dominant- negative PI3-kinase or AKT inhibits nuclear entry of MDM2, increases cellular levels of p53, and augments p53 transcriptional activity. Expression of constitutively active AKT promotes

nuclear entry of MDM2, diminishes cellular levels of p53, and decreases p53 transcriptional activity. Mutation of the AKT phosphorylation sites in MDM2 produces a mutant protein that is unable to enter the nucleus and increases p53 activity. The demonstration that PI3- kinase/AKT signaling affects MDM2 localization provided insight into how this pathway, which is inappropriately activated in many malignancies, affects the function of p53. Testa and Bellacosa (2001) reviewed the central role of AKT in tumorigenesis.

[30588]

[30589] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30590] Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.; Sasazuki, T.; McMahon, M.; Oren, M.; McCormick, F. : Opposing effects of Ras on p53: transcriptional activation of mdm2 and induction of p19(ARF). Cell 103: 321- 330, 2000. ; and

[30591] Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S. A.; Albitar, M. : The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82: 2617- 2623, 1993.

[30592] Further studies establishing the function and utilities of MDM2 are found in John Hopkins OMIM database record ID 164785, and in cited publications listed in Table 5, which are hereby incorporated by reference.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_002383.1) is another GAM189 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30593] Another function of GAM189 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_002383.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may

be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[30594] The function of MDM2 has been established by previous studies. MDM2 acts as a major regulator of the tumor suppressor p53 (OMIM Ref. No. 191170) by targeting its destruction. Oliner et al. (1992) used MDM2 clones to localize the human gene to 12q13- q14 by analysis of human- hamster somatic cell hybrids. By fluorescence in situ hybridization onto simultaneously DAPI- banded metaphase chromosomes and interphase nuclei, Mitchell et al. (1995) mapped MDM2 to 12q14.3- q15 distal to CDK4 (OMIM Ref. No. 123829) and flanked by Genethon microsatellites D12S80 and D12S83. On both the physical and the genetic maps of chromosome 12, Bureau et al. (1995) mapped the IFG gene (OMIM Ref. No. 147570) close to the D12S335 and D12S313 microsatellites. They also physically mapped it close to the locus of the MDM2 oncogene on 12q15, a localization proximal to that arrived at earlier. They described the organization of the Ifg,

Myf6 (OMIM Ref. No. 159991), Mdm1, and Mdm2 loci on mouse chromosome 10 in a region with homology of synteny to human 12q15. . Bueso- Ramos et al. (1993) found overexpression of the MDM2 oncogene in leukemias. Inactivation of tumor suppressor genes leads to deregulated cell proliferation and is a key factor in human tumorigenesis. Mutations in the p53 and retinoblastoma (OMIM Ref. No. 180200) genes are frequently associated with human cancers, and simultaneous inactivation of both RB and p53 is frequently observed in naturally occurring tumors. Additionally, 3 distinct DNA tumor virus groups (papovaviruses, adenoviruses, and human papillomaviruses) transform cells by targeting and inactivating certain functions of both the p53 and RB1 gene products. Xiao et al. (1995) showed that MDM2 interacts physically and functionally with the RB protein and can inhibit its growth regulatory capacity. They thus demonstrated that both RB and p53 can be subjected to negative regulation by the product of a single cellular protooncogene. Mdm2 acts as a major regulator of the tumor suppressor p53 by targeting its destruction. Ries et al. (2000) showed that the mdm2 gene is also regulated by the Ras- driven Raf/MEK/MAP kinase pathway, in a p53- independent manner.

Mdm2 induced by activated Raf degrades p53 in the absence of the Mdm2 inhibitor p19(ARF) (OMIM Ref. No. 600160). This regulatory pathway accounts for the observation that cells transformed by oncogenic Ras are more resistant to p53- dependent apoptosis following exposure to DNA damage. Activation of the Ras- induced Raf/MEK/MAP kinase may therefore play a key role in suppressing p53 during tumor development and treatment. In primary cells, Raf also activates the Mdm2 inhibitor p19(ARF). Levels of p53 are therefore determined by opposing effects of Raf- induced p19(ARF) and Mdm2. The MDM2 oncoprotein promotes cell survival and cell cycle progression by inhibiting the p53 tumor suppressor protein (OMIM Ref. No. 191170). To regulate p53, MDM2 must gain nuclear entry; Mayo and Donner (2001) identified the mechanism that induces this. Mitogen- induced activation of phosphatidylinositol 3- kinase (see OMIM Ref. No. PIK3CA; 171834) and its downstream target, the AKT/PKB serine- threonine kinase (OMIM Ref. No. 164730), results in phosphorylation of MDM2 on serine-166 and serine- 186. Phosphorylation on these sites is necessary for translocation of MDM2 from the cytoplasm into the nucleus. Pharmacologic blockade of PI3- kinase/

AKT signaling or expression of dominant- negative PI3-kinase or AKT inhibits nuclear entry of MDM2, increases cellular levels of p53, and augments p53 transcriptional activity. Expression of constitutively active AKT promotes nuclear entry of MDM2, diminishes cellular levels of p53, and decreases p53 transcriptional activity. Mutation of the AKT phosphorylation sites in MDM2 produces a mutant protein that is unable to enter the nucleus and increases p53 activity. The demonstration that PI3- kinase/AKT signaling affects MDM2 localization provided insight into how this pathway, which is inappropriately activated in many malignancies, affects the function of p53. Testa and Bellacosa (2001) reviewed the central role of AKT in tumorigenesis.

[30595]

[30596] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30597] Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.; Sasazuki, T.; McMahon, M.; Oren, M.; McCormick, F. : Opposing effects of Ras on p53: transcriptional activation of mdm2 and induction of p19(ARF). Cell 103: 321- 330, 2000. ; and

[30598] Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S. A.; Albitar, M. : The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82: 2617- 2623, 1993.

[30599] Further studies establishing the function and utilities of MDM2 are found in John Hopkins OMIM database record ID 164785, and in cited publications listed in Table 5, which are hereby incorporated by reference.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006871.1) is another GAM189 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30600] Another function of GAM189 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006871.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may

be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[30601] The function of MDM2 has been established by previous studies. MDM2 acts as a major regulator of the tumor suppressor p53 (OMIM Ref. No. 191170) by targeting its destruction. Oliner et al. (1992) used MDM2 clones to localize the human gene to 12q13- q14 by analysis of human- hamster somatic cell hybrids. By fluorescence in situ hybridization onto simultaneously DAPI- banded metaphase chromosomes and interphase nuclei, Mitchell et al. (1995) mapped MDM2 to 12q14.3- q15 distal to CDK4 (OMIM Ref. No. 123829) and flanked by Genethon microsatellites D12S80 and D12S83. On both the physical and the genetic maps of chromosome 12, Bureau et al. (1995) mapped the IFG gene (OMIM Ref. No. 147570) close to the D12S335 and D12S313 microsatellites. They also physically mapped it close to the locus of the MDM2 oncogene on 12q15, a localization proximal to that arrived at earlier. They described the organization of the Ifg,

Myf6 (OMIM Ref. No. 159991), Mdm1, and Mdm2 loci on mouse chromosome 10 in a region with homology of synteny to human 12q15. . Bueso- Ramos et al. (1993) found overexpression of the MDM2 oncogene in leukemias. Inactivation of tumor suppressor genes leads to deregulated cell proliferation and is a key factor in human tumorigenesis. Mutations in the p53 and retinoblastoma (OMIM Ref. No. 180200) genes are frequently associated with human cancers, and simultaneous inactivation of both RB and p53 is frequently observed in naturally occurring tumors. Additionally, 3 distinct DNA tumor virus groups (papovaviruses, adenoviruses, and human papillomaviruses) transform cells by targeting and inactivating certain functions of both the p53 and RB1 gene products. Xiao et al. (1995) showed that MDM2 interacts physically and functionally with the RB protein and can inhibit its growth regulatory capacity. They thus demonstrated that both RB and p53 can be subjected to negative regulation by the product of a single cellular protooncogene. Mdm2 acts as a major regulator of the tumor suppressor p53 by targeting its destruction. Ries et al. (2000) showed that the mdm2 gene is also regulated by the Ras- driven Raf/MEK/MAP kinase pathway, in a p53- independent manner.

Mdm2 induced by activated Raf degrades p53 in the absence of the Mdm2 inhibitor p19(ARF) (OMIM Ref. No. 600160). This regulatory pathway accounts for the observation that cells transformed by oncogenic Ras are more resistant to p53- dependent apoptosis following exposure to DNA damage. Activation of the Ras- induced Raf/MEK/MAP kinase may therefore play a key role in suppressing p53 during tumor development and treatment. In primary cells, Raf also activates the Mdm2 inhibitor p19(ARF). Levels of p53 are therefore determined by opposing effects of Raf- induced p19(ARF) and Mdm2. The MDM2 oncoprotein promotes cell survival and cell cycle progression by inhibiting the p53 tumor suppressor protein (OMIM Ref. No. 191170). To regulate p53, MDM2 must gain nuclear entry; Mayo and Donner (2001) identified the mechanism that induces this. Mitogen- induced activation of phosphatidylinositol 3- kinase (see OMIM Ref. No. PIK3CA; 171834) and its downstream target, the AKT/PKB serine- threonine kinase (OMIM Ref. No. 164730), results in phosphorylation of MDM2 on serine-166 and serine- 186. Phosphorylation on these sites is necessary for translocation of MDM2 from the cytoplasm into the nucleus. Pharmacologic blockade of PI3- kinase/

AKT signaling or expression of dominant- negative PI3-kinase or AKT inhibits nuclear entry of MDM2, increases cellular levels of p53, and augments p53 transcriptional activity. Expression of constitutively active AKT promotes nuclear entry of MDM2, diminishes cellular levels of p53, and decreases p53 transcriptional activity. Mutation of the AKT phosphorylation sites in MDM2 produces a mutant protein that is unable to enter the nucleus and increases p53 activity. The demonstration that PI3- kinase/AKT signaling affects MDM2 localization provided insight into how this pathway, which is inappropriately activated in many malignancies, affects the function of p53. Testa and Bellacosa (2001) reviewed the central role of AKT in tumorigenesis.

[30602]

[30603] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30604] Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.; Sasazuki, T.; McMahon, M.; Oren, M.; McCormick, F. : Opposing effects of Ras on p53: transcriptional activation of mdm2 and induction of p19(ARF). Cell 103: 321- 330, 2000. ; and

[30605] Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S. A.; Albitar, M. : The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82: 2617- 2623, 1993.

[30606] Further studies establishing the function and utilities of MDM2 are found in John Hopkins OMIM database record ID 164785, and in cited publications listed in Table 5, which are hereby incorporated by reference.Mdm4, transformed 3t3 cell double minute 4, p53 binding protein (mouse) (MDM4, Accession NP_002384.1) is another GAM189 target gene, herein designated TARGET GENE. MDM4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MDM4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM4 BINDING SITE, designated SEQ ID:7078, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30607] Another function of GAM189 is therefore inhibition of Mdm4, transformed 3t3 cell double minute 4, p53 binding protein (mouse) (MDM4, Accession NP_002384.1), a gene which Strongly similar to murine Mdm4; may interact with p53. Accordingly, utilities of GAM189 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with MDM4.

[30608] The function of MDM4 has been established by previous studies. Shvarts et al. (1997) isolated cDNAs encoding MDM4 by screening a human cDNA library from a colonic tumorigenic cell line with a mouse mdmx probe. The human MDM4 gene encodes a 490- amino acid protein containing a RING finger domain and a putative nuclear localization signal. The predicted mass of the protein was 54 kD, while the observed mass was 80 kD, a difference which Shvarts et al. (1997) stated was probably due to phosphorylation or other posttranslational modification. Northern blot analysis revealed a 10- kb mRNA expressed at a high level in thymus and at lower levels in all other tissues tested. A 2.2- kb mRNA was detected in testis. MDM4 protein produced by in vitro translation interacts with p53 (OMIM Ref. No. 191170) via a binding domain located in the N- terminal region of the MDM4 protein. MDM4 shows significant structural similarity to p53-binding protein MDM2 (OMIM Ref. No. 164785), an E3 ubiquitin ligase. The interaction between MDM2 and p53 is critical for cell viability; loss of Mdm2 causes cell death in vitro and in vivo in a p53- dependent manner. MDM4

has some of the same properties as MDM2, but unlike MDM2, it does not cause nuclear export or degradation of p53. To study MDM4 function in vivo, Parant et al. (2001) deleted the Mdm4 gene in mice. Mdm4- null mice died at 7.5 to 8.5 days postcoitum due to loss of cell proliferation. When Parant et al. (2001) crossed in a p53- null allele, they found that loss of p53 completely rescued the Mdm4 - /- embryonic lethality. Thus, MDM2 and MDM4 are nonoverlapping critical regulators of p53 in vivo. These data defined a new pathway of p53 regulation and raised the possibility that increased MDM4 levels and the resulting inactivation of p53 contribute to the development of human tumors. By fluorescence in situ hybridization, Shvarts et al. (1997) mapped the MDM4 gene to human chromosome 1q32.

[30609]

[30610] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30611] Parant, J.; Chavez- Reyes, A.; Little, N. A.; Yan, W.; Reinke, V.; Jochemsen, A. G.; Lozano, G. : Rescue of embryonic lethality in Mdm4- null mice by loss of Trp53 suggests a nonoverlapping pathway with MDM2 to regulate p53. Na-

ture Genet. 29: 92- 95, 2001. ; and

[30612] Shvarts, A.; Bazuine, M.; Dekker, P.; Ramos, Y. F. M.; Steegenga, W. T.; Merckx, G.; van Ham, R. C. A.; van der Houven van Oordt, W.; van der Eb, A. J.; Jochemsen, A. G. : Isolation an.

[30613] Further studies establishing the function and utilities of MDM4 are found in John Hopkins OMIM database record ID 602704, and in cited publications listed in Table 5, which are hereby incorporated by reference.Mediterranean fever (MEFV, Accession NP_000234.1) is another GAM189 target gene, herein designated TARGET GENE. MEFV BINDING SITE1 and MEFV BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MEFV, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MEFV BINDING SITE1 and MEFV BINDING SITE2, designated SEQ ID:19829 and SEQ ID:5443 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30614] Another function of GAM189 is therefore inhibition of Mediterranean fever (MEFV, Accession NP_000234.1) . Accordingly, utilities of GAM189 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with MEFV.

[30615] Mesoderm development candidate 2 (MESDC2, Accession XP_051854.1) is another GAM189 target gene, herein designated TARGET GENE. MESDC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MESDC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MESDC2 BINDING SITE, designated SEQ ID:6523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30616] Another function of GAM189 is therefore inhibition of Mesoderm development candidate 2 (MESDC2, Accession XP_051854.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MESDC2.

[30617] MFTC (Accession NP_110407.2) is another GAM189 target gene, herein designated TARGET GENE. MFTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MFTC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MFTC BINDING SITE, designated SEQ ID:16545, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30618] Another function of GAM189 is therefore inhibition of MFTC (Accession NP_110407.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MFTC.

[30619] Mannosyl (alpha-1,6-)-glycoprotein beta-1,2-n-acetylglucosaminyltransferase (MGAT2, Accession NP_079374.1) is another GAM189 target gene, herein designated TARGET GENE. MGAT2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MGAT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGAT2 BINDING SITE, designated SEQ ID:9699, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30620] Another function of GAM189 is therefore inhibition of Mannosyl (alpha-1,6-)-glycoprotein beta-

1,2-n-acetylglucosaminyltransferase (MGAT2, Accession NP_079374.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAT2.

[30621] MGC10772 (Accession NP_085044.2) is another GAM189 target gene, herein designated TARGET GENE. MGC10772 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC10772, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10772 BINDING SITE, designated SEQ ID:5386, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30622] Another function of GAM189 is therefore inhibition of MGC10772 (Accession NP_085044.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10772.

[30623] MGC10818 (Accession NP_085045.2) is another GAM189 target gene, herein designated TARGET GENE. MGC10818 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10818, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10818 BINDING SITE, designated SEQ ID:2199, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30624] Another function of GAM189 is therefore inhibition of MGC10818 (Accession NP_085045.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10818.

[30625] MGC11102 (Accession NP_115701.2) is another GAM189 target gene, herein designated TARGET GENE. MGC11102 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC11102, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC11102 BINDING SITE, designated SEQ ID:17609, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30626] Another function of GAM189 is therefore inhibition of MGC11102 (Accession NP_115701.2) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11102.

[30627] MGC12262 (Accession NP_116085.1) is another GAM189 target gene, herein designated TARGET GENE. MGC12262 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC12262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC12262 BINDING SITE, designated SEQ ID:12220, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30628] Another function of GAM189 is therefore inhibition of MGC12262 (Accession NP_116085.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12262.

[30629] MGC12518 (Accession NP_291026.1) is another GAM189 target gene, herein designated TARGET GENE. MGC12518 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC12518, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC12518 BINDING SITE, designated SEQ ID:18251, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30630] Another function of GAM189 is therefore inhibition of MGC12518 (Accession NP_291026.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12518.

[30631] MGC13017 (Accession NP_542387.1) is another GAM189 target gene, herein designated TARGET GENE. MGC13017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13017 BINDING SITE, designated SEQ ID:11562, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30632] Another function of GAM189 is therefore inhibition of MGC13017 (Accession NP_542387.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC13017.

[30633] MGC13024 (Accession NP_689501.1) is another GAM189 target gene, herein designated TARGET GENE. MGC13024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13024 BINDING SITE, designated SEQ ID:13564, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30634] Another function of GAM189 is therefore inhibition of MGC13024 (Accession NP_689501.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13024.

[30635] MGC13138 (Accession NP_219363.1) is another GAM189 target gene, herein designated TARGET GENE. MGC13138 BINDING SITE1 and MGC13138 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC13138, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13138 BINDING SITE1 and MGC13138 BINDING SITE2, designated SEQ ID:6646 and SEQ ID:9543 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30636] Another function of GAM189 is therefore inhibition of MGC13138 (Accession NP_219363.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13138.

[30637] MGC13170 (Accession NP_116101.1) is another GAM189 target gene, herein designated TARGET GENE. MGC13170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13170 BINDING SITE, designated SEQ ID:20116, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30638] Another function of GAM189 is therefore inhibition of MGC13170 (Accession NP_116101.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13170.

[30639] MGC13204 (Accession NP_113653.1) is another GAM189 target gene, herein designated TARGET GENE. MGC13204 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13204, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13204 BINDING SITE, designated SEQ ID:9494, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30640] Another function of GAM189 is therefore inhibition of MGC13204 (Accession NP_113653.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13204.

[30641] MGC14289 (Accession NP_542391.1) is another GAM189 target gene, herein designated TARGET GENE. MGC14289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14289, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14289 BINDING SITE, designated SEQ ID:3677, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30642] Another function of GAM189 is therefore inhibition of MGC14289 (Accession NP_542391.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14289.

[30643] MGC14436 (Accession NP_116286.1) is another GAM189 target gene, herein designated TARGET GENE. MGC14436 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC14436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14436 BINDING SITE, designated SEQ ID:17347, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30644] Another function of GAM189 is therefore inhibition of MGC14436 (Accession NP_116286.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC14436.

[30645] MGC14836 (Accession NP_219480.1) is another GAM189 target gene, herein designated TARGET GENE. MGC14836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14836 BINDING SITE, designated SEQ ID:15044, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30646] Another function of GAM189 is therefore inhibition of MGC14836 (Accession NP_219480.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14836.

[30647] MGC15419 (Accession NP_079011.2) is another GAM189 target gene, herein designated TARGET GENE. MGC15419 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC15419, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC15419 BINDING SITE, designated SEQ ID:15115, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30648] Another function of GAM189 is therefore inhibition of MGC15419 (Accession NP_079011.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15419.

[30649] MGC15606 (Accession NP_659474.1) is another GAM189 target gene, herein designated TARGET GENE. MGC15606 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC15606, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15606 BINDING SITE, designated SEQ ID:10968, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30650] Another function of GAM189 is therefore inhibition of MGC15606 (Accession NP_659474.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC15606.

[30651] MGC15668 (Accession NP_116145.1) is another GAM189 target gene, herein designated TARGET GENE. MGC15668 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC15668, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15668 BINDING SITE, designated SEQ ID:3620, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30652] Another function of GAM189 is therefore inhibition of MGC15668 (Accession NP_116145.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15668.

[30653] MGC15873 (Accession NP_116309.1) is another GAM189 target gene, herein designated TARGET GENE. MGC15873 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC15873, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC15873 BINDING SITE, designated SEQ ID:2894, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30654] Another function of GAM189 is therefore inhibition of MGC15873 (Accession NP_116309.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15873.

[30655] MGC1842 (Accession XP_037797.2) is another GAM189 target gene, herein designated TARGET GENE. MGC1842 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC1842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC1842 BINDING SITE, designated SEQ ID:15046, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30656] Another function of GAM189 is therefore inhibition of MGC1842 (Accession XP_037797.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC1842.

[30657] MGC21675 (Accession NP_443093.1) is another GAM189 target gene, herein designated TARGET GENE. MGC21675 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC21675, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC21675 BINDING SITE, designated SEQ ID:16916, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30658] Another function of GAM189 is therefore inhibition of MGC21675 (Accession NP_443093.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21675.

[30659] MGC21738 (Accession NP_659481.1) is another GAM189 target gene, herein designated TARGET GENE. MGC21738 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC21738, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC21738 BINDING SITE, designated SEQ ID:8134, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30660] Another function of GAM189 is therefore inhibition of MGC21738 (Accession NP_659481.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21738.

[30661] MGC2306 (Accession NP_002041.2) is another GAM189 target gene, herein designated TARGET GENE. MGC2306 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2306, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2306 BINDING SITE, designated SEQ ID:7160, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30662] Another function of GAM189 is therefore inhibition of MGC2306 (Accession NP_002041.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2306.

[30663] MGC2474 (Accession NP_076420.1) is another GAM189

target gene, herein designated TARGET GENE. MGC2474 BINDING SITE1 and MGC2474 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC2474, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2474 BINDING SITE1 and MGC2474 BINDING SITE2, designated SEQ ID:7797 and SEQ ID:18665 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30664] Another function of GAM189 is therefore inhibition of MGC2474 (Accession NP_076420.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2474.

[30665] MGC2477 (Accession NP_077004.1) is another GAM189 target gene, herein designated TARGET GENE. MGC2477 BINDING SITE1 through MGC2477 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by MGC2477, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of MGC2477 BINDING SITE1 through MGC2477 BINDING SITE3, designated SEQ ID:8610, SEQ ID:19729 and SEQ ID:5609 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30666] Another function of GAM189 is therefore inhibition of MGC2477 (Accession NP_077004.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2477.

[30667] MGC2603 (Accession NP_076942.1) is another GAM189 target gene, herein designated TARGET GENE. MGC2603 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2603 BINDING SITE, designated SEQ ID:5845, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30668] Another function of GAM189 is therefore inhibition of MGC2603 (Accession NP_076942.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MGC2603.

[30669] MGC2718 (Accession NP_076972.2) is another GAM189 target gene, herein designated TARGET GENE. MGC2718 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2718, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2718 BINDING SITE, designated SEQ ID:3976, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30670] Another function of GAM189 is therefore inhibition of MGC2718 (Accession NP_076972.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2718.

[30671] MGC27345 (Accession XP_300964.1) is another GAM189 target gene, herein designated TARGET GENE. MGC27345 BINDING SITE1 and MGC27345 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MGC27345, corresponding to target binding sites such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC27345 BINDING SITE1 and MGC27345 BINDING SITE2, designated SEQ ID:19385 and SEQ ID:18352 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30672] Another function of GAM189 is therefore inhibition of MGC27345 (Accession XP_300964.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC27345.

[30673] MGC29891 (Accession NP_653219.1) is another GAM189 target gene, herein designated TARGET GENE. MGC29891 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC29891, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC29891 BINDING SITE, designated SEQ ID:14858, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30674] Another function of GAM189 is therefore inhibition of MGC29891 (Accession NP_653219.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29891.

[30675] MGC29898 (Accession NP_659485.1) is another GAM189 target gene, herein designated TARGET GENE. MGC29898 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC29898, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC29898 BINDING SITE, designated SEQ ID:16672, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30676] Another function of GAM189 is therefore inhibition of MGC29898 (Accession NP_659485.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29898.

[30677] MGC3113 (Accession NP_076940.1) is another GAM189 target gene, herein designated TARGET GENE. MGC3113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3113, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3113 BINDING SITE, designated SEQ ID:10136, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30678] Another function of GAM189 is therefore inhibition of MGC3113 (Accession NP_076940.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3113.

[30679] MGC3207 (Accession NP_115661.1) is another GAM189 target gene, herein designated TARGET GENE. MGC3207 BINDING SITE1 and MGC3207 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC3207, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3207 BINDING SITE1 and MGC3207 BINDING SITE2, designated SEQ ID:5157 and SEQ ID:13812 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30680] Another function of GAM189 is therefore inhibition of

MGC3207 (Accession NP_115661.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3207.

[30681] MGC3329 (Accession NP_076991.2) is another GAM189 target gene, herein designated TARGET GENE. MGC3329 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3329 BINDING SITE, designated SEQ ID:4477, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30682] Another function of GAM189 is therefore inhibition of MGC3329 (Accession NP_076991.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3329.

[30683] MGC33637 (Accession NP_689809.1) is another GAM189 target gene, herein designated TARGET GENE. MGC33637 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC33637, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC33637 BINDING SITE, designated SEQ ID:12069, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30684] Another function of GAM189 is therefore inhibition of MGC33637 (Accession NP_689809.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33637.

[30685] MGC33887 (Accession NP_659473.1) is another GAM189 target gene, herein designated TARGET GENE. MGC33887 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC33887, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC33887 BINDING SITE, designated SEQ ID:8724, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30686] Another function of GAM189 is therefore inhibition of MGC33887 (Accession NP_659473.1) . Accordingly, utili-

ties of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33887.

[30687] MGC34034 (Accession NP_694956.1) is another GAM189 target gene, herein designated TARGET GENE. MGC34034 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC34034, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34034 BINDING SITE, designated SEQ ID:9529, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30688] Another function of GAM189 is therefore inhibition of MGC34034 (Accession NP_694956.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34034.

[30689] MGC34079 (Accession NP_689688.1) is another GAM189 target gene, herein designated TARGET GENE. MGC34079 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC34079, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34079 BINDING SITE, designated SEQ ID:19817, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30690] Another function of GAM189 is therefore inhibition of MGC34079 (Accession NP_689688.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34079.

[30691] MGC34132 (Accession XP_291029.1) is another GAM189 target gene, herein designated TARGET GENE. MGC34132 BINDING SITE1 and MGC34132 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC34132, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34132 BINDING SITE1 and MGC34132 BINDING SITE2, designated SEQ ID:9087 and SEQ ID:8232 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30692] Another function of GAM189 is therefore inhibition of

MGC34132 (Accession XP_291029.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34132.

[30693] MGC35136 (Accession NP_689640.1) is another GAM189 target gene, herein designated TARGET GENE. MGC35136 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC35136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35136 BINDING SITE, designated SEQ ID:8535, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30694] Another function of GAM189 is therefore inhibition of MGC35136 (Accession NP_689640.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35136.

[30695] MGC35440 (Accession NP_694952.1) is another GAM189 target gene, herein designated TARGET GENE. MGC35440 BINDING SITE1 and MGC35440 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by MGC35440, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35440 BINDING SITE1 and MGC35440 BINDING SITE2, designated SEQ ID:7378 and SEQ ID:6886 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30696] Another function of GAM189 is therefore inhibition of MGC35440 (Accession NP_694952.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35440.

[30697] MGC35468 (Accession NP_694976.1) is another GAM189 target gene, herein designated TARGET GENE. MGC35468 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35468, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35468 BINDING SITE, designated SEQ ID:7484, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30698] Another function of GAM189 is therefore inhibition of MGC35468 (Accession NP_694976.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35468.

[30699] MGC35521 (Accession NP_659502.1) is another GAM189 target gene, herein designated TARGET GENE. MGC35521 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35521, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35521 BINDING SITE, designated SEQ ID:18741, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30700] Another function of GAM189 is therefore inhibition of MGC35521 (Accession NP_659502.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35521.

[30701] MGC3771 (Accession NP_112232.1) is another GAM189 target gene, herein designated TARGET GENE. MGC3771 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by MGC3771, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3771 BINDING SITE, designated SEQ ID:3231, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30702] Another function of GAM189 is therefore inhibition of MGC3771 (Accession NP_112232.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3771.

[30703] MGC39320 (Accession NP_689642.2) is another GAM189 target gene, herein designated TARGET GENE. MGC39320 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC39320, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC39320 BINDING SITE, designated SEQ ID:13428, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30704] Another function of GAM189 is therefore inhibition of

MGC39320 (Accession NP_689642.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC39320.

[30705] MGC40157 (Accession NP_689563.1) is another GAM189 target gene, herein designated TARGET GENE. MGC40157 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC40157, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40157 BINDING SITE, designated SEQ ID:10743, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30706] Another function of GAM189 is therefore inhibition of MGC40157 (Accession NP_689563.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40157.

[30707] MGC40168 (Accession NP_714920.1) is another GAM189 target gene, herein designated TARGET GENE. MGC40168 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC40168, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40168 BINDING SITE, designated SEQ ID:7220, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30708] Another function of GAM189 is therefore inhibition of MGC40168 (Accession NP_714920.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40168.

[30709] MGC40579 (Accession NP_689989.1) is another GAM189 target gene, herein designated TARGET GENE. MGC40579 BINDING SITE1 and MGC40579 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC40579, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40579 BINDING SITE1 and MGC40579 BINDING SITE2, designated SEQ ID:19220 and SEQ ID:16218 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30710] Another function of GAM189 is therefore inhibition of MGC40579 (Accession NP_689989.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40579.

[30711] MGC4248 (Accession NP_115709.2) is another GAM189 target gene, herein designated TARGET GENE. MGC4248 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC4248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4248 BINDING SITE, designated SEQ ID:3338, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30712] Another function of GAM189 is therefore inhibition of MGC4248 (Accession NP_115709.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4248.

[30713] MGC43122 (Accession NP_775784.1) is another GAM189 target gene, herein designated TARGET GENE. MGC43122 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC43122, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC43122 BINDING SITE, designated SEQ ID:12783, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30714] Another function of GAM189 is therefore inhibition of MGC43122 (Accession NP_775784.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC43122.

[30715] MGC50337 (Accession NP_848604.1) is another GAM189 target gene, herein designated TARGET GENE. MGC50337 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC50337, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC50337 BINDING SITE, designated SEQ ID:2959, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30716] Another function of GAM189 is therefore inhibition of

MGC50337 (Accession NP_848604.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC50337.

[30717] MGC50452 (Accession NP_775733.1) is another GAM189 target gene, herein designated TARGET GENE. MGC50452 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC50452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC50452 BINDING SITE, designated SEQ ID:16867, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30718] Another function of GAM189 is therefore inhibition of MGC50452 (Accession NP_775733.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC50452.

[30719] MGC50559 (Accession NP_776163.1) is another GAM189 target gene, herein designated TARGET GENE. MGC50559 BINDING SITE1 and MGC50559 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by MGC50559, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC50559 BINDING SITE1 and MGC50559 BINDING SITE2, designated SEQ ID:11296 and SEQ ID:15151 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30720] Another function of GAM189 is therefore inhibition of MGC50559 (Accession NP_776163.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC50559.

[30721] MGC9912 (Accession NP_542395.1) is another GAM189 target gene, herein designated TARGET GENE. MGC9912 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC9912, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC9912 BINDING SITE, designated SEQ ID:12221, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30722] Another function of GAM189 is therefore inhibition of MGC9912 (Accession NP_542395.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC9912.

[30723] MGRN1 (Accession XP_048119.4) is another GAM189 target gene, herein designated TARGET GENE. MGRN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGRN1 BINDING SITE, designated SEQ ID:16616, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30724] Another function of GAM189 is therefore inhibition of MGRN1 (Accession XP_048119.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGRN1.

[30725] Mhc class ii transactivator (MHC2TA, Accession NP_000237.1) is another GAM189 target gene, herein designated TARGET GENE. MHC2TA BINDING SITE1 through MHC2TA BINDING SITE3 are target binding sites

found in untranslated regions of mRNA encoded by MHC2TA, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MHC2TA BINDING SITE1 through MHC2TA BINDING SITE3, designated SEQ ID:2053, SEQ ID:783 and SEQ ID:922 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30726] Another function of GAM189 is therefore inhibition of Mhc class ii transactivator (MHC2TA, Accession NP_000237.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MHC2TA.

[30727] MIRAB13 (Accession NP_203744.1) is another GAM189 target gene, herein designated TARGET GENE. MIRAB13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MIRAB13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIRAB13 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM189

RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30728] Another function of GAM189 is therefore inhibition of MIRAB13 (Accession NP_203744.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIRAB13.

[30729] MIRAB13 (Accession XP_039236.6) is another GAM189 target gene, herein designated TARGET GENE. MIRAB13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MIRAB13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIRAB13 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30730] Another function of GAM189 is therefore inhibition of MIRAB13 (Accession XP_039236.6) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIRAB13.

[30731] Makorin, ring finger protein, 4 (MKRN4, Accession NP_110384.1) is another GAM189 target gene, herein designated TARGET GENE. MKRN4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MKRN4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MKRN4 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30732] Another function of GAM189 is therefore inhibition of Makorin, ring finger protein, 4 (MKRN4, Accession NP_110384.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKRN4.

[30733] Melan-a (MLANA, Accession NP_005502.1) is another GAM189 target gene, herein designated TARGET GENE. MLANA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MLANA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of MLANA BINDING SITE, designated SEQ ID:13029, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30734] Another function of GAM189 is therefore inhibition of Melan-a (MLANA, Accession NP_005502.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLANA.

[30735] Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_055981.1) is another GAM189 target gene, herein designated TARGET GENE. MLC1 BINDING SITE1 and MLC1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MLC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLC1 BINDING SITE1 and MLC1 BINDING SITE2, designated SEQ ID:14833 and SEQ ID:19859 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30736] Another function of GAM189 is therefore inhibition of Megalencephalic leukoencephalopathy with subcortical

cysts 1 (MLC1, Accession NP_055981.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLC1.

[30737] Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_055981.1) is another GAM189 target gene, herein designated TARGET GENE. MLC1 BINDING SITE1 and MLC1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MLC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLC1 BINDING SITE1 and MLC1 BINDING SITE2, designated SEQ ID:19859 and SEQ ID:19859 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30738] Another function of GAM189 is therefore inhibition of Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_055981.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLC1.

[30739] Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_055981.1) is another GAM189 target gene, herein designated TARGET GENE. MLC1 BINDING SITE1 and MLC1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MLC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLC1 BINDING SITE1 and MLC1 BINDING SITE2, designated SEQ ID:19859 and SEQ ID:14833 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30740] Another function of GAM189 is therefore inhibition of Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_055981.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLC1.

[30741] Melanoma-derived leucine zipper, extra-nuclear factor (MLZE, Accession NP_113603.1) is another GAM189 target gene, herein designated TARGET GENE. MLZE BINDING SITE is a target binding site found in the 5` untranslated

region of mRNA encoded by MLZE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLZE BINDING SITE, designated SEQ ID:9728, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30742] Another function of GAM189 is therefore inhibition of Melanoma-derived leucine zipper, extra-nuclear factor (MLZE, Accession NP_113603.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLZE.

[30743] Matrix metalloproteinase-like 1 (MMPL1, Accession NP_004133.1) is another GAM189 target gene, herein designated TARGET GENE. MMPL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MMPL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MMPL1 BINDING SITE, designated SEQ ID:4374, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30744] Another function of GAM189 is therefore inhibition of Ma-

trix metalloproteinase-like 1 (MMPL1, Accession NP_004133.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMPL1.

[30745] Modulator of apoptosis 1 (MOAP1, Accession NP_071434.2) is another GAM189 target gene, herein designated TARGET GENE. MOAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MOAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MOAP1 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30746] Another function of GAM189 is therefore inhibition of Modulator of apoptosis 1 (MOAP1, Accession NP_071434.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOAP1.

[30747] moblak (Accession NP_570719.1) is another GAM189 target gene, herein designated TARGET GENE. moblak BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by moblak, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of moblak BINDING SITE, designated SEQ ID:19657, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30748] Another function of GAM189 is therefore inhibition of moblak (Accession NP_570719.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with moblak.

[30749] Molybdenum cofactor synthesis 3 (MOCS3, Accession NP_055299.1) is another GAM189 target gene, herein designated TARGET GENE. MOCS3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MOCS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MOCS3 BINDING SITE, designated SEQ ID:12064, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30750] Another function of GAM189 is therefore inhibition of Molybdenum cofactor synthesis 3 (MOCS3, Accession

NP_055299.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOCS3.

[30751] Myeloproliferative leukemia virus oncogene (MPL, Accession NP_005364.1) is another GAM189 target gene, herein designated TARGET GENE. MPL BINDING SITE1 and MPL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MPL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPL BINDING SITE1 and MPL BINDING SITE2, designated SEQ ID:11185 and SEQ ID:16608 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30752] Another function of GAM189 is therefore inhibition of Myeloproliferative leukemia virus oncogene (MPL, Accession NP_005364.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPL.

[30753] Mitochondrial ribosomal protein l35 (MRPL35, Accession NP_057706.2) is another GAM189 target gene, herein designated TARGET GENE. MRPL35 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL35, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL35 BINDING SITE, designated SEQ ID:9545, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30754] Another function of GAM189 is therefore inhibition of Mitochondrial ribosomal protein l35 (MRPL35, Accession NP_057706.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL35.

[30755] Mitochondrial ribosomal protein l44 (MRPL44, Accession NP_075066.1) is another GAM189 target gene, herein designated TARGET GENE. MRPL44 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPL44, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL44 BINDING SITE, designated SEQ ID:14596, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA,

also designated SEQ ID:246.

[30756] Another function of GAM189 is therefore inhibition of Mitochondrial ribosomal protein l44 (MRPL44, Accession NP_075066.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL44.

[30757] Mitochondrial ribosomal protein l49 (MRPL49, Accession NP_004918.1) is another GAM189 target gene, herein designated TARGET GENE. MRPL49 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPL49, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL49 BINDING SITE, designated SEQ ID:5438, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30758] Another function of GAM189 is therefore inhibition of Mitochondrial ribosomal protein l49 (MRPL49, Accession NP_004918.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL49.

[30759] Mitochondrial ribosomal protein s27 (MRPS27, Accession

NP_055899.1) is another GAM189 target gene, herein designated TARGET GENE. MRPS27 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPS27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPS27 BINDING SITE, designated SEQ ID:4179, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30760] Another function of GAM189 is therefore inhibition of Mitochondrial ribosomal protein s27 (MRPS27, Accession NP_055899.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS27.

[30761] MSTP028 (Accession NP_114160.1) is another GAM189 target gene, herein designated TARGET GENE. MSTP028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MSTP028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MSTP028 BINDING SITE, designated SEQ ID:12951, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30762] Another function of GAM189 is therefore inhibition of MSTP028 (Accession NP_114160.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSTP028.

[30763] MTH2 (Accession NP_060753.1) is another GAM189 target gene, herein designated TARGET GENE. MTH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTH2 BINDING SITE, designated SEQ ID:15874, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30764] Another function of GAM189 is therefore inhibition of MTH2 (Accession NP_060753.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTH2.

[30765] V-myc myelocytomatosis viral oncogene homolog 2 (avian) (MYCL2, Accession NP_005368.1) is another

GAM189 target gene, herein designated TARGET GENE. MYCL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYCL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYCL2 BINDING SITE, designated SEQ ID:16868, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30766] Another function of GAM189 is therefore inhibition of V-myc myelocytomatosis viral oncogene homolog 2 (avian) (MYCL2, Accession NP_005368.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYCL2.

[30767] MYLC2PL (Accession NP_612412.1) is another GAM189 target gene, herein designated TARGET GENE. MYLC2PL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MYLC2PL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYLC2PL BINDING SITE, designated SEQ ID:3580, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[30768] Another function of GAM189 is therefore inhibition of MYLC2PL (Accession NP_612412.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLC2PL.

[30769] Myosin 5c (MYO5C, Accession NP_061198.1) is another GAM189 target gene, herein designated TARGET GENE. MYO5C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYO5C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYO5C BINDING SITE, designated SEQ ID:4306, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30770] Another function of GAM189 is therefore inhibition of Myosin 5c (MYO5C, Accession NP_061198.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYO5C.

[30771] NACT (Accession NP_808218.1) is another GAM189 target gene, herein designated TARGET GENE. NACT BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NACT BINDING SITE, designated SEQ ID:19968, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30772] Another function of GAM189 is therefore inhibition of NACT (Accession NP_808218.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NACT.

[30773] Nanog (Accession NP_079141.1) is another GAM189 target gene, herein designated TARGET GENE. Nanog BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Nanog, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Nanog BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30774] Another function of GAM189 is therefore inhibition of

Nanog (Accession NP_079141.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Nanog.

[30775] NCAG1 (Accession NP_115536.1) is another GAM189 target gene, herein designated TARGET GENE. NCAG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCAG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCAG1 BINDING SITE, designated SEQ ID:3766, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30776] Another function of GAM189 is therefore inhibition of NCAG1 (Accession NP_115536.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCAG1.

[30777] Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1) is another GAM189 target gene, herein designated TARGET GENE. NCOA6 BINDING SITE1 and NCOA6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCOA6, corresponding to target binding sites such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE1 and NCOA6 BINDING SITE2, designated SEQ ID:19446 and SEQ ID:12826 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30778] Another function of GAM189 is therefore inhibition of Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1), a gene which activates gene transcription through ligand- dependent association with coactivators. and therefore may be associated with Breast cancer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Breast cancer., and of other diseases and clinical conditions associated with NCOA6.

[30779] The function of NCOA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NP_079107.5) is another GAM189 target gene, herein designated TARGET GENE. NCOA6IP BINDING SITE1 and NCOA6IP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCOA6IP, corresponding to target

binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6IP BINDING SITE1 and NCOA6IP BINDING SITE2, designated SEQ ID:10534 and SEQ ID:8841 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30780] Another function of GAM189 is therefore inhibition of Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NP_079107.5) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6IP.

[30781] NDP52 (Accession NP_005822.1) is another GAM189 target gene, herein designated TARGET GENE. NDP52 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDP52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDP52 BINDING SITE, designated SEQ ID:15337, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30782] Another function of GAM189 is therefore inhibition of

NDP52 (Accession NP_005822.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDP52.

[30783] Ndrg family member 3 (NDRG3, Accession NP_114402.1) is another GAM189 target gene, herein designated TARGET GENE. NDRG3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NDRG3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDRG3 BINDING SITE, designated SEQ ID:15102, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30784] Another function of GAM189 is therefore inhibition of Ndrg family member 3 (NDRG3, Accession NP_114402.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG3.

[30785] Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) is another GAM189 target gene, herein designated TARGET GENE. NDUFC2 BINDING SITE is a target binding site found

in the 3` untranslated region of mRNA encoded by NDUFC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDUFC2 BINDING SITE, designated SEQ ID:10192, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30786] Another function of GAM189 is therefore inhibition of Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDUFC2.

[30787] Sialidase 3 (membrane sialidase) (NEU3, Accession NP_006647.2) is another GAM189 target gene, herein designated TARGET GENE. NEU3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NEU3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEU3 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM189

RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30788] Another function of GAM189 is therefore inhibition of Sialidase 3 (membrane sialidase) (NEU3, Accession NP_006647.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEU3.

[30789] Neurofibromin 2 (bilateral acoustic neuroma) (NF2, Accession NP_057502.1) is another GAM189 target gene, herein designated TARGET GENE. NF2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NF2 BINDING SITE, designated SEQ ID:9169, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30790] Another function of GAM189 is therefore inhibition of Neurofibromin 2 (bilateral acoustic neuroma) (NF2, Accession NP_057502.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NF2.

[30791] Non-pou domain containing, octamer-binding (NONO, Accession NP_031389.2) is another GAM189 target gene, herein designated TARGET GENE. NONO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NONO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NONO BINDING SITE, designated SEQ ID:17960, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30792] Another function of GAM189 is therefore inhibition of Non-pou domain containing, octamer-binding (NONO, Accession NP_031389.2), a gene which is a nuclear protein which contains RNA recognition motifs. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NONO.

[30793] The function of NONO has been established by previous studies. Dong et al. (1993) purified and cloned the cDNA of HeLa cell p54nrb, a nuclear protein with 2 RNA recognition motifs and extensive homology to human splicing factor PSF and Drosophila NONA/BJ6. Brown et al. (1997)

examined the expression of 33 X- linked genes in 8 mouse/human somatic cell hybrids that contained either the human active (3 hybrids) or inactive (5 hybrids) X chromosome. They found that the p54nrb gene was expressed only in those hybrids with the active human X. Using a megabase scale from pter to qter devised by Nelson et al. (1995), they noted that the approximate physical position of the gene was 70 Mb from pter. Brown et al. (1997) placed it in almost exactly the same position as the CCG1 gene (TAF2A; 313650), which had been mapped to Xq13- q27, and approximately 2 Mb proximal to PHKA1 (OMIM Ref. No. 311870), which had been mapped to Xq13. Thus, Xq13 is the likely location. The AFX1 gene (OMIM Ref. No. 300033) and the NRB54 gene map to a yeast artificial chromosome (YAC) contig of Xq13.1 that harbors the X- linked dystonia- parkinsonism locus DYT3 (OMIM Ref. No. 314250). Peters et al. (1997) found that the AFX1 gene is composed of 3 exons with most of exon 3 being untranslated. The NRB54 gene is made up of 12 exons ranging in size from 40 to 1,227 bp. The start codon is in exon 3 and the stop codon in exon 12. Both genes are expressed in the brain, among other tissues. Peters et al. (1997) excluded both genes as candidates of

DYT3 by sequencing of the exons and the flanking intronic sequences in a patient and a control, and by Northern blot analysis.

[30794]

[30795] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30796] Brown, C. J.; Carrel, L.; Willard, H. F. : Expression of genes from the human active and inactive X chromosomes. Am. J. Hum. Genet. 60: 1333- 1343, 1997. ; and

[30797] Peters, U.; Haberhausen, G.; Kostrzewa, M.; Nolte, D.; Muller, U. : AFX1 and p54(nrb): fine mapping, genomic structure, and exclusion as candidate genes of X- linked dystonia parkinsonism.

[30798] Further studies establishing the function and utilities of NONO are found in John Hopkins OMIM database record ID 300084, and in cited publications listed in Table 5, which are hereby incorporated by reference.NOSIP (Accession NP_057037.1) is another GAM189 target gene, herein designated TARGET GENE. NOSIP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NOSIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOSIP BINDING SITE, designated SEQ ID:7311, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30799] Another function of GAM189 is therefore inhibition of NOSIP (Accession NP_057037.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOSIP.

[30800] Neuronal pentraxin receptor (NPTXR, Accession NP_055108.2) is another GAM189 target gene, herein designated TARGET GENE. NPTXR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NPTXR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE, designated SEQ ID:5189, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30801] Another function of GAM189 is therefore inhibition of Neuronal pentraxin receptor (NPTXR, Accession NP_055108.2) . Accordingly, utilities of GAM189 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR.

[30802] Neuronal pentraxin receptor (NPTXR, Accession NP_478058.1) is another GAM189 target gene, herein designated TARGET GENE. NPTXR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NPTXR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE, designated SEQ ID:5189, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30803] Another function of GAM189 is therefore inhibition of Neuronal pentraxin receptor (NPTXR, Accession NP_478058.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR.

[30804] Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1) is another GAM189 target gene, herein designated TARGET GENE. NQO1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NQO1, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NQO1 BINDING SITE, designated SEQ ID:14855, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30805] Another function of GAM189 is therefore inhibition of Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1), a gene which is cytochrome b5 reductase which reduces redox dyes and quinones. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NQO1.

[30806] The function of NQO1 has been established by previous studies. By study of man- mouse somatic cell hybrids, Grzeschik (1980) and Povey et al. (1980) identified a fourth diaphorase locus (DIA4) which segregates with chromosome 16. The regional assignment was 16q12-q22 (smallest region of overlap, SRO). Edwards et al. (1983) showed that the quantitative polymorphism of DIA4 can be attributed to the segregation of a 'low activity' allele. In 4 to 6% of persons there is a DIA4- absent phenotype. In a series of human/hamster hybrids, made

using a human parental cell heterozygous for both phosphoglycolate phosphatase (PGP; 172280) and DIA4, the low activity allele and the PGP(2) allele cosegregated except in 2 of 16 discordant hybrids. DIA4 is presumably the same as NAD(P)H:menadione oxidoreductase (NMOR1). Jaiswal et al. (1988) showed that tetrachlorodibenzo- p-dioxin (TCDD) treatment of a human hepatoblastoma cell produced a 5- fold induction of NMOR1 activity. They isolated several overlapping human NMOR1 cDNAs. Southern blot analysis of human genomic DNA suggested the presence of a single NMOR1 gene approximately 10 kb long. They identified 4 potential polyadenylation sites and found 3 mRNAs in human cells. The 3 mRNA species appeared to be differentially regulated following TCDD treatment. By means of Southern blot analysis of genomic DNA from human/rodent somatic cell hybrids, Jaiswal et al. (1988) demonstrated that the gene is located on chromosome 16, consistent with the assignment of DIA4 to that chromosome. By means of mouse/human somatic cell hybrids containing rearranged chromosome 16 together with multiple probes, Chen et al. (1991) assigned the NMOR1 locus to 16q22.1.

[30807] Animal model experiments lend further support to the

function of NQO1. Radjendirane et al. (1998) generated Nqo1- null mice by targeted disruption. Mice lacking NQO1 gene expression were indistinguishable from wild-type mice. However, Nqo1- null mice exhibited increased toxicity when administered menadione compared with wildtype mice. These results established a role for NQO1 in protection against quinone toxicity.

[30808] It is appreciated that the abovementioned animal model for NQO1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[30809] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30810] Jaiswal, A. K.; McBride, O. W.; Adesnik, M.; Nebert, D. W. : Human dioxin- inducible cytosolic NAD(P)H:menadione oxidoreductase: cDNA sequence and localization of gene to chromosome 16. J. Biol. Chem. 263: 13572- 13578, 1988. ; and

[30811] Radjendirane, V.; Joseph, P.; Lee, Y.- H.; Kimura, S.; Klein-Szanto, A. J. P.; Gonzalez, F. J.; Jaiswal, A. K. : Disruption of the DT diaphorase (NQO1) gene in mice leads to increased me.

[30812] Further studies establishing the function and utilities of NQO1 are found in John Hopkins OMIM database record ID 125860, and in cited publications listed in Table 5, which are hereby incorporated by reference.Nuclear receptor subfamily 2, group e, member 1 (NR2E1, Accession NP_003260.1) is another GAM189 target gene, herein designated TARGET GENE. NR2E1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NR2E1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NR2E1 BINDING SITE, designated SEQ ID:13178, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30813] Another function of GAM189 is therefore inhibition of Nuclear receptor subfamily 2, group e, member 1 (NR2E1, Accession NP_003260.1), a gene which may be required for brain development and be involved in the regulation of retinal development . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR2E1.

[30814] The function of NR2E1 has been established by previous

studies. The product of the Drosophila terminal/gap gene 'tailless' (tll) is expressed in the embryonic brain and is required for brain development in flies. The tll protein is a ligand- activated nuclear receptor- type transcription factor. In 2 discrete subregions of the DNA- binding domain (DBD) that modulate the mode of DNA binding, the tll protein contains changes that distinguish it from all other nuclear receptors. Yu et al. (1994) identified the chick and mouse Tlx genes, encoding the vertebrate tll homolog. The vertebrate Tlx proteins are highly conserved, and both avian and mammalian Tlx contain the distinct tll DBD sequences. In vitro DNA- binding assays demonstrated that Tlx and tll share a target gene specificity that is unique among the nuclear receptor superfamily. Ectopic expression of chick Tlx in fly embryos caused a repression of segmentation comparable to that elicited by tll. In situ hybridization to chick and mouse embryos revealed that Tlx is expressed in the head ectoderm in early embryos. At later stages, cells expressing Tlx are localized in the ventricular zone of the neuroepithelial layer, suggesting that Tlx is involved in transcriptional control in undifferentiated neuroepithelial cells in the anterior regions of the developing vertebrate brain. By searching for genes lo-

cated within the 6q21- q23 region of minimal deletion (RMD) associated with hematologic malignancies, Jackson et al. (1998) identified the human TLX homolog, also called NR2E1. The TLX gene contains 9 exons and spans 24 kb. By a combination of direct sequencing, exon trapping, and library screening, they isolated human TLX cDNAs. The predicted 386- amino acid human protein shares 97% and 99% identity with chick and mouse TLX, respectively. The highest degree of similarity between TLX and Drosophila tll is within the DBDs and the ligand-binding domains (LBDs) of the proteins. Northern blot analysis revealed that the approximately 3.9- kb TLX mRNA is expressed exclusively in brain.

[30815]

[30816] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30817] Jackson, A.; Panayiotidis, P.; Foroni, L. : The human homologue of the Drosophila tailless gene (TLX): characterization and mapping to a region of common deletion in human lymphoid leukemia on chromosome 6q21. Genomics 50: 34- 43, 1998. ; and

[30818] Yu, R. T.; McKeown, M.; Evans, R. M.; Umesono, K. : Rela-

tionship between Drosophila gap gene tailless and a vertebrate nuclear receptor Tlx. Nature 370: 375- 379, 1994.

[30819] Further studies establishing the function and utilities of NR2E1 are found in John Hopkins OMIM database record ID 603849, and in cited publications listed in Table 5, which are hereby incorporated by reference.NRLN1 (Accession NP_660277.1) is another GAM189 target gene, herein designated TARGET GENE. NRLN1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NRLN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRLN1 BINDING SITE, designated SEQ ID:15825, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30820] Another function of GAM189 is therefore inhibition of NRLN1 (Accession NP_660277.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRLN1.

[30821] 5'-nucleotidase, cytosolic ii (NT5C2, Accession NP_036361.1) is another GAM189 target gene, herein designated TARGET GENE. NT5C2 BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by NT5C2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NT5C2 BINDING SITE, designated SEQ ID:4030, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30822] Another function of GAM189 is therefore inhibition of 5'-nucleotidase, cytosolic ii (NT5C2, Accession NP_036361.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NT5C2.

[30823] Nudix (nucleoside diphosphate linked moiety x)-type motif 4 (NUDT4, Accession NP_061967.2) is another GAM189 target gene, herein designated TARGET GENE. NUDT4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NUDT4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUDT4 BINDING SITE, designated SEQ ID:18879, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30824] Another function of GAM189 is therefore inhibition of Nudix (nucleoside diphosphate linked moiety x)-type motif 4 (NUDT4, Accession NP_061967.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUDT4.

[30825] Nuclear mitotic apparatus protein 1 (NUMA1, Accession NP_006176.1) is another GAM189 target gene, herein designated TARGET GENE. NUMA1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NUMA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUMA1 BINDING SITE, designated SEQ ID:14343, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30826] Another function of GAM189 is therefore inhibition of Nuclear mitotic apparatus protein 1 (NUMA1, Accession NP_006176.1), a gene which is nuclear mitotic apparatus protein. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUMA1.

[30827] The function of NUMA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM133.1.NUP43 (Accession NP_078923.2) is another GAM189 target gene, herein designated TARGET GENE. NUP43 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NUP43, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUP43 BINDING SITE, designated SEQ ID:1900, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30828] Another function of GAM189 is therefore inhibition of NUP43 (Accession NP_078923.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUP43.

[30829] Nucleoredoxin (NXN, Accession NP_071908.1) is another GAM189 target gene, herein designated TARGET GENE. NXN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NXN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of NXN BINDING SITE, designated SEQ ID:935, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30830] Another function of GAM189 is therefore inhibition of Nucleoredoxin (NXN, Accession NP_071908.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXN.

[30831] Olfactory receptor, family 51, subfamily e, member 2 (OR51E2, Accession NP_110401.1) is another GAM189 target gene, herein designated TARGET GENE. OR51E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OR51E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OR51E2 BINDING SITE, designated SEQ ID:4096, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30832] Another function of GAM189 is therefore inhibition of Olfactory receptor, family 51, subfamily e, member 2 (OR51E2, Accession NP_110401.1) . Accordingly, utilities

of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OR51E2.

[30833] Origin recognition complex, subunit 1-like (yeast) (ORC1L, Accession NP_004144.1) is another GAM189 target gene, herein designated TARGET GENE. ORC1L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ORC1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ORC1L BINDING SITE, designated SEQ ID:17969, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30834] Another function of GAM189 is therefore inhibition of Origin recognition complex, subunit 1-like (yeast) (ORC1L, Accession NP_004144.1), a gene which may be required for initiation of DNA replication. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ORC1L.

[30835] The function of ORC1L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM136.1.Oxysterol binding protein-like 2 (OSBPL2, Accession NP_055650.1) is another GAM189 target gene, herein designated TARGET GENE. OSBPL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL2 BINDING SITE, designated SEQ ID:7553, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30836] Another function of GAM189 is therefore inhibition of Oxysterol binding protein-like 2 (OSBPL2, Accession NP_055650.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL2.

[30837] Oxysterol binding protein-like 2 (OSBPL2, Accession NP_653081.1) is another GAM189 target gene, herein designated TARGET GENE. OSBPL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates

the complementarity of the nucleotide sequences of OSBPL2 BINDING SITE, designated SEQ ID:7553, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30838] Another function of GAM189 is therefore inhibition of Oxysterol binding protein-like 2 (OSBPL2, Accession NP_653081.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL2.

[30839] Purinergic receptor p2x-like 1, orphan receptor (P2RXL1, Accession NP_005437.1) is another GAM189 target gene, herein designated TARGET GENE. P2RXL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P2RXL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P2RXL1 BINDING SITE, designated SEQ ID:4425, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30840] Another function of GAM189 is therefore inhibition of Purinergic receptor p2x-like 1, orphan receptor (P2RXL1, Accession NP_005437.1) . Accordingly, utilities of

GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RXL1.

[30841] Purinergic receptor p2y, g-protein coupled, 1 (P2RY1, Accession NP_002554.1) is another GAM189 target gene, herein designated TARGET GENE. P2RY1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P2RY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P2RY1 BINDING SITE, designated SEQ ID:8453, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30842] Another function of GAM189 is therefore inhibition of Purinergic receptor p2y, g-protein coupled, 1 (P2RY1, Accession NP_002554.1), a gene which plays an essential role in thrombotic states. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RY1.

[30843] The function of P2RY1 has been established by previous studies. P2 purinoceptors have been broadly classified as P2X receptors (e.g., 600843), which are ATP- gated channels; P2Z receptors, which mediate nonselective pores in

mast cells; and P2Y receptors, a family of G protein- coupled receptors. Based on the recommendation for nomenclature of P2 purinoceptors, the P2Y purinoceptors were numbered in the order of cloning. Ayyanathan et al. (1996) noted that P2Y1, P2Y2 (PR2Y2; 600041), and P2Y3 have been cloned from a variety of species. P2Y1 responds to both ADP and ATP. The P2Y2 receptor cDNA was cloned in the human and this receptor was known as P2U under previous nomenclature. Ayyanathan et al. (1996) cloned the human P2Y1 receptor (P2RY1) and its 2 alternately polyadenylated forms of mRNA. The P2Y1 purinoceptor was also cloned from a human placenta cDNA library by Leon et al. (1996). They found that the gene encodes a 372- amino acid polypeptide. Northern blot analysis revealed 2 transcripts of 4.6 and 7.5 kb which were expressed in many tissues. Using oligonucleotide primers specific for the human P2Y1 purinergic receptor, Ayyanathan et al. (1996) amplified a region from genomic DNA from a panel of mouse/human somatic cell hybrid cell lines and localized the P2Y1 gene to human chromosome 3. By sequence tagged site (STS) mapping utilizing the National Center for Biotechnology Information (NCBI) database, Somers et al. (1997) mapped the

P2RY1 gene between flanking markers D3S1279 and D3S1280 at a position 173 to 174 cM from the most telomeric markers on the short arm of chromosome 3.

[30844] Animal model experiments lend further support to the function of P2RY1. Leon et al. (1999) generated P2Y1-null mice to define the physiologic role of the P2Y1 receptor. These mice were viable with no apparent abnormalities affecting their development, survival, reproduction, or morphology of platelets, and the platelet count in these animals was identical to that of wildtype mice. However, platelets from P2Y1- deficient mice were unable to aggregate in response to usual concentrations of ADP and displayed impaired aggregation to other agonists, while high concentrations of ADP induced platelet aggregation without shape change. In addition, ADP- induced inhibition of adenylyl cyclase still occurred, demonstrating the existence of an ADP receptor distinct from P2Y1. P2Y1- null mice had no spontaneous bleeding tendency but were resistant to thromboembolism induced by intravenous injection of ADP or collagen and adrenaline. Hence, the P2Y1 receptor plays an essential role in thrombotic states and represents a potential target for antithrombotic drugs.

[30845] It is appreciated that the abovementioned animal model for P2RY1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[30846] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30847] Ayyanathan, K.; Webbs, T. E.; Sandhu, A. K.; Athwal, R. S.; Barnard, E. A.; Kunapuli, S. P. : Cloning and chromosomal localization of the human P2Y1 purinoceptor. Biochem. Biophys. Res. Commun. 218: 783- 788, 1996. ; and

[30848] Leon, C.; Hechler, B.; Freund, M.; Eckly, A.; Vial, C.; Ohlmann, P.; Dierich, A.; LeMeur, M.; Cazenave, J.- P.; Gachet, C. : Defective platelet aggregation and increased resistance to thr.

[30849] Further studies establishing the function and utilities of P2RY1 are found in John Hopkins OMIM database record ID 601167, and in cited publications listed in Table 5, which are hereby incorporated by reference.P450RAI-2 (Accession NP_063938.1) is another GAM189 target gene, herein designated TARGET GENE. P450RAI-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P450RAI-2, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P450RAI-2 BINDING SITE, designated SEQ ID:18160, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30850] Another function of GAM189 is therefore inhibition of P450RAI-2 (Accession NP_063938.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P450RAI-2.

[30851] Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS, Accession NP_006443.1) is another GAM189 target gene, herein designated TARGET GENE. PAICS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PAICS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PAICS BINDING SITE, designated SEQ ID:16852, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30852] Another function of GAM189 is therefore inhibition of Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS, Accession NP_006443.1), a gene which is required for purine biosynthesis. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAICS.

[30853] The function of PAICS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) is another GAM189 target gene, herein designated TARGET GENE. PASK BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PASK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PASK BINDING SITE, designated SEQ ID:2769, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30854] Another function of GAM189 is therefore inhibition of Pas domain containing serine/threonine kinase (PASK, Acces-

sion NP_055963.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PASK.

[30855] Protocadherin alpha 9 (PCDHA9, Accession NP_054724.1) is another GAM189 target gene, herein designated TARGET GENE. PCDHA9 BINDING SITE1 and PCDHA9 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PCDHA9, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA9 BINDING SITE1 and PCDHA9 BINDING SITE2, designated SEQ ID:16048 and SEQ ID:10427 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30856] Another function of GAM189 is therefore inhibition of Protocadherin alpha 9 (PCDHA9, Accession NP_054724.1), a gene which is a calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA9.

[30857] The function of PCDHA9 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Protocadherin beta 11 (PCDHB11, Accession NP_061754.1) is another GAM189 target gene, herein designated TARGET GENE. PCDHB11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB11 BINDING SITE, designated SEQ ID:10723, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30858] Another function of GAM189 is therefore inhibition of Protocadherin beta 11 (PCDHB11, Accession NP_061754.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB11.

[30859] Protocadherin beta 16 (PCDHB16, Accession NP_066008.1) is another GAM189 target gene, herein designated TARGET GENE. PCDHB16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB16, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB16 BINDING SITE, designated SEQ ID:4617, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30860] Another function of GAM189 is therefore inhibition of Protocadherin beta 16 (PCDHB16, Accession NP_066008.1), a gene which is a potential calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB16.

[30861] The function of PCDHB16 has been established by previous studies. Cadherins are calcium- dependent cell- cell adhesion molecules that mediate neural cell- cell interactions. Protocadherins constitute a subfamily of nonclassic cadherins. PCDHB16 is a member of the beta cluster of protocadherin genes on 5q31. For specific information on the PCDHB genes, see 604967. Using PCR with degenerate primers to screen melanoma cell lines, Matsuyoshi et al. (1997) obtained a cDNA fragment encoding part of PCDHB16, which they termed ME1. RT- PCR analysis detected expression of ME1 in melanoma cell lines and nor-

mal fibroblast cell lines, but not in a squamous carcinoma cell lines or normal melanocytes, suggesting that ME1 may play a role in the strong cell- cell adhesiveness of melanoma cells.

[30862]

[30863] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30864] Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S. : Identification of novel cadherins expressed in human melanoma cells. J. Invest. Derm. 108: 908- 913, 1997. ; and

[30865] Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz, J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis, T. : Comparative DNA sequence analysis of mouse and.

[30866] Further studies establishing the function and utilities of PCDHB16 are found in John Hopkins OMIM database record ID 606345, and in cited publications listed in Table 5, which are hereby incorporated by reference.Protocadherin beta 9 (PCDHB9, Accession NP_061992.2) is another GAM189 target gene, herein designated TARGET GENE. PCDHB9 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by PCDHB9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB9 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30867] Another function of GAM189 is therefore inhibition of Protocadherin beta 9 (PCDHB9, Accession NP_061992.2), a gene which is a potential calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB9.

[30868] The function of PCDHB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Phosphodiesterase 6b, cgmp-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NP_000274.1) is another GAM189 target gene, herein designated TARGET GENE. PDE6B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDE6B, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDE6B BINDING SITE, designated SEQ ID:936, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30869] Another function of GAM189 is therefore inhibition of Phosphodiesterase 6b, cgmp-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NP_000274.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE6B.

[30870] Platelet derived growth factor c (PDGFC, Accession NP_057289.1) is another GAM189 target gene, herein designated TARGET GENE. PDGFC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDGFC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDGFC BINDING SITE, designated SEQ ID:905, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30871] Another function of GAM189 is therefore inhibition of

Platelet derived growth factor c (PDGFC, Accession NP_057289.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFC.

[30872] Pdz and lim domain 2 (mystique) (PDLIM2, Accession NP_789847.1) is another GAM189 target gene, herein designated TARGET GENE. PDLIM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PDLIM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDLIM2 BINDING SITE, designated SEQ ID:14973, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30873] Another function of GAM189 is therefore inhibition of Pdz and lim domain 2 (mystique) (PDLIM2, Accession NP_789847.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDLIM2.

[30874] Pdz domain containing 1 (PDZK1, Accession NP_002605.2) is another GAM189 target gene, herein designated TARGET GENE. PDZK1 BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by PDZK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDZK1 BINDING SITE, designated SEQ ID:4194, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30875] Another function of GAM189 is therefore inhibition of Pdz domain containing 1 (PDZK1, Accession NP_002605.2), a gene which is a contains PDZ interaction domains, interacts with MAP17, a protein involved in control of cell proliferation. and therefore may be associated with Autosomal dominant hypophosphatemic rickets. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Autosomal dominant hypophosphatemic rickets, and of other diseases and clinical conditions associated with PDZK1.

[30876] The function of PDZK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.PDZRN1 (Accession NP_699202.1) is another GAM189 target gene, herein designated TARGET GENE. PDZRN1 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by PDZRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDZRN1 BINDING SITE, designated SEQ ID:5270, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30877] Another function of GAM189 is therefore inhibition of PDZRN1 (Accession NP_699202.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDZRN1.

[30878] Pellino homolog 1 (drosophila) (PELI1, Accession NP_065702.2) is another GAM189 target gene, herein designated TARGET GENE. PELI1 BINDING SITE1 through PELI1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PELI1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PELI1 BINDING SITE1 through PELI1 BINDING SITE3, designated SEQ ID:7382, SEQ ID:14861 and SEQ ID:5491 respectively, to the nucleotide sequence of GAM189 RNA,

herein designated GAM RNA, also designated SEQ ID:246.

[30879] Another function of GAM189 is therefore inhibition of Pellino homolog 1 (drosophila) (PELI1, Accession NP_065702.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PELI1.

[30880] Period homolog 2 (drosophila) (PER2, Accession NP_073728.1) is another GAM189 target gene, herein designated TARGET GENE. PER2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PER2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PER2 BINDING SITE, designated SEQ ID:19703, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30881] Another function of GAM189 is therefore inhibition of Period homolog 2 (drosophila) (PER2, Accession NP_073728.1), a gene which Period homolog 2; putative circadian clock protein; has a PAS dimerization domain and therefore may be associated with Familial advanced sleep- phase syndrome. Accordingly, utilities of GAM189

include diagnosis, prevention and treatment of Familial advanced sleep- phase syndrome, and of other diseases and clinical conditions associated with PER2.

[30882] The function of PER2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Phosphoribosylformylglycinamidine synthase (fgar amidotransferase) (PFAS, Accession NP_036525.1) is another GAM189 target gene, herein designated TARGET GENE. PFAS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PFAS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PFAS BINDING SITE, designated SEQ ID:16261, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30883] Another function of GAM189 is therefore inhibition of Phosphoribosylformylglycinamidine synthase (fgar amidotransferase) (PFAS, Accession NP_036525.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with PFAS.

[30884] PHAX (Accession NP_115553.1) is another GAM189 target gene, herein designated TARGET GENE. PHAX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PHAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PHAX BINDING SITE, designated SEQ ID:12159, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30885] Another function of GAM189 is therefore inhibition of PHAX (Accession NP_115553.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHAX.

[30886] Polymeric immunoglobulin receptor (PIGR, Accession NP_002635.2) is another GAM189 target gene, herein designated TARGET GENE. PIGR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIGR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIGR BINDING SITE, designated

SEQ ID:11059, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30887] Another function of GAM189 is therefore inhibition of Polymeric immunoglobulin receptor (PIGR, Accession NP_002635.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGR.

[30888] Phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B, Accession NP_002637.2) is another GAM189 target gene, herein designated TARGET GENE. PIK3C2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3C2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3C2B BINDING SITE, designated SEQ ID:10488, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30889] Another function of GAM189 is therefore inhibition of Phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B, Accession NP_002637.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PIK3C2B.

[30890] Phosphoinositide-3-kinase, class 3 (PIK3C3, Accession NP_002638.1) is another GAM189 target gene, herein designated TARGET GENE. PIK3C3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3C3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3C3 BINDING SITE, designated SEQ ID:8874, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30891] Another function of GAM189 is therefore inhibition of Phosphoinositide-3-kinase, class 3 (PIK3C3, Accession NP_002638.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3C3.

[30892] Phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD, Accession NP_005017.2) is another GAM189 target gene, herein designated TARGET GENE. PIK3CD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3CD, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3CD BINDING SITE, designated SEQ ID:9545, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30893] Another function of GAM189 is therefore inhibition of Phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD, Accession NP_005017.2), a gene which regulating cell growth. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3CD.

[30894] The function of PIK3CD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Pbx/knotted 1 homeobox 1 (PKNOX1, Accession NP_004562.2) is another GAM189 target gene, herein designated TARGET GENE. PKNOX1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PKNOX1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PKNOX1 BINDING SITE, designated SEQ ID:8826, to the nucleotide se-

quence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30895] Another function of GAM189 is therefore inhibition of Pbx/knotted 1 homeobox 1 (PKNOX1, Accession NP_004562.2), a gene which may regulate gene expression and control cell differentiation. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKNOX1.

[30896] The function of PKNOX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Phospholipase a2, group vi (cytosolic, calcium-independent) (PLA2G6, Accession NP_003551.1) is another GAM189 target gene, herein designated TARGET GENE. PLA2G6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLA2G6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PLA2G6 BINDING SITE, designated SEQ ID:16143, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ

ID:246.

[30897] Another function of GAM189 is therefore inhibition of Phospholipase a2, group vi (cytosolic, calcium-independent) (PLA2G6, Accession NP_003551.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLA2G6.

[30898] Pro-melanin-concentrating hormone-like 1 (PMCHL1, Accession NP_114093.1) is another GAM189 target gene, herein designated TARGET GENE. PMCHL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMCHL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMCHL1 BINDING SITE, designated SEQ ID:16917, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30899] Another function of GAM189 is therefore inhibition of Pro-melanin-concentrating hormone-like 1 (PMCHL1, Accession NP_114093.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMCHL1.

[30900] Pro-melanin-concentrating hormone-like 2 (PMCHL2, Accession NP_114094.1) is another GAM189 target gene, herein designated TARGET GENE. PMCHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMCHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMCHL2 BINDING SITE, designated SEQ ID:16917, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30901] Another function of GAM189 is therefore inhibition of Pro-melanin-concentrating hormone-like 2 (PMCHL2, Accession NP_114094.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMCHL2.

[30902] PMPCA (Accession NP_055975.1) is another GAM189 target gene, herein designated TARGET GENE. PMPCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMPCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMPCA

BINDING SITE, designated SEQ ID:7640, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30903] Another function of GAM189 is therefore inhibition of PMPCA (Accession NP_055975.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMPCA.

[30904] Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) is another GAM189 target gene, herein designated TARGET GENE. PNMA2 BINDING SITE1 and PNMA2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PNMA2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PNMA2 BINDING SITE1 and PNMA2 BINDING SITE2, designated SEQ ID:17067 and SEQ ID:8006 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30905] Another function of GAM189 is therefore inhibition of Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PNMA2.

[30906] Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) is another GAM189 target gene, herein designated TARGET GENE. POFUT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by POFUT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POFUT1 BINDING SITE, designated SEQ ID:11287, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30907] Another function of GAM189 is therefore inhibition of Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POFUT1.

[30908] Polymerase (dna directed), epsilon 3 (p17 subunit) (POLE3, Accession NP_059139.2) is another GAM189 target gene, herein designated TARGET GENE. POLE3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLE3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLE3 BINDING SITE, designated SEQ ID:6151, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30909] Another function of GAM189 is therefore inhibition of Polymerase (dna directed), epsilon 3 (p17 subunit) (POLE3, Accession NP_059139.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLE3.

[30910] Polymerase (rna) ii (dna directed) polypeptide d (POLR2D, Accession NP_004796.1) is another GAM189 target gene, herein designated TARGET GENE. POLR2D BINDING SITE1 and POLR2D BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by POLR2D, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLR2D BINDING SITE1 and POLR2D BINDING SITE2, designated SEQ ID:5412 and SEQ ID:2798 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30911] Another function of GAM189 is therefore inhibition of

Polymerase (rna) ii (dna directed) polypeptide d (POLR2D, Accession NP_004796.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLR2D.

[30912] Paraoxonase 1 (PON1, Accession NP_000437.3) is another GAM189 target gene, herein designated TARGET GENE. PON1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PON1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PON1 BINDING SITE, designated SEQ ID:2152, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30913] Another function of GAM189 is therefore inhibition of Paraoxonase 1 (PON1, Accession NP_000437.3), a gene which hydrolyzes the toxic metabolites of a variety of organophosphorus insecticides. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PON1.

[30914] The function of PON1 has been established by previous studies. Two factors result in large individual variations in PON serum levels: a substrate- dependent activity poly-

morphism and large individual differences in PON protein levels that are stable over time. Animal model studies indicated that PON activity levels are likely to play a major role in determining sensitivity to several organophosphate insecticides (Clendenning et al., 1996). The arg192 isoform (168820.0001) appears to be a risk factor in coronary artery disease. Serum paraoxonase is an esterase that is associated with high density lipoproteins (HDLs) in the plasma. It is involved in the detoxification of organophosphate insecticides such as parathion and chlorpyrifos. PON1 may also confer protection against coronary artery disease by destroying proinflammatory oxidized lipids present in oxidized low density lipoproteins (LDLs). To study the role of PON1 in vivo, Shih et al. (1998) created PON1- knockout mice by gene targeting. Compared with their wildtype littermates, PON1- deficient mice were extremely sensitive to the toxic effects of chlorpyrifos oxon, the activated form of chlorpyrifos, and were more sensitive to chlorpyrifos itself. HDLs isolated from PON1- deficient mice were unable to prevent LDL oxidation in a cocultured cell model of the artery wall, and both HDLs and LDLs isolated from PON1- knockout mice were more susceptible to oxidation by cocultured cells

than were lipoproteins from wildtype littermates. When fed on a high- fat, high- cholesterol diet, PON1- null mice were more susceptible to atherosclerosis than were their wildtype littermates.

[30915]

[30916] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30917] Clendenning, J. B.; Humbert, R.; Green, E. D.; Wood, C.; Traver, D.; Furlong, C. E. : Structural organization of the human PON1 gene. Genomics 35: 586- 589, 1996. ; and

[30918] Shih, D. M.; Gu, L.; Xia, Y.- R.; Navab, M.; Li, W.- F.; Hama, S.; Castellani, L. W.; Furlong, C. E.; Costa, L. G.; Fogelman, A. M.; Lusis, A. J. : Mice lacking serum paraoxonase are suscepti.

[30919] Further studies establishing the function and utilities of PON1 are found in John Hopkins OMIM database record ID 168820, and in cited publications listed in Table 5, which are hereby incorporated by reference.Pou domain, class 2, associating factor 1 (POU2AF1, Accession NP_006226.1) is another GAM189 target gene, herein designated TARGET GENE. POU2AF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

POU2AF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POU2AF1 BINDING SITE, designated SEQ ID:20135, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30920] Another function of GAM189 is therefore inhibition of Pou domain, class 2, associating factor 1 (POU2AF1, Accession NP_006226.1), a gene which is a transcriptional coactivator that specifically associates with either oct1 or oct2 and therefore may be associated with A form of b- cell leukemia. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of A form of b- cell leukemia, and of other diseases and clinical conditions associated with POU2AF1.

[30921] The function of POU2AF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Pou domain, class 2, transcription factor 3 (POU2F3, Accession NP_055167.1) is another GAM189 target gene, herein designated TARGET GENE. POU2F3 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by POU2F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POU2F3 BINDING SITE, designated SEQ ID:16114, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30922] Another function of GAM189 is therefore inhibition of Pou domain, class 2, transcription factor 3 (POU2F3, Accession NP_055167.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU2F3.

[30923] PP1628 (Accession NP_079477.1) is another GAM189 target gene, herein designated TARGET GENE. PP1628 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PP1628, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP1628 BINDING SITE, designated SEQ ID:10180, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30924] Another function of GAM189 is therefore inhibition of

PP1628 (Accession NP_079477.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1628.

[30925] PP3111 (Accession NP_071439.2) is another GAM189 target gene, herein designated TARGET GENE. PP3111 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PP3111, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP3111 BINDING SITE, designated SEQ ID:10883, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30926] Another function of GAM189 is therefore inhibition of PP3111 (Accession NP_071439.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP3111.

[30927] PP3856 (Accession NP_660202.1) is another GAM189 target gene, herein designated TARGET GENE. PP3856 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PP3856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of PP3856 BINDING SITE, designated SEQ ID:10744, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30928] Another function of GAM189 is therefore inhibition of PP3856 (Accession NP_660202.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP3856.

[30929] Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_803545.1) is another GAM189 target gene, herein designated TARGET GENE. PPAP2C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPAP2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPAP2C BINDING SITE, designated SEQ ID:7299, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30930] Another function of GAM189 is therefore inhibition of Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_803545.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with PPAP2C.

[30931] Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_808211.1) is another GAM189 target gene, herein designated TARGET GENE. PPAP2C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPAP2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPAP2C BINDING SITE, designated SEQ ID:7299, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30932] Another function of GAM189 is therefore inhibition of Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_808211.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPAP2C.

[30933] Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_003703.1) is another GAM189 target gene, herein designated TARGET GENE. PPAP2C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPAP2C, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPAP2C BINDING SITE, designated SEQ ID:7299, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30934] Another function of GAM189 is therefore inhibition of Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_003703.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPAP2C.

[30935] Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690911.1) is another GAM189 target gene, herein designated TARGET GENE. PPEF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPEF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPEF2 BINDING SITE, designated SEQ ID:2954, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30936] Another function of GAM189 is therefore inhibition of Protein phosphatase, ef hand calcium-binding domain 2

(PPEF2, Accession NP_690911.1), a gene which is a homolog of Drosophila rdgC. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPEF2.

[30937] The function of PPEF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690910.1) is another GAM189 target gene, herein designated TARGET GENE. PPEF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPEF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPEF2 BINDING SITE, designated SEQ ID:2954, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30938] Another function of GAM189 is therefore inhibition of Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690910.1), a gene which is a homolog of Drosophila rdgC. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with PPEF2.

[30939] The function of PPEF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_006230.2) is another GAM189 target gene, herein designated TARGET GENE. PPEF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPEF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPEF2 BINDING SITE, designated SEQ ID:2954, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30940] Another function of GAM189 is therefore inhibition of Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_006230.2), a gene which is a homolog of Drosophila rdgC. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPEF2.

[30941] The function of PPEF2 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM66.2.Protein tyrosine phosphatase, receptor type, f polypeptide (ptprf), interacting protein (liprin), alpha 4 (PPFIA4, Accession XP_046751.3) is another GAM189 target gene, herein designated TARGET GENE. PPFIA4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PPFIA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPFIA4 BINDING SITE, designated SEQ ID:16851, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30942] Another function of GAM189 is therefore inhibition of Protein tyrosine phosphatase, receptor type, f polypeptide (ptprf), interacting protein (liprin), alpha 4 (PPFIA4, Accession XP_046751.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPFIA4.

[30943] Ptprf interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1, Accession NP_003613.2) is another GAM189 target gene, herein designated TARGET GENE. PPFIBP1 BINDING SITE1 through PPFIBP1 BINDING SITE3 are target bind-

ing sites found in untranslated regions of multiple transcripts of mRNA encoded by PPFIBP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPFIBP1 BINDING SITE1 through PPFIBP1 BINDING SITE3, designated SEQ ID:12217, SEQ ID:8231 and SEQ ID:10708 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30944] Another function of GAM189 is therefore inhibition of Pt-prf interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1, Accession NP_003613.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPFIBP1.

[30945] Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession NP_005029.1) is another GAM189 target gene, herein designated TARGET GENE. PPID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPID BINDING SITE, designated

SEQ ID:7378, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30946] Another function of GAM189 is therefore inhibition of Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession NP_005029.1), a gene which catalyzes the cis- trans isomerization of proline imidic peptide bonds in oligopeptides. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPID.

[30947] The function of PPID and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) is another GAM189 target gene, herein designated TARGET GENE. PPIL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPIL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPIL2 BINDING SITE, designated SEQ ID:13122, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30948] Another function of GAM189 is therefore inhibition of Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPIL2.

[30949] Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_115288.1) is another GAM189 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE, designated SEQ ID:3861, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30950] Another function of GAM189 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_115288.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[30951] Protein phosphatase 1, regulatory (inhibitor) subunit 12b

(PPP1R12B, Accession NP_002472.1) is another GAM189 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE, designated SEQ ID:3861, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30952] Another function of GAM189 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[30953] Protein kinase, interferon-inducible double stranded rna dependent (PRKR, Accession NP_002750.1) is another GAM189 target gene, herein designated TARGET GENE. PRKR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of PRKR BINDING SITE, designated SEQ ID:4790, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30954] Another function of GAM189 is therefore inhibition of Protein kinase, interferon-inducible double stranded rna dependent (PRKR, Accession NP_002750.1), a gene which catalyze the phosphorylation of the alpha subunit of eif2. and therefore may be associated with Huntington's disease. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Huntington's disease, and of other diseases and clinical conditions associated with PRKR.

[30955] The function of PRKR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Protein kinase, lysine deficient 3 (PRKWNK3, Accession NP_065973.1) is another GAM189 target gene, herein designated TARGET GENE. PRKWNK3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKWNK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of PRKWNK3 BINDING SITE, designated SEQ ID:14862, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30956] Another function of GAM189 is therefore inhibition of Protein kinase, lysine deficient 3 (PRKWNK3, Accession NP_065973.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKWNK3.

[30957] Prion protein 2 (dublet) (PRND, Accession NP_036541.1) is another GAM189 target gene, herein designated TARGET GENE. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, designated SEQ ID:1539 and SEQ ID:4170 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30958] Another function of GAM189 is therefore inhibition of Prion protein 2 (dublet) (PRND, Accession NP_036541.1), a

gene which is similar to prion protein PRNP. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRND.

[30959] The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.PRO0297 (Accession NP_054800.1) is another GAM189 target gene, herein designated TARGET GENE. PRO0297 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0297, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0297 BINDING SITE, designated SEQ ID:10574, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30960] Another function of GAM189 is therefore inhibition of PRO0297 (Accession NP_054800.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0297.

[30961] PRO0365 (Accession NP_054845.1) is another GAM189 target gene, herein designated TARGET GENE. PRO0365 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0365, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0365 BINDING SITE, designated SEQ ID:18148, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30962] Another function of GAM189 is therefore inhibition of PRO0365 (Accession NP_054845.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0365.

[30963] PRO1048 (Accession NP_060967.1) is another GAM189 target gene, herein designated TARGET GENE. PRO1048 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO1048, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO1048 BINDING SITE, designated SEQ ID:12596, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30964] Another function of GAM189 is therefore inhibition of PRO1048 (Accession NP_060967.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1048.

[30965] PRO2730 (Accession NP_079498.1) is another GAM189 target gene, herein designated TARGET GENE. PRO2730 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO2730, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO2730 BINDING SITE, designated SEQ ID:2048, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30966] Another function of GAM189 is therefore inhibition of PRO2730 (Accession NP_079498.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2730.

[30967] PROM2 (Accession NP_653308.1) is another GAM189 tar-

get gene, herein designated TARGET GENE. PROM2 BINDING SITE1 and PROM2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PROM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PROM2 BINDING SITE1 and PROM2 BINDING SITE2, designated SEQ ID:2147 and SEQ ID:13176 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30968] Another function of GAM189 is therefore inhibition of PROM2 (Accession NP_653308.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROM2.

[30969] Prp31 pre-mrna processing factor 31 homolog (yeast) (PRPF31, Accession NP_056444.1) is another GAM189 target gene, herein designated TARGET GENE. PRPF31 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRPF31, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRPF31 BINDING SITE, designated SEQ ID:11313, to the nucleotide

sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30970] Another function of GAM189 is therefore inhibition of Prp31 pre-mrna processing factor 31 homolog (yeast) (PRPF31, Accession NP_056444.1), a gene which is likely to be involved in pre- mRNA splicing and therefore is associated with Retinitis pigmentosa. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Retinitis pigmentosa, and of other diseases and clinical conditions associated with PRPF31.

[30971] The function of PRPF31 has been established by previous studies. Using a positional cloning approach supported by bioinformatics, Vithana et al. (2001) narrowed the genomic region of the autosomal dominant retinitis pigmentosa- 11 locus (RP11; 600138) to an approximately 600-kb region between markers D19S927 and D19S781.2 on 19q13.4. Within this region, they identified the PRPF31 gene, a homolog of the S. cerevisiae pre- mRNA splicing gene Prp31 (Weidenhammer et al., 1996). PRPF31 encodes a putative 499- amino acid protein that is 20% and 38% identical to its S. cerevisiae and S. pombe homologs, respectively. The level of sequence identity to the yeast genes indicates that PRPF31 is likely to be involved in pre-

mRNA splicing. PRPF31 and its homologs all contain a region homologous to Nop, a putative snoRNA- binding domain. In yeast Prp31, the Nop domain is thought to mediate protein- RNA interactions required for spliceosome assembly. PRPF31 also has putative nuclear localization signals in its medial region, providing further evidence for a nuclear role.

[30972]

[30973] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[30974] Al- Maghtheh, M.; Vithana, E.; Tarttelin, E.; Jay, M.; Evans, K.; Moore, T.; Bhattacharya, S.; Inglehearn, C. F. : Evidence for a major retinitis pigmentosa locus on 19q13.4 (RP11), and association with a unique bimodal expressivity phenotype. Am. J. Hum. Genet. 59: 864- 871, 1996. ; and

[30975] Vithana, E. N.; Abu- Safieh, L.; Allen, M. J.; Carey, A.; Papaioannou, M.; Chakarova, C.; Al- Maghtheh, M.; Ebenezer, N. D.; Willis, C.; Moore, A. T.; Bird, A. C.; Hunt, D. M.; Bhattachary.

[30976] Further studies establishing the function and utilities of PRPF31 are found in John Hopkins OMIM database record ID 606419, and in cited publications listed in Table 5,

which are hereby incorporated by reference.Proteasome (prosome, macropain) 26s subunit, non-atpase, 9 (PSMD9, Accession NP_002804.2) is another GAM189 target gene, herein designated TARGET GENE. PSMD9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSMD9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSMD9 BINDING SITE, designated SEQ ID:17758, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30977] Another function of GAM189 is therefore inhibition of Proteasome (prosome, macropain) 26s subunit, non-atpase, 9 (PSMD9, Accession NP_002804.2), a gene which acts as a regulatory subunit of the 26 proteasome. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSMD9.

[30978] The function of PSMD9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Phosphoserine phosphatase (PSPH, Accession

NP_004568.1) is another GAM189 target gene, herein designated TARGET GENE. PSPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSPH BINDING SITE, designated SEQ ID:15044, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30979] Another function of GAM189 is therefore inhibition of Phosphoserine phosphatase (PSPH, Accession NP_004568.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSPH.

[30980] Prostaglandin e synthase (PTGES, Accession NP_004869.1) is another GAM189 target gene, herein designated TARGET GENE. PTGES BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGES BINDING SITE, designated

SEQ ID:16070, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30981] Another function of GAM189 is therefore inhibition of Prostaglandin e synthase (PTGES, Accession NP_004869.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGES.

[30982] Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1) is another GAM189 target gene, herein designated TARGET GENE. PTGIS BINDING SITE1 and PTGIS BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PTGIS, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGIS BINDING SITE1 and PTGIS BINDING SITE2, designated SEQ ID:17361 and SEQ ID:10783 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30983] Another function of GAM189 is therefore inhibition of Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1), a gene which catalyzes the isomerization

of prostaglandin h2 to prostacyclin (= prostaglandin i2). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGIS.

[30984] The function of PTGIS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Ptk2 protein tyrosine kinase 2 (PTK2, Accession NP_005598.3) is another GAM189 target gene, herein designated TARGET GENE. PTK2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PTK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTK2 BINDING SITE, designated SEQ ID:10355, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30985] Another function of GAM189 is therefore inhibition of Ptk2 protein tyrosine kinase 2 (PTK2, Accession NP_005598.3), a gene which involves in intracellular signal transduction pathway and is a putative homolog of chicken focal adhesion associated kinase. Accordingly,

utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTK2.

[30986] The function of PTK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.2.Phosphorylase, glycogen; muscle (mcardle syndrome, glycogen storage disease type v) (PYGM, Accession NP_005600.1) is another GAM189 target gene, herein designated TARGET GENE. PYGM BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PYGM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PYGM BINDING SITE, designated SEQ ID:15938, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30987] Another function of GAM189 is therefore inhibition of Phosphorylase, glycogen; muscle (mcardle syndrome, glycogen storage disease type v) (PYGM, Accession NP_005600.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PYGM.

[30988] RAB11-FIP4 (Accession NP_116321.2) is another GAM189 target gene, herein designated TARGET GENE. RAB11-FIP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB11-FIP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB11-FIP4 BINDING SITE, designated SEQ ID:13848, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30989] Another function of GAM189 is therefore inhibition of RAB11-FIP4 (Accession NP_116321.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB11-FIP4.

[30990] Rab21, member ras oncogene family (RAB21, Accession NP_055814.1) is another GAM189 target gene, herein designated TARGET GENE. RAB21 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of RAB21 BINDING SITE, designated SEQ ID:7076, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30991] Another function of GAM189 is therefore inhibition of Rab21, member ras oncogene family (RAB21, Accession NP_055814.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB21.

[30992] Rab33b, member ras oncogene family (RAB33B, Accession NP_112586.1) is another GAM189 target gene, herein designated TARGET GENE. RAB33B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB33B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB33B BINDING SITE, designated SEQ ID:7910, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30993] Another function of GAM189 is therefore inhibition of Rab33b, member ras oncogene family (RAB33B, Accession NP_112586.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with RAB33B.

[30994] Rab36, member ras oncogene family (RAB36, Accession NP_004905.1) is another GAM189 target gene, herein designated TARGET GENE. RAB36 BINDING SITE1 and RAB36 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by RAB36, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB36 BINDING SITE1 and RAB36 BINDING SITE2, designated SEQ ID:808 and SEQ ID:1652 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30995] Another function of GAM189 is therefore inhibition of Rab36, member ras oncogene family (RAB36, Accession NP_004905.1), a gene which is involved in protein transport. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB36.

[30996] The function of RAB36 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Rab39, member ras oncogene family

(RAB39, Accession XP_084662.1) is another GAM189 target gene, herein designated TARGET GENE. RAB39 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB39, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB39 BINDING SITE, designated SEQ ID:3754, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30997] Another function of GAM189 is therefore inhibition of Rab39, member ras oncogene family (RAB39, Accession XP_084662.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB39.

[30998] Rab4a, member ras oncogene family (RAB4A, Accession NP_004569.2) is another GAM189 target gene, herein designated TARGET GENE. RAB4A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAB4A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB4A BINDING SITE, designated

SEQ ID:16568, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[30999] Another function of GAM189 is therefore inhibition of Rab4a, member ras oncogene family (RAB4A, Accession NP_004569.2), a gene which is involved in protein transport. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB4A.

[31000] The function of RAB4A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.2.Rab, member of ras oncogene family-like 2a (RABL2A, Accession NP_038198.1) is another GAM189 target gene, herein designated TARGET GENE. RABL2A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RABL2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RABL2A BINDING SITE, designated SEQ ID:2648, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31001] Another function of GAM189 is therefore inhibition of Rab, member of ras oncogene family-like 2a (RABL2A, Accession NP_038198.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2A.

[31002] Rab, member of ras oncogene family-like 2b (RABL2B, Accession NP_009012.1) is another GAM189 target gene, herein designated TARGET GENE. RABL2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RABL2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RABL2B BINDING SITE, designated SEQ ID:2648, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31003] Another function of GAM189 is therefore inhibition of Rab, member of ras oncogene family-like 2b (RABL2B, Accession NP_009012.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2B.

[31004] RAI (Accession NP_006654.1) is another GAM189 target gene, herein designated TARGET GENE. RAI BINDING SITE

is a target binding site found in the 5` untranslated region of mRNA encoded by RAI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI BINDING SITE, designated SEQ ID:8937, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31005] Another function of GAM189 is therefore inhibition of RAI (Accession NP_006654.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI.

[31006] Retinoic acid induced 16 (RAI16, Accession NP_073586.3) is another GAM189 target gene, herein designated TARGET GENE. RAI16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAI16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI16 BINDING SITE, designated SEQ ID:4335, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31007] Another function of GAM189 is therefore inhibition of

Retinoic acid induced 16 (RAI16, Accession NP_073586.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI16.

[31008] Retinoic acid induced 17 (RAI17, Accession XP_166091.2) is another GAM189 target gene, herein designated TARGET GENE. RAI17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAI17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI17 BINDING SITE, designated SEQ ID:7523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31009] Another function of GAM189 is therefore inhibition of Retinoic acid induced 17 (RAI17, Accession XP_166091.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI17.

[31010] Retinoic acid induced 17 (RAI17, Accession NP_065071.1) is another GAM189 target gene, herein designated TARGET GENE. RAI17 BINDING SITE is a target binding site

found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAI17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI17 BINDING SITE, designated SEQ ID:7523, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31011] Another function of GAM189 is therefore inhibition of Retinoic acid induced 17 (RAI17, Accession NP_065071.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI17.

[31012] Retinoic acid induced 3 (RAI3, Accession NP_003970.1) is another GAM189 target gene, herein designated TARGET GENE. RAI3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAI3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI3 BINDING SITE, designated SEQ ID:12784, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31013] Another function of GAM189 is therefore inhibition of Retinoic acid induced 3 (RAI3, Accession NP_003970.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI3.

[31014] RAP140 (Accession NP_056039.1) is another GAM189 target gene, herein designated TARGET GENE. RAP140 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAP140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAP140 BINDING SITE, designated SEQ ID:16472, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31015] Another function of GAM189 is therefore inhibition of RAP140 (Accession NP_056039.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP140.

[31016] Retinoic acid receptor, gamma (RARG, Accession NP_000957.1) is another GAM189 target gene, herein designated TARGET GENE. RARG BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by RARG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RARG BINDING SITE, designated SEQ ID:11090, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31017] Another function of GAM189 is therefore inhibition of Retinoic acid receptor, gamma (RARG, Accession NP_000957.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RARG.

[31018] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_055552.1) is another GAM189 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:19336, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[31019] Another function of GAM189 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_055552.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[31020] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739579.1) is another GAM189 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:19336, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31021] Another function of GAM189 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739579.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[31022] Ras association (ralgds/af-6) domain family 2 (RASSF2,

Accession NP_739580.1) is another GAM189 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:19336, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31023] Another function of GAM189 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739580.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[31024] Retinoblastoma binding protein 1 (RBBP1, Accession NP_002883.2) is another GAM189 target gene, herein designated TARGET GENE. RBBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RBBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RBBP1

BINDING SITE, designated SEQ ID:11014, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31025] Another function of GAM189 is therefore inhibition of Retinoblastoma binding protein 1 (RBBP1, Accession NP_002883.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP1.

[31026] Retinoblastoma binding protein 1 (RBBP1, Accession NP_075376.1) is another GAM189 target gene, herein designated TARGET GENE. RBBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RBBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RBBP1 BINDING SITE, designated SEQ ID:11014, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31027] Another function of GAM189 is therefore inhibition of Retinoblastoma binding protein 1 (RBBP1, Accession NP_075376.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with RBBP1.

[31028] Retinoblastoma binding protein 1 (RBBP1, Accession NP_075377.1) is another GAM189 target gene, herein designated TARGET GENE. RBBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RBBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RBBP1 BINDING SITE, designated SEQ ID:11014, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31029] Another function of GAM189 is therefore inhibition of Retinoblastoma binding protein 1 (RBBP1, Accession NP_075377.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP1.

[31030] Retinoblastoma binding protein 9 (RBBP9, Accession NP_006597.2) is another GAM189 target gene, herein designated TARGET GENE. RBBP9 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RBBP9, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RBBP9 BINDING SITE, designated SEQ ID:16100, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31031] Another function of GAM189 is therefore inhibition of Retinoblastoma binding protein 9 (RBBP9, Accession NP_006597.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP9.

[31032] Retinoblastoma-like 2 (p130) (RBL2, Accession NP_005602.2) is another GAM189 target gene, herein designated TARGET GENE. RBL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RBL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RBL2 BINDING SITE, designated SEQ ID:6615, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31033] Another function of GAM189 is therefore inhibition of Retinoblastoma-like 2 (p130) (RBL2, Accession NP_005602.2), a gene which may be a tumor suppressor

and therefore may be associated with Cancer. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with RBL2.

[31034] The function of RBL2 has been established by previous studies. Mayol et al. (1993) cloned a retinoblastoma- related human gene, referred to as RB2, on the basis of sequence homology of the E1A- binding domain of the retinoblastoma gene (RB1; 180200). Structural homology with RB1 suggested a possible function of RB2 as a tumor suppressor gene. Yeung et al. (1993) mapped the gene to human chromosome 16q12.2 and rat chromosome 19, using fluorescence in situ hybridization and somatic hybrid cell analysis, respectively. Based on known syntenic relationships among human, rat and mouse, the data suggested that the mouse homolog resides on chromosome 8. Deletions of chromosome 16q have been found in several human neoplasms, including breast, ovarian, hepatic, and prostatic cancers, which supports the involvement of RB2 in human cancer as a tumor suppressor gene. This locus is symbolized RBL2 because it was identified after the gene on chromosome 20, which is symbolized RBL1 (OMIM Ref. No. 116957). RBL1 has a molecular weight of

107 kD; RBL2 has a molecular weight of about 120 kD.

[31035]

[31036] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31037] Baldi, A.; Boccia, V.; Claudio, P. P.; De Luca, A.; Giordano, A. : Genomic structure of the human retinoblastoma- related Rb2/p130 gene. Proc. Nat. Acad. Sci. 93: 4629-4632, 1996. ; and

[31038] Mayol, X.; Grana, X.; Baldi, A.; Sang, N.; Hu, Q.; Giordano, A. : Cloning of a new member of the retinoblastoma gene family (pRb2) which binds to the E1A transforming domain. Oncogene.

[31039] Further studies establishing the function and utilities of RBL2 are found in John Hopkins OMIM database record ID 180203, and in cited publications listed in Table 5, which are hereby incorporated by reference.RCBTB1 (Accession NP_060661.2) is another GAM189 target gene, herein designated TARGET GENE. RCBTB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RCBTB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of RCBTB1 BINDING SITE, designated SEQ ID:13829, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31040] Another function of GAM189 is therefore inhibition of RCBTB1 (Accession NP_060661.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RCBTB1.

[31041] RCD-8 (Accession NP_055144.2) is another GAM189 target gene, herein designated TARGET GENE. RCD-8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RCD-8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RCD-8 BINDING SITE, designated SEQ ID:13335, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31042] Another function of GAM189 is therefore inhibition of RCD-8 (Accession NP_055144.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RCD-8.

[31043] RDH13 (Accession NP_612421.1) is another GAM189 target gene, herein designated TARGET GENE. RDH13 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RDH13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RDH13 BINDING SITE, designated SEQ ID:9713, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31044] Another function of GAM189 is therefore inhibition of RDH13 (Accession NP_612421.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RDH13.

[31045] Regulator of g-protein signalling 3 (RGS3, Accession NP_570613.1) is another GAM189 target gene, herein designated TARGET GENE. RGS3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by RGS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RGS3 BINDING SITE, designated SEQ ID:3344, to the nucleotide

sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31046] Another function of GAM189 is therefore inhibition of Regulator of g-protein signalling 3 (RGS3, Accession NP_570613.1), a gene which negatively regulates G protein- coupled receptor signalling. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS3.

[31047] The function of RGS3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM146.1.Rhesus blood group, d antigen (RHD, Accession NP_057208.2) is another GAM189 target gene, herein designated TARGET GENE. RHD BINDING SITE1 and RHD BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by RHD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE1 and RHD BINDING SITE2, designated SEQ ID:13465 and SEQ ID:4143 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31048] Another function of GAM189 is therefore inhibition of Rhesus blood group, d antigen (RHD, Accession NP_057208.2), a gene which Major antigen of the RH system. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[31049] The function of RHD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Rhesus blood group, d antigen (RHD, Accession NP_057309.2) is another GAM189 target gene, herein designated TARGET GENE. RHD BINDING SITE1 and RHD BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by RHD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE1 and RHD BINDING SITE2, designated SEQ ID:4143 and SEQ ID:13465 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31050] Another function of GAM189 is therefore inhibition of Rhesus blood group, d antigen (RHD, Accession

NP_057309.2), a gene which Major antigen of the RH system. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[31051] The function of RHD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.RHPN2 (Accession NP_149094.2) is another GAM189 target gene, herein designated TARGET GENE. RHPN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RHPN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHPN2 BINDING SITE, designated SEQ ID:11803, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31052] Another function of GAM189 is therefore inhibition of RHPN2 (Accession NP_149094.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHPN2.

[31053] RIP60 (Accession NP_037532.1) is another GAM189 target gene, herein designated TARGET GENE. RIP60 BINDING

SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RIP60, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RIP60 BINDING SITE, designated SEQ ID:5556, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31054] Another function of GAM189 is therefore inhibition of RIP60 (Accession NP_037532.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIP60.

[31055] RIP60 (Accession NP_055189.1) is another GAM189 target gene, herein designated TARGET GENE. RIP60 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RIP60, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RIP60 BINDING SITE, designated SEQ ID:5556, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31056] Another function of GAM189 is therefore inhibition of

RIP60 (Accession NP_055189.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIP60.

[31057] RNF137 (Accession NP_060543.4) is another GAM189 target gene, herein designated TARGET GENE. RNF137 BINDING SITE1 and RNF137 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by RNF137, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF137 BINDING SITE1 and RNF137 BINDING SITE2, designated SEQ ID:7446 and SEQ ID:16940 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31058] Another function of GAM189 is therefore inhibition of RNF137 (Accession NP_060543.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF137.

[31059] RNF144 (Accession NP_055561.1) is another GAM189 target gene, herein designated TARGET GENE. RNF144 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF144, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF144 BINDING SITE, designated SEQ ID:4727, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31060] Another function of GAM189 is therefore inhibition of RNF144 (Accession NP_055561.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF144.

[31061] Ring finger protein (c3hc4 type) 8 (RNF8, Accession NP_003949.1) is another GAM189 target gene, herein designated TARGET GENE. RNF8 BINDING SITE1 and RNF8 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by RNF8, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF8 BINDING SITE1 and RNF8 BINDING SITE2, designated SEQ ID:13778 and SEQ ID:9745 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31062] Another function of GAM189 is therefore inhibition of Ring finger protein (c3hc4 type) 8 (RNF8, Accession NP_003949.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF8.

[31063] Retinitis pigmentosa 2 (x-linked recessive) (RP2, Accession NP_008846.1) is another GAM189 target gene, herein designated TARGET GENE. RP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RP2 BINDING SITE, designated SEQ ID:6582, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31064] Another function of GAM189 is therefore inhibition of Retinitis pigmentosa 2 (x-linked recessive) (RP2, Accession NP_008846.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RP2.

[31065] Rabphilin 3a-like (without c2 domains) (RPH3AL, Accession NP_008918.1) is another GAM189 target gene, herein designated TARGET GENE. RPH3AL BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by RPH3AL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RPH3AL BINDING SITE, designated SEQ ID:2614, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31066] Another function of GAM189 is therefore inhibition of Rabphilin 3a-like (without c2 domains) (RPH3AL, Accession NP_008918.1), a gene which is a protein transporter. could play a role in neurotransmitter release by regulating membrane flow in the nerve terminal. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPH3AL.

[31067] The function of RPH3AL has been established by previous studies. Secretions of hormones and neurotransmitters from endocrine cells and neurons, respectively, are regulated by calcium ions, which trigger exocytosis. The RAS-associated protein RAB3A (OMIM Ref. No. 179490) is involved in the recruitment of synaptic vesicles for exocytosis. Using a DNA fragment encoding the Rab3A- binding

domain of a mouse rabphilin- 3A cDNA, Kotake et al. (1997) probed a rat islet cDNA library under low stringency. A partial rabphilin- 3A- related protein was identified and designated Noc2; a full- length Noc2 clone was isolated from a rat insulin- secreting cell line cDNA library. The Noc2 cDNA encodes a 302- amino acid protein that shows 40.7% amino acid identity and 77.9% similarity to the N- terminal region of rat rabphilin- 3A. However, it lacks the C2 domains, and hence the Noc2 (no C2 domain) designation. Noc2 contains 1 potential protein kinase A and 3 potential protein kinase C phosphorylation sites. RNA blot analysis revealed that a single 2.2- or 2.6- kb transcript of Noc2 is expressed at very high levels in pancreatic islets, and at low to moderate or high levels in other endocrine tissues and hormone- secreting cell lines, but at very low levels in brain. Screening a mouse embryonic cDNA library with the yeast 2- hybrid system, Kotake et al. (1997) showed that Noc2 interacts with the LIM domain- containing protein zyxin (OMIM Ref. No. 602002), a component of the cytoskeleton. The authors suggested that Noc2 is probably involved in regulated exocytosis in endocrine cells by interacting with the cytoskeleton Using cDNA selection, Smith et al. (1999) identified a human

transcript spanning a common deletion on 17p13.3 found in approximately 40% of medulloblastomas. The full-length coding sequence predicted a 315- amino acid protein displaying 77% amino acid identity with the rat Noc2 (OMIM Ref. No. Rph3al) protein. Northern blot analysis detected moderate to high expression of a 2.6- kb RPH3AL transcript in thyroid, ovary, stomach, heart, pancreas, skeletal muscle, kidney, and liver

[31068]

[31069] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31070] Kotake, K.; Ozaki, N.; Mizuta, M.; Sekiya, S.; Inagaki, N.; Seino, S. : Noc2, a putative zinc finger protein involved in exocytosis in endocrine cells. J. Biol. Chem. 272: 29407-29410, 1997. ; and

[31071] Smith, J. S.; Tachibana, I.; Allen, C.; Chiappa, S. A.; Lee, H. K.; McIver, B.; Jenkins, R. B.; Raffel, C. : Cloning of a human ortholog (RPH3AL) of (RNO)Rph3al from a candidate 17p13.3 med.

[31072] Further studies establishing the function and utilities of RPH3AL are found in John Hopkins OMIM database record ID 604881, and in cited publications listed in Table 5,

which are hereby incorporated by reference.RPP30 (Accession NP_006404.1) is another GAM189 target gene, herein designated TARGET GENE. RPP30 BINDING SITE1 and RPP30 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by RPP30, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RPP30 BINDING SITE1 and RPP30 BINDING SITE2, designated SEQ ID:445 and SEQ ID:19325 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31073] Another function of GAM189 is therefore inhibition of RPP30 (Accession NP_006404.1), a gene which is a component of ribonuclease p that processes 5' ends of precursor tRNAs. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPP30.

[31074] The function of RPP30 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.S100A15 (Accession NP_789793.1) is another GAM189 target gene, herein designated TARGET

GENE. S100A15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100A15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of S100A15 BINDING SITE, designated SEQ ID:19723, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31075] Another function of GAM189 is therefore inhibition of S100A15 (Accession NP_789793.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with S100A15.

[31076] SARM1 (Accession NP_055892.1) is another GAM189 target gene, herein designated TARGET GENE. SARM1 BINDING SITE1 and SARM1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SARM1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SARM1 BINDING SITE1 and SARM1 BINDING SITE2, designated SEQ ID:4282 and SEQ ID:7147

respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31077] Another function of GAM189 is therefore inhibition of SARM1 (Accession NP_055892.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SARM1.

[31078] Sarcoma amplified sequence (SAS, Accession NP_005972.1) is another GAM189 target gene, herein designated TARGET GENE. SAS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SAS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SAS BINDING SITE, designated SEQ ID:17726, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31079] Another function of GAM189 is therefore inhibition of Sarcoma amplified sequence (SAS, Accession NP_005972.1), a gene which is a member of the trans-membrane 4 superfamily (TM4SF) and may be involved in growth- related cellular processes T. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with SAS.

[31080] The function of SAS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM88.1.SBLF (Accession NP_006864.2) is another GAM189 target gene, herein designated TARGET GENE. SBLF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SBLF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SBLF BINDING SITE, designated SEQ ID:14551, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31081] Another function of GAM189 is therefore inhibition of SBLF (Accession NP_006864.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SBLF.

[31082] SCAMP-4 (Accession NP_524558.1) is another GAM189 target gene, herein designated TARGET GENE. SCAMP-4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCAMP-4, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAMP-4 BINDING SITE, designated SEQ ID:2153, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31083] Another function of GAM189 is therefore inhibition of SCAMP-4 (Accession NP_524558.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP-4.

[31084] Scan domain containing 2 (SCAND2, Accession NP_071333.2) is another GAM189 target gene, herein designated TARGET GENE. SCAND2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SCAND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAND2 BINDING SITE, designated SEQ ID:7179, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31085] Another function of GAM189 is therefore inhibition of Scan domain containing 2 (SCAND2, Accession

NP_071333.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAND2.

[31086] Scavenger receptor class f, member 1 (SCARF1, Accession NP_003684.1) is another GAM189 target gene, herein designated TARGET GENE. SCARF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCARF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCARF1 BINDING SITE, designated SEQ ID:5158, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31087] Another function of GAM189 is therefore inhibition of Scavenger receptor class f, member 1 (SCARF1, Accession NP_003684.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCARF1.

[31088] Stearoyl-coa desaturase (delta-9-desaturase) (SCD, Accession NP_005054.2) is another GAM189 target gene, herein designated TARGET GENE. SCD BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by SCD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCD BINDING SITE, designated SEQ ID:3800, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31089] Another function of GAM189 is therefore inhibition of Stearoyl-coa desaturase (delta-9-desaturase) (SCD, Accession NP_005054.2), a gene which functions in the synthesis of unsaturated fatty acids. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCD.

[31090] The function of SCD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.Sex comb on midleg-like 2 (drosophila) (SCML2, Accession NP_006080.1) is another GAM189 target gene, herein designated TARGET GENE. SCML2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCML2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of SCML2 BINDING SITE, designated SEQ ID:3898, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31091] Another function of GAM189 is therefore inhibition of Sex comb on midleg-like 2 (drosophila) (SCML2, Accession NP_006080.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCML2.

[31092] Sodium channel, voltage-gated, type ii, beta polypeptide (SCN2B, Accession NP_004579.1) is another GAM189 target gene, herein designated TARGET GENE. SCN2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCN2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCN2B BINDING SITE, designated SEQ ID:13704, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31093] Another function of GAM189 is therefore inhibition of Sodium channel, voltage-gated, type ii, beta polypeptide (SCN2B, Accession NP_004579.1), a gene which modulates

channel properties. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN2B.

[31094] The function of SCN2B has been established by previous studies. Jones et al. (1996) used a rat brain Scn2b cDNA to map the mouse gene in interspecific backcrosses. They found that it is linked to markers from the central region of mouse chromosome 9 and noted that the neurologic mutation 'staggerer' (Imai and Kingsley, 1994) had been mapped there also. No recombination was found with the Il10r gene (OMIM Ref. No. 146933). Thus, mouse Scn2b is located within a conserved linkage group with orthologs on human chromosome 11q22- qter. By fluorescence in situ hybridization, Eubanks et al. (1997) mapped the SCN2B gene to 11q23. Bolino et al. (1998) reported that the SCN2B gene consists of 4 exons and 3 introns spanning a region of approximately 12 kb

[31095]

[31096] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31097] Bolino, A.; Seri, M.; Caroli, F.; Eubanks, J.; Srinivasan, J.; Mandich, P.; Schenone, A.; Quattrone, A.; Romeo, G.; Cat-

terall, W. A.; Devoto, M. : Exclusion of the SCN2B gene as candidate for CMT4B. Europ. J. Hum. Genet. 6: 629- 634, 1998. ; and

[31098] Eubanks, J.; Srinivasan, J.; Dinulos, M. B.; Disteche, C. M.; Catterall, W. A. : Structure and chromosomal localization of the beta2 subunit of the human brain sodium channel. Neurorepo.

[31099] Further studies establishing the function and utilities of SCN2B are found in John Hopkins OMIM database record ID 601327, and in cited publications listed in Table 5, which are hereby incorporated by reference.SCN3B (Accession NP_060870.1) is another GAM189 target gene, herein designated TARGET GENE. SCN3B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCN3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCN3B BINDING SITE, designated SEQ ID:4399, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31100] Another function of GAM189 is therefore inhibition of SCN3B (Accession NP_060870.1) . Accordingly, utilities of

GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN3B.

[31101] SDS-RS1 (Accession NP_612441.1) is another GAM189 target gene, herein designated TARGET GENE. SDS-RS1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SDS-RS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SDS-RS1 BINDING SITE, designated SEQ ID:14127, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31102] Another function of GAM189 is therefore inhibition of SDS-RS1 (Accession NP_612441.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDS-RS1.

[31103] Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1) is another GAM189 target gene, herein designated TARGET GENE. SEDL BINDING SITE1 through SEDL BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by SEDL, corresponding to target binding sites such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEDL BINDING SITE1 through SEDL BINDING SITE3, designated SEQ ID:15576, SEQ ID:11591 and SEQ ID:926 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31104] Another function of GAM189 is therefore inhibition of Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1), a gene which may play role in vesicular transport from endoplasmic reticulum to golgi. and therefore may be associated with Spondyloepiphyseal dysplasia. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Spondyloepiphyseal dysplasia, and of other diseases and clinical conditions associated with SEDL.

[31105] The function of SEDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Sema domain, immunoglobulin domain (ig), short basic domain, secreted, (semaphorin) 3e (SEMA3E, Accession NP_036563.1) is another GAM189 target gene, herein designated TARGET GENE. SEMA3E BINDING SITE is a target binding site found in the 3` untranslated region

of mRNA encoded by SEMA3E, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEMA3E BINDING SITE, designated SEQ ID:13353, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31106] Another function of GAM189 is therefore inhibition of Sema domain, immunoglobulin domain (ig), short basic domain, secreted, (semaphorin) 3e (SEMA3E, Accession NP_036563.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA3E.

[31107] Selenoprotein n, 1 (SEPN1, Accession NP_065184.1) is another GAM189 target gene, herein designated TARGET GENE. SEPN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEPN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEPN1 BINDING SITE, designated SEQ ID:18255, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31108] Another function of GAM189 is therefore inhibition of Selenoprotein n, 1 (SEPN1, Accession NP_065184.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEPN1.

[31109] Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) is another GAM189 target gene, herein designated TARGET GENE. SERF1A BINDING SITE1 and SERF1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERF1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1A BINDING SITE1 and SERF1A BINDING SITE2, designated SEQ ID:15849 and SEQ ID:9219 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31110] Another function of GAM189 is therefore inhibition of Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1A.

[31111] Small edrk-rich factor 1b (centromeric) (SERF1B, Accession

NP_075267.1) is another GAM189 target gene, herein designated TARGET GENE. SERF1B BINDING SITE1 and SERF1B BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERF1B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1B BINDING SITE1 and SERF1B BINDING SITE2, designated SEQ ID:15849 and SEQ ID:9219 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31112] Another function of GAM189 is therefore inhibition of Small edrk-rich factor 1b (centromeric) (SERF1B, Accession NP_075267.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1B.

[31113] Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 9 (SERPINB9, Accession NP_004146.1) is another GAM189 target gene, herein designated TARGET GENE. SERPINB9 BINDING SITE1 and SERPINB9 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERPINB9, corresponding to target binding sites such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERPINB9 BINDING SITE1 and SERPINB9 BINDING SITE2, designated SEQ ID:4363 and SEQ ID:9152 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31114] Another function of GAM189 is therefore inhibition of Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 9 (SERPINB9, Accession NP_004146.1), a gene which may be a serpin serine protease inhibitor that interacts with granzyme B (GZMB). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB9.

[31115] The function of SERPINB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM88.2.Sideroflexin 2 (SFXN2, Accession XP_058359.2) is another GAM189 target gene, herein designated TARGET GENE. SFXN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SFXN2, corresponding to a target binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SFXN2 BINDING SITE, designated SEQ ID:3678, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31116] Another function of GAM189 is therefore inhibition of Sideroflexin 2 (SFXN2, Accession XP_058359.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN2.

[31117] Sideroflexin 2 (SFXN2, Accession NP_849189.1) is another GAM189 target gene, herein designated TARGET GENE. SFXN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SFXN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SFXN2 BINDING SITE, designated SEQ ID:3678, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31118] Another function of GAM189 is therefore inhibition of Sideroflexin 2 (SFXN2, Accession NP_849189.1) . Accordingly, utilities of GAM189 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with SFXN2.

[31119] Sh3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2, Accession NP_113657.1) is another GAM189 target gene, herein designated TARGET GENE. SH3BGRL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SH3BGRL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SH3BGRL2 BINDING SITE, designated SEQ ID:2741, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31120] Another function of GAM189 is therefore inhibition of Sh3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2, Accession NP_113657.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BGRL2.

[31121] Sh3-domain binding protein 2 (SH3BP2, Accession NP_003014.2) is another GAM189 target gene, herein designated TARGET GENE. SH3BP2 BINDING SITE1 through SH3BP2 BINDING SITE3 are target binding sites found in

untranslated regions of mRNA encoded by SH3BP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SH3BP2 BINDING SITE1 through SH3BP2 BINDING SITE3, designated SEQ ID:3836, SEQ ID:9440 and SEQ ID:1122 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31122] Another function of GAM189 is therefore inhibition of Sh3-domain binding protein 2 (SH3BP2, Accession NP_003014.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BP2.

[31123] Short stature homeobox (SHOX, Accession NP_006874.1) is another GAM189 target gene, herein designated TARGET GENE. SHOX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SHOX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SHOX BINDING SITE, designated SEQ ID:4375, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:246.

[31124] Another function of GAM189 is therefore inhibition of Short stature homeobox (SHOX, Accession NP_006874.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHOX.

[31125] Sialic acid binding ig-like lectin 8 (SIGLEC8, Accession NP_055257.1) is another GAM189 target gene, herein designated TARGET GENE. SIGLEC8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIGLEC8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIGLEC8 BINDING SITE, designated SEQ ID:4513, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31126] Another function of GAM189 is therefore inhibition of Sialic acid binding ig-like lectin 8 (SIGLEC8, Accession NP_055257.1), a gene which is a cell adhesion molecule for postnatal neural development. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIGLEC8.

[31127] The function of SIGLEC8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Tal1 (scl) interrupting locus (SIL, Accession NP_003026.1) is another GAM189 target gene, herein designated TARGET GENE. SIL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIL BINDING SITE, designated SEQ ID:12411, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31128] Another function of GAM189 is therefore inhibition of Tal1 (scl) interrupting locus (SIL, Accession NP_003026.1), a gene which may be required for axial development and left- right specification and therefore may be associated with Prominent midline neural tube defects, abnormal left- right development. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Prominent midline neural tube defects, abnormal left- right development, and of other diseases and clinical conditions associated with SIL.

[31129] The function of SIL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Signal-regulatory protein beta 1 (SIRPB1, Accession NP_006056.1) is another GAM189 target gene, herein designated TARGET GENE. SIRPB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIRPB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIRPB1 BINDING SITE, designated SEQ ID:14771, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31130] Another function of GAM189 is therefore inhibition of Signal-regulatory protein beta 1 (SIRPB1, Accession NP_006056.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIRPB1.

[31131] Src-like-adaptor 2 (SLA2, Accession NP_115590.1) is another GAM189 target gene, herein designated TARGET GENE. SLA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of

mRNA encoded by SLA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLA2 BINDING SITE, designated SEQ ID:19573, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31132] Another function of GAM189 is therefore inhibition of Src-like-adaptor 2 (SLA2, Accession NP_115590.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA2.

[31133] Src-like-adaptor 2 (SLA2, Accession NP_778252.1) is another GAM189 target gene, herein designated TARGET GENE. SLA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLA2 BINDING SITE, designated SEQ ID:19573, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31134] Another function of GAM189 is therefore inhibition of Src-like-adaptor 2 (SLA2, Accession NP_778252.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA2.

[31135] Solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8, Accession NP_078904.1) is another GAM189 target gene, herein designated TARGET GENE. SLC12A8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC12A8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC12A8 BINDING SITE, designated SEQ ID:5190, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31136] Another function of GAM189 is therefore inhibition of Solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8, Accession NP_078904.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC12A8.

[31137] Solute carrier family 13 (sodium/sulfate symporters),

member 1 (SLC13A1, Accession NP_071889.2) is another GAM189 target gene, herein designated TARGET GENE. SLC13A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC13A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC13A1 BINDING SITE, designated SEQ ID:4370, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31138] Another function of GAM189 is therefore inhibition of Solute carrier family 13 (sodium/sulfate symporters), member 1 (SLC13A1, Accession NP_071889.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC13A1.

[31139] Solute carrier family 14 (urea transporter), member 2 (SLC14A2, Accession NP_009094.2) is another GAM189 target gene, herein designated TARGET GENE. SLC14A2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC14A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of SLC14A2 BINDING SITE, designated SEQ ID:4514, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31140] Another function of GAM189 is therefore inhibition of Solute carrier family 14 (urea transporter), member 2 (SLC14A2, Accession NP_009094.2), a gene which is a renal urea transporter 2. and therefore may be associated with Orthostatic hypotension. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Orthostatic hypotension, and of other diseases and clinical conditions associated with SLC14A2.

[31141] The function of SLC14A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM97.1.Solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1, Accession NP_005064.1) is another GAM189 target gene, herein designated TARGET GENE. SLC15A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC15A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of SLC15A1 BINDING SITE, designated SEQ ID:18930, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31142] Another function of GAM189 is therefore inhibition of Solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1, Accession NP_005064.1), a gene which is a H(+)- coupled peptide transporter. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC15A1.

[31143] The function of SLC15A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Solute carrier family 16 (monocarboxylic acid transporters), member 4 (SLC16A4, Accession NP_004687.1) is another GAM189 target gene, herein designated TARGET GENE. SLC16A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC16A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A4 BIND-

ING SITE, designated SEQ ID:611, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31144] Another function of GAM189 is therefore inhibition of Solute carrier family 16 (monocarboxylic acid transporters), member 4 (SLC16A4, Accession NP_004687.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A4.

[31145] Solute carrier family 19, member 3 (SLC19A3, Accession NP_079519.1) is another GAM189 target gene, herein designated TARGET GENE. SLC19A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC19A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC19A3 BINDING SITE, designated SEQ ID:6713, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31146] Another function of GAM189 is therefore inhibition of Solute carrier family 19, member 3 (SLC19A3, Accession NP_079519.1) . Accordingly, utilities of GAM189 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC19A3.

[31147] Solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5, Accession NP_005619.1) is another GAM189 target gene, herein designated TARGET GENE. SLC1A5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC1A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC1A5 BINDING SITE, designated SEQ ID:1277, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31148] Another function of GAM189 is therefore inhibition of Solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5, Accession NP_005619.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC1A5.

[31149] Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1, Accession NP_004718.1) is another GAM189 target gene, herein designated TARGET GENE. SLC24A1 BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by SLC24A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC24A1 BINDING SITE, designated SEQ ID:10966, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31150] Another function of GAM189 is therefore inhibition of Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1, Accession NP_004718.1), a gene which is a critical component of the visual transduction cascade, controlling the calcium concentration of outer segments during light and darkness. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC24A1.

[31151] The function of SLC24A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.SLC30A5 (Accession NP_076960.1) is another GAM189 target gene, herein designated TARGET GENE. SLC30A5 BINDING SITE is a target binding site

found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLC30A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC30A5 BINDING SITE, designated SEQ ID:3692, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31152] Another function of GAM189 is therefore inhibition of SLC30A5 (Accession NP_076960.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC30A5.

[31153] SLC30A6 (Accession NP_060434.2) is another GAM189 target gene, herein designated TARGET GENE. SLC30A6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC30A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC30A6 BINDING SITE, designated SEQ ID:5362, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31154] Another function of GAM189 is therefore inhibition of SLC30A6 (Accession NP_060434.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC30A6.

[31155] SLC35E2 (Accession XP_049733.6) is another GAM189 target gene, herein designated TARGET GENE. SLC35E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC35E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC35E2 BINDING SITE, designated SEQ ID:13336, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31156] Another function of GAM189 is therefore inhibition of SLC35E2 (Accession XP_049733.6) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35E2.

[31157] Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2) is another GAM189 target gene, herein designated TARGET GENE. SLC39A1

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC39A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC39A1 BINDING SITE, designated SEQ ID:9528, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31158] Another function of GAM189 is therefore inhibition of Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2), a gene which is a divalent (zinc/iron) metal ion transporter. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC39A1.

[31159] The function of SLC39A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.1.Solute carrier family 4, sodium bicarbonate transporter-like, member 11 (SLC4A11, Accession NP_114423.1) is another GAM189 target gene, herein designated TARGET GENE. SLC4A11 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by SLC4A11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC4A11 BINDING SITE, designated SEQ ID:806, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31160] Another function of GAM189 is therefore inhibition of Solute carrier family 4, sodium bicarbonate transporter-like, member 11 (SLC4A11, Accession NP_114423.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC4A11.

[31161] Solute carrier family 5 (sodium/glucose cotransporter), member 1 (SLC5A1, Accession NP_000334.1) is another GAM189 target gene, herein designated TARGET GENE. SLC5A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC5A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC5A1 BINDING SITE, designated SEQ ID:2571, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[31162] Another function of GAM189 is therefore inhibition of Solute carrier family 5 (sodium/glucose cotransporter), member 1 (SLC5A1, Accession NP_000334.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC5A1.

[31163] Solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14, Accession NP_009162.1) is another GAM189 target gene, herein designated TARGET GENE. SLC6A14 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC6A14 BINDING SITE, designated SEQ ID:13830, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31164] Another function of GAM189 is therefore inhibition of Solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14, Accession NP_009162.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with SLC6A14.

[31165] Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (SLC6A3, Accession NP_001035.1) is another GAM189 target gene, herein designated TARGET GENE. SLC6A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC6A3 BINDING SITE, designated SEQ ID:12941, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31166] Another function of GAM189 is therefore inhibition of Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (SLC6A3, Accession NP_001035.1), a gene which terminates the action of dopamine by its high affinity sodium- dependent reuptake into presynaptic terminals. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A3.

[31167] The function of SLC6A3 has been established by previous studies. Giros et al. (1996) found that the disruption of

the mouse dopamine transporter gene results in spontaneous hyperlocomotion despite major adaptive changes such as decreases in neurotransmitter and receptor levels. In homozygous mice, dopamine persisted at least 100 times longer in the extracellular space, providing a biochemical explanation of the hyperdopaminergic phenotype and demonstrating the critical role of the transporter in regulating neurotransmission. The authors noted that the dopamine transporter is an obligatory target of cocaine and amphetamine, as demonstrated by the fact that these psychostimulants had no effect on locomotor activity or dopamine release and uptake in mice lacking the transporter. Giros et al. (1996) stated that the DAT knockout mice should be an excellent tool for the study and development of drugs used in the management of dopaminergic dysfunction. There are similarities between the hyperdopaminergic phenotype of the knockout mice and some of the positive symptoms of schizophrenic patients. Specific blockade of the dopamine transporter with high-affinity inhibitors may be beneficial in illnesses such as Parkinson disease, where the effective levels of dopamine are markedly reduced.

[31168]

[31169] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31170] Gainetdinov, R. R.; Wetsel, W. C.; Jones, S. R.; Levin, E. D.; Jaber, M.; Caron, M. G. : Role of serotonin in the paradoxical calming effect of psychostimulants on hyperactivity. Science 283: 397- 401, 1999. ; and

[31171] Giros, B.; Jaber, M.; Jones, S. R.; Wightman, R. M.; Caron, M. G. : Hyperlocomotion and indifference to cocaine and amphetamine in mice lacking the dopamine receptor. Nature 370: 606- 612, 1.

[31172] Further studies establishing the function and utilities of SLC6A3 are found in John Hopkins OMIM database record ID 126455, and in cited publications listed in Table 5, which are hereby incorporated by reference.SMAC (Accession NP_620308.1) is another GAM189 target gene, herein designated TARGET GENE. SMAC BINDING SITE1 and SMAC BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by SMAC, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMAC BINDING SITE1 and SMAC

BINDING SITE2, designated SEQ ID:18165 and SEQ ID:1861 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31173] Another function of GAM189 is therefore inhibition of SMAC (Accession NP_620308.1), a gene which promotes apoptosis via caspase activation. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMAC.

[31174] The function of SMAC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_570710.1) is another GAM189 target gene, herein designated TARGET GENE. SNAP23 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNAP23, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP23 BINDING SITE, designated SEQ ID:19007, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31175] Another function of GAM189 is therefore inhibition of Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_570710.1), a gene which is essential component of the high affinity receptor for the general membrane fusion machinery. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP23.

[31176] The function of SNAP23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_003816.2) is another GAM189 target gene, herein designated TARGET GENE. SNAP23 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNAP23, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP23 BINDING SITE, designated SEQ ID:19007, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31177] Another function of GAM189 is therefore inhibition of

Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_003816.2), a gene which is essential component of the high affinity receptor for the general membrane fusion machinery. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP23.

[31178] The function of SNAP23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.SNARK (Accession NP_112214.1) is another GAM189 target gene, herein designated TARGET GENE. SNARK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNARK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNARK BINDING SITE, designated SEQ ID:18622, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31179] Another function of GAM189 is therefore inhibition of SNARK (Accession NP_112214.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNARK.

[31180] Syntaphilin (SNPH, Accession NP_055538.1) is another GAM189 target gene, herein designated TARGET GENE. SNPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNPH BINDING SITE, designated SEQ ID:15041, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31181] Another function of GAM189 is therefore inhibition of Syntaphilin (SNPH, Accession NP_055538.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNPH.

[31182] Sorting nexin 15 (SNX15, Accession NP_037438.2) is another GAM189 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE,

designated SEQ ID:7625, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31183] Another function of GAM189 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NP_037438.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15.

[31184] Sorting nexin 15 (SNX15, Accession NP_680086.1) is another GAM189 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:7625, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31185] Another function of GAM189 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NP_680086.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with SNX15.

[31186] SNX22 (Accession NP_079074.1) is another GAM189 target gene, herein designated TARGET GENE. SNX22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNX22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX22 BINDING SITE, designated SEQ ID:13596, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31187] Another function of GAM189 is therefore inhibition of SNX22 (Accession NP_079074.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX22.

[31188] SNX27 (Accession NP_112180.4) is another GAM189 target gene, herein designated TARGET GENE. SNX27 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNX27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX27 BINDING SITE, designated SEQ ID:16941, to the nucleotide

sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31189] Another function of GAM189 is therefore inhibition of SNX27 (Accession NP_112180.4) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX27.

[31190] Sialophorin (gpl115, leukosialin, cd43) (SPN, Accession NP_003114.1) is another GAM189 target gene, herein designated TARGET GENE. SPN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPN BINDING SITE, designated SEQ ID:16209, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31191] Another function of GAM189 is therefore inhibition of Sialophorin (gpl115, leukosialin, cd43) (SPN, Accession NP_003114.1), a gene which plays a role in the physico-chemical properties of the t- cell surface and in lectin binding. presents carbohydrate ligands to selectins. . and therefore may be associated with Wiskott- aldrich syn-

drome. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Wiskott- aldrich syndrome, and of other diseases and clinical conditions associated with SPN.

[31192] The function of SPN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Speckle-type poz protein (SPOP, Accession NP_003554.1) is another GAM189 target gene, herein designated TARGET GENE. SPOP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SPOP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPOP BINDING SITE, designated SEQ ID:5610, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31193] Another function of GAM189 is therefore inhibition of Speckle-type poz protein (SPOP, Accession NP_003554.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPOP.

[31194] SQV7L (Accession XP_047287.1) is another GAM189 target

gene, herein designated TARGET GENE. SQV7L BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SQV7L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SQV7L BINDING SITE, designated SEQ ID:7375, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31195] Another function of GAM189 is therefore inhibition of SQV7L (Accession XP_047287.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SQV7L.

[31196] Sarcalumenin (SRL, Accession XP_064152.3) is another GAM189 target gene, herein designated TARGET GENE. SRL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SRL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRL BINDING SITE, designated SEQ ID:6681, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31197] Another function of GAM189 is therefore inhibition of Sarcalumenin (SRL, Accession XP_064152.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRL.

[31198] Serine/arginine repetitive matrix 2 (SRRM2, Accession NP_057417.2) is another GAM189 target gene, herein designated TARGET GENE. SRRM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SRRM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRRM2 BINDING SITE, designated SEQ ID:18975, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31199] Another function of GAM189 is therefore inhibition of Serine/arginine repetitive matrix 2 (SRRM2, Accession NP_057417.2), a gene which RELATED NUCLEAR MATRIX PROTEIN. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRRM2.

[31200] The function of SRRM2 has been established by previous

studies. For background information on SRM proteins, see SRM160 (OMIM Ref. No. 605975). By biochemical purification, micropeptide sequence analysis, EST database searching, and screening a monocytoid cDNA library, Blencowe et al. (2000) isolated a cDNA encoding SRM300. Like SRM160, the deduced 2,296- amino acid SRM300 protein is rich in serine (S), arginine (R), and proline (P), has numerous SR dipeptides and 2 long polyserine domains, and lacks an RNA recognition domain. A portion of the SRM300 protein is identical to a partial protein, KIAA0324, identified by Nagase et al. (1997). By RT- PCR analysis, Nagase et al. (1997) detected ubiquitous expression of KIAA0324. Using immunoblot and immunoprecipitation analyses and confocal microscopy, Blencowe et al. (2000) confirmed that SRM300 associates with SRM160 and pre- mRNA and is localized in nuclear speckles. Reconstitution of SRM160/SRM300- depleted splicing reactions with recombinant SRM160 restored splicing activity, suggesting that SRM160 is the more important component of the complex. By screening a cDNA library for RNA ligands, Sawada et al. (2000) identified a cDNA encoding SRM300, which they termed SRL300. The deduced 2,752- amino acid protein has multiple R, S, and P residues, nu-

merous phosphorylation sites, and a predicted molecular mass of 300 kD, suggesting that it may be the full- length protein. Immunoblot analysis detected GST fusion proteins of greater than 300 kD in human and rat cells. Northern blot analysis revealed expression of a 9.0- to 10.0- kb SRL300 transcript in all tissues and cell lines tested. By radiation hybrid analysis, Nagase et al. (1997) mapped the SRM300 gene, or KIAA0324, to chromosome 16. By genomic sequence analysis, Blencowe et al. (2000) mapped the SRM300 gene to chromosome 16.

[31201]

[31202] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31203] Blencowe, B. J.; Bauren, G.; Eldridge, A. G.; Issner, R.; Nickerson, J. A.; Rosonina, E.; Sharp, P. A. : The SRm160/300 splicing coactivator subunits. RNA 6: 111-120, 2000. ; and

[31204] Sawada, Y.; Miura, Y.; Umeki, K.; Tamaoki, T.; Fujinaga, K.; Ohtaki, S. : Cloning and characterization of a novel RNA-binding protein SRL300 with RS domains. Biochim. Biophys. Acta 1492.

[31205] Further studies establishing the function and utilities of

SRRM2 are found in John Hopkins OMIM database record ID 606032, and in cited publications listed in Table 5, which are hereby incorporated by reference.Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1) is another GAM189 target gene, herein designated TARGET GENE. SS18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SS18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SS18 BINDING SITE, designated SEQ ID:17762, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31206] Another function of GAM189 is therefore inhibition of Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1), a gene which is a putative transcriptional activator. and therefore is associated with Human synovial sarcomas. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Human synovial sarcomas., and of other diseases and clinical conditions associated with SS18.

[31207] The function of SS18 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.STAF65(gamma) (Accession NP_055675.1) is another GAM189 target gene, herein designated TARGET GENE. STAF65(gamma) BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STAF65(gamma), corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAF65(gamma) BINDING SITE, designated SEQ ID:2196, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31208] Another function of GAM189 is therefore inhibition of STAF65(gamma) (Accession NP_055675.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAF65(gamma).

[31209] Staufen, rna binding protein (drosophila) (STAU, Accession NP_004593.1) is another GAM189 target gene, herein designated TARGET GENE. STAU BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by STAU, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAU BINDING SITE, designated SEQ ID:3950, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31210] Another function of GAM189 is therefore inhibition of Staufen, rna binding protein (drosophila) (STAU, Accession NP_004593.1), a gene which may play a role in specific positioning of mrnas at given sites in the cell and in stimulating their translation at the site. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAU.

[31211] The function of STAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM37.1.Sulfotransferase, estrogen-preferring (STE, Accession NP_005411.1) is another GAM189 target gene, herein designated TARGET GENE. STE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of STE BINDING SITE, designated SEQ ID:3303, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31212] Another function of GAM189 is therefore inhibition of Sulfotransferase, estrogen-preferring (STE, Accession NP_005411.1), a gene which sulfates estrone and dehydroepiandrosterone, but not dopamine. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STE.

[31213] The function of STE has been established by previous studies. Sulfation is an important pathway in the biotransformation of steroid hormones such as estrogens. Human liver contains 2 different types of sulfotransferases, dehydroepiandrosterone (DHEA) sulfotransferase (OMIM Ref. No. 125263) and phenol sulfotransferase (STP1; 171150). Aksoy et al. (1994) set out to test the possibility that human tissues may contain 1 or more estrogen sulfotransferases orthologous to the proteins encoded by EST cDNAs that had been cloned from other mammalian species. They succeeded in cloning a cDNA for human liver EST and studied selected properties of the protein that it encodes. Estrone sulfate is the predominant form of estro-

gen found in the circulation in women and could thus serve as precursor for active estrogens in target tissues by removal of the sulfate group through the action of endogenous steroid sulfatase. Bernier et al. (1994) used a cDNA encoding human placental estrogen sulfotransferase as a probe for isolating a clone containing almost the whole genomic sequence. The gene contains 9 short exons separated by 8 introns in an expanse of approximately 7.7 kb. The first 2 exons, named exon 1a and exon 1b, are noncoding and correspond to the 5- prime untranslated sequences of human brain and human placental estrogen sulfotransferase cDNAs, respectively. Transfection of chloramphenicol acetyltransferase reporter gene vectors containing the 5- prime flanking sequence upstream from exon 1a and exon 1b into human adrenal adenocarcinoma cells indicated that both sequences possess promoter activity. The results were interpreted as indicating that human brain aryl sulfotransferase and placental estrogen sulfotransferase mRNA species are transcribed from a single gene by alternate exon 1a and exon 1b promoters, respectively. Using DNA from panels of human- rodent somatic cell hybrids and amplification of the gene by PCR, Bernier et al. (1994) assigned the placental

estrogen sulfotransferase gene to chromosome 16. On the other hand, Her et al. (1995) mapped liver estrogen sulfotransferase cDNA to 4q13.1 by fluorescence in situ hybridization, suggesting that these may be 2 separate genes. They found that the liver STE gene spans approximately 20 kb and consists of 8 exons, ranging in length from 95 to 181 bp. The locations of most exon- intron splice junctions within STE were identical to those found in a human phenol ST gene (STM; 600641). (The STM gene maps to chromosome 16p11.2. Indeed, STM is the same as the 'placental estrogen sulfotransferase' gene mapped by Bernier et al. (1994) to chromosome 16 (Weinshilboum, 1995).) In addition, the locations of 5 STE introns were conserved in the human DHEA- sulfotransferase gene, which is located on chromosome 19. Weinshilboum et al. (1997) reviewed the genes in the mouse corresponding to the sulfotransferase genes in the human. The Ste gene is located on mouse chromosome 5.

[31214]

[31215] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31216] Aksoy, I. A.; Wood, T. C.; Weinshilboum, R. : Human liver

estrogen sulfotransferase: identification by cDNA cloning and expression. Biochem. Biophys. Res. Commun. 200: 1621- 1629, 1994. ; and

[31217] Bernier, F.; Leblanc, G.; Labrie, F.; Luu- The, V. : Structure of human estrogen and aryl sulfotransferase gene: two mRNA species issued from a single gene. J. Biol. Chem. 269: 28200- 282.

[31218] Further studies establishing the function and utilities of STE are found in John Hopkins OMIM database record ID 600043, and in cited publications listed in Table 5, which are hereby incorporated by reference.Six transmembrane epithelial antigen of prostate 2 (STEAP2, Accession NP_694544.1) is another GAM189 target gene, herein designated TARGET GENE. STEAP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STEAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STEAP2 BINDING SITE, designated SEQ ID:9147, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31219] Another function of GAM189 is therefore inhibition of Six

transmembrane epithelial antigen of prostate 2 (STEAP2, Accession NP_694544.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STEAP2.

[31220] Stomatin (STOM, Accession NP_004090.3) is another GAM189 target gene, herein designated TARGET GENE. STOM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STOM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STOM BINDING SITE, designated SEQ ID:2907, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31221] Another function of GAM189 is therefore inhibition of Stomatin (STOM, Accession NP_004090.3) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STOM.

[31222] Syntaxin 12 (STX12, Accession NP_803173.1) is another GAM189 target gene, herein designated TARGET GENE. STX12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STX12, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STX12 BINDING SITE, designated SEQ ID:12575, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31223] Another function of GAM189 is therefore inhibition of Syntaxin 12 (STX12, Accession NP_803173.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STX12.

[31224] Synaptotagmin xi (SYT11, Accession NP_689493.2) is another GAM189 target gene, herein designated TARGET GENE. SYT11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYT11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYT11 BINDING SITE, designated SEQ ID:9033, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31225] Another function of GAM189 is therefore inhibition of Synaptotagmin xi (SYT11, Accession NP_689493.2) . Ac-

cordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT11.

[31226] Synaptotagmin xiii (SYT13, Accession NP_065877.1) is another GAM189 target gene, herein designated TARGET GENE. SYT13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYT13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYT13 BINDING SITE, designated SEQ ID:15294, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31227] Another function of GAM189 is therefore inhibition of Synaptotagmin xiii (SYT13, Accession NP_065877.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT13.

[31228] TADA3L (Accession NP_597814.1) is another GAM189 target gene, herein designated TARGET GENE. TADA3L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TADA3L, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TADA3L BINDING SITE, designated SEQ ID:9087, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31229] Another function of GAM189 is therefore inhibition of TADA3L (Accession NP_597814.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TADA3L.

[31230] T-cell acute lymphocytic leukemia 1 (TAL1, Accession NP_003180.1) is another GAM189 target gene, herein designated TARGET GENE. TAL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TAL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAL1 BINDING SITE, designated SEQ ID:18260, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31231] Another function of GAM189 is therefore inhibition of T-cell acute lymphocytic leukemia 1 (TAL1, Accession

NP_003180.1), a gene which may help control cell growth and differentiation. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAL1.

[31232] The function of TAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tap binding protein (tapasin) (TAPBP, Accession NP_003181.3) is another GAM189 target gene, herein designated TARGET GENE. TAPBP BINDING SITE1 through TAPBP BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TAPBP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAPBP BINDING SITE1 through TAPBP BINDING SITE3, designated SEQ ID:11523, SEQ ID:12247 and SEQ ID:16940 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31233] Another function of GAM189 is therefore inhibition of Tap binding protein (tapasin) (TAPBP, Accession NP_003181.3), a gene which is involved in MHC class I-

restricted antigen processing. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAPBP.

[31234] The function of TAPBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Tyrosine aminotransferase (TAT, Accession NP_000344.1) is another GAM189 target gene, herein designated TARGET GENE. TAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAT BINDING SITE, designated SEQ ID:18942, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31235] Another function of GAM189 is therefore inhibition of Tyrosine aminotransferase (TAT, Accession NP_000344.1), a gene which is tyrosine aminotransferase and strongly similar to rat Rn.9947, which plays a role in gluconeogenesis. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with TAT.

[31236] The function of TAT has been established by previous studies. Richner (1938) and Hanhart (1947) described an oculocutaneous syndrome characterized by herpetiform corneal ulcers and painful punctate keratoses of digits, palms, and soles. Richner (1938) described skin lesions in brother and sister. Only the brother had corneal lesions. Hanhart (1947) reported that the parents of his patient were second cousins. Hanhart (1947) also described associated severe mental and somatic retardation. The pedigree he reported was reproduced by Waardenburg et al. (1961). Waardenburg et al. (1961) described children of a first- cousin marriage, one with the full syndrome and one with only corneal changes. Ventura et al. (1965) described the syndrome in 2 sons of first- cousin parents. Buist (1967) referred to studies of a child with tyrosinemia and tyrosine transaminase deficiency, but normal p- hydroxyphenylpyruvic acid oxidase. Phenylalanine level was normal. Hydroxyphenylpyruvic acid was elevated in the urine. Fellman et al. (1969) reported chemical studies on the same patient. Only the mitochondrial form of tyrosine aminotransferase (TAT) was present in the liver. The soluble form of TAT (EC 2.6.1.5) was lacking. The patient had

markedly elevated tyrosine blood levels and an increase in urinary p- hydroxyphenylpyruvate and p- hydroxyphenyl-lactate. A regulator gene for tyrosine transaminase is X-linked (OMIM Ref. No. 314350). Goldsmith et al. (1973) demonstrated tyrosinemia and phenylaceticacidemia in this disorder. Their patient was the 14- year- old son of consanguineous Italian parents. The urine contained excessive P- hydroxyphenylactic acid. Urinary P- hydroxyphenylpyruvic acid was normal. Clinical and biochemical improvement accompanied low phenylalanine- low tyrosine diet. They suggested that soluble TAT may be deficient. Mitochondrial tyrosine transaminase is normal. Beinfang et al. (1976) described the ophthalmologic findings in the patient reported by Goldsmith et al. (1973). This condition is also known as tyrosinemia with palmar and plantar keratosis and keratitis. Garibaldi et al. (1977) observed this disorder, which they called oculocutaneous tyrosinosis, in a 42- month- old girl and her maternal aunt. The parents of the maternal aunt were first cousins. They emphasized the importance of early diagnosis in order to prevent mental retardation by means of a diet restricted in phenylalanine and tyrosine. Hunziker (1980) reported brother and sister with unusually late onset (about age

15). Their patients' skin lesions were improved with a diet restricted in phenylalanine and tyrosine. In a consanguineous sibship, Rehak et al. (1981) reported 4 cases of Richner- Hanhart syndrome. Cutaneous manifestations were typical but the eyes were not involved, suggesting heterogeneity in this disorder. Bohnert and Anton- Lamprecht (1982) reported unique ultrastructural changes: thickening of the granular layer and increased synthesis of tonofibrils and keratohyalin; in the ridged palmar or plantar skin, large numbers of microtubules and unusually tight packing of tonofibrillar masses, which contained tubular channels or inclusions of microtubules. The authors assumed that increased cohesion and tight packing of tonofilaments prevent normal spreading of keratohyalin and result in its globular appearance. Further, they suggested that excessive amounts of intracellular tyrosine enhance crosslinks between aggregated tonofilaments. In an Ashkenazi Jewish family, Chitayat et al. (1992) observed 2 adult sibs, offspring of a first- cousin marriage, with persistent hypertyrosinemia. A curious feature was that the affected female sib, aged 41 years, had hypertyrosinemia and characteristic oculocutaneous signs; the brother, aged 39 years, had hypertyrosinemia but no ocu-

locutaneous disease. Both sibs had 2 children; none had signs of metabolic fetopathy.

[31237]

[31238] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31239] Goldsmith, L. A.; Kang, E. S.; Bienfang, D. C.; Jimbow, K.; Gerald, P. S.; Baden, H. P. : Tyrosinemia with plantar and palmar keratosis and keratitis. J. Pediat. 83: 798- 805, 1973. ; and

[31240] Hunziker, N. : Richner- Hanhart syndrome and tyrosinemia type II. Dermatologica 160: 180- 189, 1980.

[31241] Further studies establishing the function and utilities of TAT are found in John Hopkins OMIM database record ID 276600, and in cited publications listed in Table 5, which are hereby incorporated by reference.Tbc1 domain family, member 5 (TBC1D5, Accession NP_055559.1) is another GAM189 target gene, herein designated TARGET GENE. TBC1D5 BINDING SITE1 and TBC1D5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TBC1D5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of TBC1D5 BINDING SITE1 and TBC1D5 BINDING SITE2, designated SEQ ID:14859 and SEQ ID:16449 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31242] Another function of GAM189 is therefore inhibition of Tbc1 domain family, member 5 (TBC1D5, Accession NP_055559.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBC1D5.

[31243] T-box 3 (ulnar mammary syndrome) (TBX3, Accession NP_005987.2) is another GAM189 target gene, herein designated TARGET GENE. TBX3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TBX3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TBX3 BINDING SITE, designated SEQ ID:19690, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31244] Another function of GAM189 is therefore inhibition of T-box 3 (ulnar mammary syndrome) (TBX3, Accession

NP_005987.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBX3.

[31245] T-box 3 (ulnar mammary syndrome) (TBX3, Accession NP_057653.2) is another GAM189 target gene, herein designated TARGET GENE. TBX3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TBX3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TBX3 BINDING SITE, designated SEQ ID:19690, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31246] Another function of GAM189 is therefore inhibition of T-box 3 (ulnar mammary syndrome) (TBX3, Accession NP_057653.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBX3.

[31247] Transcription factor 2, hepatic; lf-b3; variant hepatic nuclear factor (TCF2, Accession NP_006472.1) is another GAM189 target gene, herein designated TARGET GENE. TCF2 BINDING SITE is a target binding site found in the 3`

untranslated region of multiple transcripts of mRNA encoded by TCF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCF2 BINDING SITE, designated SEQ ID:625, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31248] Another function of GAM189 is therefore inhibition of Transcription factor 2, hepatic; lf-b3; variant hepatic nuclear factor (TCF2, Accession NP_006472.1), a gene which probably binds to the inverted palindrome 5'- gttaatnattaac- 3'. and therefore is associated with Maturity- onset diabetes of the young type 5 (mody5), familial hypoplastic glomerulocystic kidney disease (gckd). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Maturity- onset diabetes of the young type 5 (mody5), familial hypoplastic glomerulocystic kidney disease (gckd), and of other diseases and clinical conditions associated with TCF2.

[31249] The function of TCF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.T-cell leukemia/lymphoma 6 (TCL6, Acces-

sion NP_065575.1) is another GAM189 target gene, herein designated TARGET GENE. TCL6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TCL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE, designated SEQ ID:17450, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31250] Another function of GAM189 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065575.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[31251] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_036600.2) is another GAM189 target gene, herein designated TARGET GENE. TCL6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TCL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6

BINDING SITE, designated SEQ ID:17450, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31252] Another function of GAM189 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_036600.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[31253] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065577.2) is another GAM189 target gene, herein designated TARGET GENE. TCL6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TCL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE, designated SEQ ID:17450, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31254] Another function of GAM189 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065577.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with TCL6.

[31255] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_055233.1) is another GAM189 target gene, herein designated TARGET GENE. TCL6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TCL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE, designated SEQ ID:17450, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31256] Another function of GAM189 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_055233.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[31257] Teratocarcinoma-derived growth factor 1 (TDGF1, Accession NP_003203.1) is another GAM189 target gene, herein designated TARGET GENE. TDGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TDGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TDGF1 BINDING SITE, designated SEQ ID:8563, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31258] Another function of GAM189 is therefore inhibition of Teratocarcinoma-derived growth factor 1 (TDGF1, Accession NP_003203.1), a gene which can play a role in the determination of the epiblastic cells that subsequently give rise to the mesoderm. and therefore may be associated with Forebrain defects. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Forebrain defects, and of other diseases and clinical conditions associated with TDGF1.

[31259] The function of TDGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.TERA (Accession NP_067061.1) is another GAM189 target gene, herein designated TARGET GENE. TERA BINDING SITE1 and TERA BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TERA, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of TERA BINDING SITE1 and TERA BINDING SITE2, designated SEQ ID:17755 and SEQ ID:14491 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31260] Another function of GAM189 is therefore inhibition of TERA (Accession NP_067061.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERA.

[31261] Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_059523.1) is another GAM189 target gene, herein designated TARGET GENE. TERF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TERF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF1 BINDING SITE, designated SEQ ID:1745, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31262] Another function of GAM189 is therefore inhibition of Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_059523.1), a gene which negatively

regulates telomere length, involves in regulation of the mitotic spindle. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF1.

[31263] The function of TERF1 has been established by previous studies. Human chromosomes carry at their termini long arrays of double- stranded hexamers (OMIM Ref. No. TTAGGG) that are maintained by the enzyme telomerase (OMIM Ref. No. 187270). Chong et al. (1995) noted that telomeric DNA is thought to form a protective nucleoprotein cap through its association with telomere- specific proteins; also see review by Zakian (1995). Because the loss of telomere function can induce cell cycle arrest and genome instability, the telomeric complex is probably required in all human cells. Changes in the structure and function of human telomeres are thought to play a role in malignant transformation and cellular senescence. Protein components of the telomeric complex had been identified in ciliates and yeast, but not in vertebrate systems. Quests for vertebrate telomeric proteins had yielded a single candidate that could potentially bind along the length of the telomeric TTAGGG repeat array. This protein, called TRF (telomeric repeat- binding factor) by Chong et al. (1995),

was shown by the authors to associate with double-stranded TTAGGG repeat arrays in vitro. TRF displays strong specificity for vertebrate telomere DNA. Human TRF activity is detectable in HeLa cell nuclear extracts on the basis of its ability to alter the mobility of double-stranded DNA fragments containing the sequence (OMIM Ref. No. TTAGGG)12. Using this assay, Chong et al. (1995) purified HeLa TRF to near homogeneity. Three independent preparations of purified TRF contained a protein in the 60- kD apparent molecular mass range, which copurified with TRF activity over a column containing double-stranded TTAGGG repeats. Amino acid sequences revealed sequence identity to an anonymous partial cDNA in the GenBank database. On the basis of this nucleotide sequence, cDNAs were isolated from a HeLa cell library, sequenced, and found to contain an open reading frame encoding all sequence peptides. The cDNA hybridized 2 mRNAs of approximately 1.8 and 3.0 kb that are expressed in a variety of human tissues. The cDNA derived from the larger mRNA revealed an open reading frame encoding a 439- amino acid protein. In vitro transcription and translation of the cloned cDNA produced a protein of the same size as purified HeLa TRF. Comparison with the sequence

information in the databases indicated that human TRF is a novel protein with 3 previously recognized sequence motifs. There is one DNA- binding repeat resembling that of MYB (OMIM Ref. No. 189990) and an N- terminal acidic domain. Immunofluorescent labeling showed that TRF specifically colocalizes with telomeric DNA in human metaphase cells and is located at chromosome ends during metaphase. Chong et al. (1995) stated that the presence of TRF along the telomeric TTAGGG repeat array demonstrates that human telomeres form a specialized nuclear protein complex. In yeast, Marcand et al. (1997) demonstrated a protein- counting mechanism for regulation of the length of telomeres. This mechanism involves the telomere repeat- binding protein Rap1p. Because the structural and functional properties of telomeres appear to be highly conserved, Marcand et al. (1997) suggested that their findings may be relevant to telomere length regulation in humans, which has been associated with aging and cancer. Okabe et al. (2000) investigated cellular factors required for telomere formation using the frequency of telomere seeding as an index and identified TRF1 as an essential transacting factor. The exogenous telomere repeat induced telomere formation at a fre-

quency determined by the availability of TRF1, even in telomerase- negative cells. The authors concluded that TRF1 has a novel physiologic significance distinct from its role as a regulator of telomere length in the endogenous chromosome.

[31264]

[31265] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31266] Chong, L.; van Steensel, B.; Broccoli, D.; Erdjument- Bromage, H.; Hanish, J.; Tempst, P.; de Lange, T. : A human telomeric protein. Science 270: 1663- 1667, 1995. ; and

[31267] Okabe, J.; Eguchi, A.; Masago, A.; Hayakawa, T.; Nakanishi, M. : TRF1 is a critical trans- acting factor required for de novo telomere formation in human cells. Hum. Molec. Genet. 9: 263.

[31268] Further studies establishing the function and utilities of TERF1 are found in John Hopkins OMIM database record ID 600951, and in cited publications listed in Table 5, which are hereby incorporated by reference.Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_003209.1) is another GAM189 target gene, herein designated TARGET GENE. TERF1 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TERF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF1 BINDING SITE, designated SEQ ID:1745, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31269] Another function of GAM189 is therefore inhibition of Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_003209.1), a gene which negatively regulates telomere length, involves in regulation of the mitotic spindle. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF1.

[31270] The function of TERF1 has been established by previous studies. Human chromosomes carry at their termini long arrays of double- stranded hexamers (OMIM Ref. No. TTAGGG) that are maintained by the enzyme telomerase (OMIM Ref. No. 187270). Chong et al. (1995) noted that telomeric DNA is thought to form a protective nucleoprotein cap through its association with telomere- specific proteins; also see review by Zakian (1995). Because the

loss of telomere function can induce cell cycle arrest and genome instability, the telomeric complex is probably required in all human cells. Changes in the structure and function of human telomeres are thought to play a role in malignant transformation and cellular senescence. Protein components of the telomeric complex had been identified in ciliates and yeast, but not in vertebrate systems. Quests for vertebrate telomeric proteins had yielded a single candidate that could potentially bind along the length of the telomeric TTAGGG repeat array. This protein, called TRF (telomeric repeat- binding factor) by Chong et al. (1995), was shown by the authors to associate with double-stranded TTAGGG repeat arrays in vitro. TRF displays strong specificity for vertebrate telomere DNA. Human TRF activity is detectable in HeLa cell nuclear extracts on the basis of its ability to alter the mobility of double-stranded DNA fragments containing the sequence (OMIM Ref. No. TTAGGG)12. Using this assay, Chong et al. (1995) purified HeLa TRF to near homogeneity. Three independent preparations of purified TRF contained a protein in the 60- kD apparent molecular mass range, which copurified with TRF activity over a column containing double-stranded TTAGGG repeats. Amino acid sequences revealed

sequence identity to an anonymous partial cDNA in the GenBank database. On the basis of this nucleotide sequence, cDNAs were isolated from a HeLa cell library, sequenced, and found to contain an open reading frame encoding all sequence peptides. The cDNA hybridized 2 mRNAs of approximately 1.8 and 3.0 kb that are expressed in a variety of human tissues. The cDNA derived from the larger mRNA revealed an open reading frame encoding a 439- amino acid protein. In vitro transcription and translation of the cloned cDNA produced a protein of the same size as purified HeLa TRF. Comparison with the sequence information in the databases indicated that human TRF is a novel protein with 3 previously recognized sequence motifs. There is one DNA- binding repeat resembling that of MYB (OMIM Ref. No. 189990) and an N- terminal acidic domain. Immunofluorescent labeling showed that TRF specifically colocalizes with telomeric DNA in human metaphase cells and is located at chromosome ends during metaphase. Chong et al. (1995) stated that the presence of TRF along the telomeric TTAGGG repeat array demonstrates that human telomeres form a specialized nuclear protein complex. In yeast, Marcand et al. (1997) demonstrated a protein- counting mechanism for regula-

tion of the length of telomeres. This mechanism involves the telomere repeat- binding protein Rap1p. Because the structural and functional properties of telomeres appear to be highly conserved, Marcand et al. (1997) suggested that their findings may be relevant to telomere length regulation in humans, which has been associated with aging and cancer. Okabe et al. (2000) investigated cellular factors required for telomere formation using the frequency of telomere seeding as an index and identified TRF1 as an essential transacting factor. The exogenous telomere repeat induced telomere formation at a frequency determined by the availability of TRF1, even in telomerase- negative cells. The authors concluded that TRF1 has a novel physiologic significance distinct from its role as a regulator of telomere length in the endogenous chromosome.

[31271]

[31272] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31273] Chong, L.; van Steensel, B.; Broccoli, D.; Erdjument- Bromage, H.; Hanish, J.; Tempst, P.; de Lange, T. : A human telomeric protein. Science 270: 1663- 1667, 1995. ; and

[31274] Okabe, J.; Eguchi, A.; Masago, A.; Hayakawa, T.; Nakanishi, M. : TRF1 is a critical trans- acting factor required for de novo telomere formation in human cells. Hum. Molec. Genet. 9: 263.

[31275] Further studies establishing the function and utilities of TERF1 are found in John Hopkins OMIM database record ID 600951, and in cited publications listed in Table 5, which are hereby incorporated by reference.Telomeric repeat binding factor 2 (TERF2, Accession NP_005643.1) is another GAM189 target gene, herein designated TARGET GENE. TERF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TERF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF2 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31276] Another function of GAM189 is therefore inhibition of Telomeric repeat binding factor 2 (TERF2, Accession NP_005643.1), a gene which plays a key role in the protective activity of telomeres. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with TERF2.

[31277] The function of TERF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM133.2.Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) is another GAM189 target gene, herein designated TARGET GENE. TGIF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGIF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGIF2 BINDING SITE, designated SEQ ID:6881, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31278] Another function of GAM189 is therefore inhibition of Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGIF2.

[31279] Tigger transposable element derived 6 (TIGD6, Accession NP_112215.1) is another GAM189 target gene, herein designated TARGET GENE. TIGD6 BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by TIGD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TIGD6 BINDING SITE, designated SEQ ID:4933, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31280] Another function of GAM189 is therefore inhibition of Tigger transposable element derived 6 (TIGD6, Accession NP_112215.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIGD6.

[31281] TIM50L (Accession XP_053074.2) is another GAM189 target gene, herein designated TARGET GENE. TIM50L BINDING SITE1 and TIM50L BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TIM50L, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TIM50L BINDING SITE1 and TIM50L BINDING SITE2, designated SEQ ID:5989 and SEQ ID:10157 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31282] Another function of GAM189 is therefore inhibition of TIM50L (Accession XP_053074.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIM50L.

[31283] Tousled-like kinase 1 (TLK1, Accession NP_036422.2) is another GAM189 target gene, herein designated TARGET GENE. TLK1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TLK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLK1 BINDING SITE, designated SEQ ID:6551, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31284] Another function of GAM189 is therefore inhibition of Tousled-like kinase 1 (TLK1, Accession NP_036422.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLK1.

[31285] Toll-like receptor 5 (TLR5, Accession NP_003259.2) is another GAM189 target gene, herein designated TARGET GENE. TLR5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TLR5,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLR5 BINDING SITE, designated SEQ ID:16229, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31286] Another function of GAM189 is therefore inhibition of Toll-like receptor 5 (TLR5, Accession NP_003259.2), a gene which participates in the innate immune response to bacterial flagellins. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLR5.

[31287] The function of TLR5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Transmembrane, cochlear expressed, 1 (TMC1, Accession NP_619636.2) is another GAM189 target gene, herein designated TARGET GENE. TMC1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TMC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMC1 BIND-

ING SITE, designated SEQ ID:2152, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31288] Another function of GAM189 is therefore inhibition of Transmembrane, cochlear expressed, 1 (TMC1, Accession NP_619636.2), a gene which is required for normal function of cochlear hair cells and therefore may be associated with Autosomal recessive nonsyndromic neurosensory deafness and autosomal dominant nonsyndromic sensorineural hearing loss . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Autosomal recessive nonsyndromic neurosensory deafness and autosomal dominant nonsyndromic sensorineural hearing loss ., and of other diseases and clinical conditions associated with TMC1.

[31289] The function of TMC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.TMEM14A (Accession NP_054770.1) is another GAM189 target gene, herein designated TARGET GENE. TMEM14A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TMEM14A, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMEM14A BINDING SITE, designated SEQ ID:5271, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31290] Another function of GAM189 is therefore inhibition of TMEM14A (Accession NP_054770.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEM14A.

[31291] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_076927.1) is another GAM189 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE, designated SEQ ID:6625, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31292] Another function of GAM189 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession

NP_076927.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[31293] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115777.1) is another GAM189 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE, designated SEQ ID:6625, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31294] Another function of GAM189 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115777.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[31295] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115780.1) is another GAM189 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE, designated SEQ ID:6625, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31296] Another function of GAM189 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115780.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[31297] Tumor necrosis factor, alpha-induced protein 2 (TNFAIP2, Accession NP_006282.2) is another GAM189 target gene, herein designated TARGET GENE. TNFAIP2 BINDING SITE1 and TNFAIP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TNFAIP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFAIP2 BINDING SITE1 and TNFAIP2 BINDING SITE2, designated SEQ ID:13948 and SEQ ID:17621 respectively, to the nucleotide sequence of GAM189 RNA,

herein designated GAM RNA, also designated SEQ ID:246.

[31298] Another function of GAM189 is therefore inhibition of Tumor necrosis factor, alpha-induced protein 2 (TNFAIP2, Accession NP_006282.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFAIP2.

[31299] Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_003833.3) is another GAM189 target gene, herein designated TARGET GENE. TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF10B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2, designated SEQ ID:4398 and SEQ ID:4398 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31300] Another function of GAM189 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_003833.3), a gene which forms complex that induces apoptosis. and therefore may be as-

sociated with Squamous cell carcinoma . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Squamous cell carcinoma ., and of other diseases and clinical conditions associated with TNFRSF10B.

[31301] The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_671716.1) is another GAM189 target gene, herein designated TARGET GENE. TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF10B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2, designated SEQ ID:15107 and SEQ ID:15107 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31302] Another function of GAM189 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10b

(TNFRSF10B, Accession NP_671716.1), a gene which forms complex that induces apoptosis. and therefore may be associated with Squamous cell carcinoma . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Squamous cell carcinoma ., and of other diseases and clinical conditions associated with TNFRSF10B.

[31303] The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tumor necrosis factor receptor superfamily, member 11a, activator of nfkb (TNFRSF11A, Accession NP_003830.1) is another GAM189 target gene, herein designated TARGET GENE. TNFRSF11A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF11A BINDING SITE, designated SEQ ID:2200, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31304] Another function of GAM189 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 11a,

activator of nfkb (TNFRSF11A, Accession NP_003830.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF11A.

[31305] Tumor necrosis factor receptor superfamily, member 21 (TNFRSF21, Accession NP_055267.1) is another GAM189 target gene, herein designated TARGET GENE. TNFRSF21 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF21 BINDING SITE, designated SEQ ID:16759, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31306] Another function of GAM189 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 21 (TNFRSF21, Accession NP_055267.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF21.

[31307] Tumor necrosis factor receptor superfamily, member 9 (TNFRSF9, Accession NP_001552.2) is another GAM189

target gene, herein designated TARGET GENE. TNFRSF9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF9 BINDING SITE, designated SEQ ID:13464, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31308] Another function of GAM189 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 9 (TNFRSF9, Accession NP_001552.2), a gene which inhibits proliferation of activated T lymphocytes. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF9.

[31309] The function of TNFRSF9 has been established by previous studies. Schwarz et al. (1996) reported that ILA inhibits proliferation of activated T lymphocytes and induces programmed cell death. Loo et al. (1997) reported that, unlike its mouse counterpart, human 4- 1BB binds only to its ligand, TNFSF9, and not to extracellular matrix proteins such as laminin (see OMIM Ref. No. 150240). The authors

attributed this species distinction to sequence differences in the N- terminal laminin- homologous domain of human 4- 1BB.

[31310]

[31311] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31312] Loo, D. T.; Chalupny, N. J.; Bajorath, J.; Shuford, W. W.; Mittler, R. S.; Aruffo, A. : Analysis of 4- 1BBL and laminin binding to murine 4- 1BB, a member of the tumor necrosis factor receptor superfamily, and comparison with human 4- 1BB. J. Biol. Chem. 272: 6448- 6456, 1997. ; and

[31313] Schwarz, H.; Arden, K.; Lotz, M. : CD137, a member of the tumor necrosis factor receptor family, is located on chromosome 1p36, in a cluster of related genes, and colocalizes with sever.

[31314] Further studies establishing the function and utilities of TNFRSF9 are found in John Hopkins OMIM database record ID 602250, and in cited publications listed in Table 5, which are hereby incorporated by reference.Tensin (TNS, Accession NP_072174.2) is another GAM189 target gene, herein designated TARGET GENE. TNS BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by TNS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNS BINDING SITE, designated SEQ ID:8787, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31315] Another function of GAM189 is therefore inhibition of Tensin (TNS, Accession NP_072174.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNS.

[31316] TOLLIP (Accession NP_061882.2) is another GAM189 target gene, herein designated TARGET GENE. TOLLIP BINDING SITE1 and TOLLIP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TOLLIP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOLLIP BINDING SITE1 and TOLLIP BINDING SITE2, designated SEQ ID:13694 and SEQ ID:3306 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31317] Another function of GAM189 is therefore inhibition of TOLLIP (Accession NP_061882.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOLLIP.

[31318] Topoisomerase (dna) iii beta (TOP3B, Accession NP_003926.1) is another GAM189 target gene, herein designated TARGET GENE. TOP3B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TOP3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOP3B BINDING SITE, designated SEQ ID:4495, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31319] Another function of GAM189 is therefore inhibition of Topoisomerase (dna) iii beta (TOP3B, Accession NP_003926.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOP3B.

[31320] Torsin family 1, member b (torsin b) (TOR1B, Accession NP_055321.1) is another GAM189 target gene, herein designated TARGET GENE. TOR1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by TOR1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOR1B BINDING SITE, designated SEQ ID:14221, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31321] Another function of GAM189 is therefore inhibition of Torsin family 1, member b (torsin b) (TOR1B, Accession NP_055321.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOR1B.

[31322] TOSO (Accession NP_005440.1) is another GAM189 target gene, herein designated TARGET GENE. TOSO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TOSO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOSO BINDING SITE, designated SEQ ID:5682, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31323] Another function of GAM189 is therefore inhibition of

TOSO (Accession NP_005440.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOSO.

[31324] Tumor protein p53 (li-fraumeni syndrome) (TP53, Accession NP_000537.2) is another GAM189 target gene, herein designated TARGET GENE. TP53 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TP53, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TP53 BINDING SITE, designated SEQ ID:4654, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31325] Another function of GAM189 is therefore inhibition of Tumor protein p53 (li-fraumeni syndrome) (TP53, Accession NP_000537.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53.

[31326] TP53I11 (Accession XP_029347.6) is another GAM189 target gene, herein designated TARGET GENE. TP53I11 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TP53I11, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TP53I11 BINDING SITE, designated SEQ ID:14987, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31327] Another function of GAM189 is therefore inhibition of TP53I11 (Accession XP_029347.6) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53I11.

[31328] Thiopurine s-methyltransferase (TPMT, Accession NP_000358.1) is another GAM189 target gene, herein designated TARGET GENE. TPMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TPMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPMT BINDING SITE, designated SEQ ID:19670, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31329] Another function of GAM189 is therefore inhibition of

Thiopurine s-methyltransferase (TPMT, Accession NP_000358.1), a gene which catalyzes the s- methylation of thiopurine drugs such as 6- mercaptopurine. and therefore may be associated with Thiopurine s- methyl-transferase polymorphism. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Thiopurine s- methyltransferase polymorphism, and of other diseases and clinical conditions associated with TPMT.

[31330] The function of TPMT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Tnf receptor-associated factor 5 (TRAF5, Accession NP_004610.1) is another GAM189 target gene, herein designated TARGET GENE. TRAF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRAF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:7045, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31331] Another function of GAM189 is therefore inhibition of Tnf receptor-associated factor 5 (TRAF5, Accession NP_004610.1), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5.

[31332] The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Tnf receptor-associated factor 5 (TRAF5, Accession NP_665702.1) is another GAM189 target gene, herein designated TARGET GENE. TRAF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRAF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:7045, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31333] Another function of GAM189 is therefore inhibition of Tnf receptor-associated factor 5 (TRAF5, Accession

NP_665702.1), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5.

[31334] The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Tripartite motif-containing 16 (TRIM16, Accession NP_006461.2) is another GAM189 target gene, herein designated TARGET GENE. TRIM16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRIM16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM16 BINDING SITE, designated SEQ ID:4601, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31335] Another function of GAM189 is therefore inhibition of Tripartite motif-containing 16 (TRIM16, Accession NP_006461.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with TRIM16.

[31336] Tripartite motif-containing 5 (TRIM5, Accession NP_149023.1) is another GAM189 target gene, herein designated TARGET GENE. TRIM5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRIM5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM5 BINDING SITE, designated SEQ ID:5879, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31337] Another function of GAM189 is therefore inhibition of Tripartite motif-containing 5 (TRIM5, Accession NP_149023.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM5.

[31338] Tripartite motif-containing 6 (TRIM6, Accession NP_477514.1) is another GAM189 target gene, herein designated TARGET GENE. TRIM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRIM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM6 BINDING SITE, designated SEQ ID:13572, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31339] Another function of GAM189 is therefore inhibition of Tripartite motif-containing 6 (TRIM6, Accession NP_477514.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM6.

[31340] TRIP-Br2 (Accession NP_055570.1) is another GAM189 target gene, herein designated TARGET GENE. TRIP-Br2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRIP-Br2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIP-Br2 BINDING SITE, designated SEQ ID:19574, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31341] Another function of GAM189 is therefore inhibition of TRIP-Br2 (Accession NP_055570.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with TRIP-Br2.

[31342] Transient receptor potential cation channel, subfamily m, member 6 (TRPM6, Accession NP_060132.3) is another GAM189 target gene, herein designated TARGET GENE. TRPM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPM6 BINDING SITE, designated SEQ ID:18177, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31343] Another function of GAM189 is therefore inhibition of Transient receptor potential cation channel, subfamily m, member 6 (TRPM6, Accession NP_060132.3), a gene which contains a predicted ion channel domain and a protein kinase domain. and therefore is associated with Hypomagnesemia with secondary hypocalcemia. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Hypomagnesemia with secondary hypocalcemia, and of other diseases and clinical conditions associated with TRPM6.

[31344] The function of TRPM6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1) is another GAM189 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:16980 and SEQ ID:19833 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31345] Another function of GAM189 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[31346] The function of TRPV1 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542437.1) is another GAM189 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:16980 and SEQ ID:16980 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31347] Another function of GAM189 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542437.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[31348] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1) is another GAM189 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:19833 and SEQ ID:19833 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31349] Another function of GAM189 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[31350] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542435.1) is another GAM189 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:19833 and SEQ ID:16980 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31351] Another function of GAM189 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542435.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[31352] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Tuberous sclerosis 1 (TSC1, Accession

NP_000359.1) is another GAM189 target gene, herein designated TARGET GENE. TSC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TSC1 BINDING SITE, designated SEQ ID:15082, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31353] Another function of GAM189 is therefore inhibition of Tuberous sclerosis 1 (TSC1, Accession NP_000359.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSC1.

[31354] Tspy-like (TSPYL, Accession XP_166325.1) is another GAM189 target gene, herein designated TARGET GENE. TSPYL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSPYL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TSPYL BINDING SITE, designated SEQ ID:15042, to the nu-

cleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31355] Another function of GAM189 is therefore inhibition of Tspy-like (TSPYL, Accession XP_166325.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSPYL.

[31356] TTY7 (Accession NP_114132.1) is another GAM189 target gene, herein designated TARGET GENE. TTY7 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TTY7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TTY7 BINDING SITE, designated SEQ ID:1016, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31357] Another function of GAM189 is therefore inhibition of TTY7 (Accession NP_114132.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTY7.

[31358] TU12B1-TY (Accession NP_057659.1) is another GAM189 target gene, herein designated TARGET GENE. TU12B1-TY

BINDING SITE1 through TU12B1-TY BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by TU12B1-TY, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TU12B1-TY BINDING SITE1 through TU12B1-TY BINDING SITE3, designated SEQ ID:4256, SEQ ID:16036 and SEQ ID:15780 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31359] Another function of GAM189 is therefore inhibition of TU12B1-TY (Accession NP_057659.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TU12B1-TY.

[31360] TUCAN (Accession NP_055774.1) is another GAM189 target gene, herein designated TARGET GENE. TUCAN BINDING SITE1 and TUCAN BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TUCAN, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUCAN BINDING SITE1 and TUCAN

BINDING SITE2, designated SEQ ID:9530 and SEQ ID:7106 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31361] Another function of GAM189 is therefore inhibition of TUCAN (Accession NP_055774.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUCAN.

[31362] TXL-2 (Accession NP_835231.1) is another GAM189 target gene, herein designated TARGET GENE. TXL-2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TXL-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TXL-2 BINDING SITE, designated SEQ ID:15381, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31363] Another function of GAM189 is therefore inhibition of TXL-2 (Accession NP_835231.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TXL-2.

[31364] Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) is another GAM189 target gene, herein designated TARGET

GENE. TXNL2 BINDING SITE1 and TXNL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TXNL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TXNL2 BINDING SITE1 and TXNL2 BINDING SITE2, designated SEQ ID:19232 and SEQ ID:9147 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31365] Another function of GAM189 is therefore inhibition of Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TXNL2.

[31366] U1SNRNPBP (Accession NP_851034.1) is another GAM189 target gene, herein designated TARGET GENE. U1SNRNPBP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by U1SNRNPBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of U1SNRNPBP BINDING SITE, desig-

nated SEQ ID:9590, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31367] Another function of GAM189 is therefore inhibition of U1SNRNPBP (Accession NP_851034.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U1SNRNPBP.

[31368] U1SNRNPBP (Accession NP_851030.1) is another GAM189 target gene, herein designated TARGET GENE. U1SNRNPBP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by U1SNRNPBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of U1SNRNPBP BINDING SITE, designated SEQ ID:9590, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31369] Another function of GAM189 is therefore inhibition of U1SNRNPBP (Accession NP_851030.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

U1SNRNPBP.

[31370] U1SNRNPBP (Accession NP_008951.1) is another GAM189 target gene, herein designated TARGET GENE. U1SNRNPBP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by U1SNRNPBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of U1SNRNPBP BINDING SITE, designated SEQ ID:9590, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31371] Another function of GAM189 is therefore inhibition of U1SNRNPBP (Accession NP_008951.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U1SNRNPBP.

[31372] UCK1 (Accession NP_113620.1) is another GAM189 target gene, herein designated TARGET GENE. UCK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UCK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of UCK1 BINDING SITE, designated SEQ ID:11791, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31373] Another function of GAM189 is therefore inhibition of UCK1 (Accession NP_113620.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UCK1.

[31374] Udp-glucose dehydrogenase (UGDH, Accession NP_003350.1) is another GAM189 target gene, herein designated TARGET GENE. UGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGDH BINDING SITE, designated SEQ ID:7909, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31375] Another function of GAM189 is therefore inhibition of Udp-glucose dehydrogenase (UGDH, Accession NP_003350.1), a gene which is an UDP- glucose dehydrogenase. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical con-

ditions associated with UGDH.

[31376] The function of UGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Udp glycosyltransferase 1 family, polypeptide a1 (UGT1A1, Accession NP_000454.1) is another GAM189 target gene, herein designated TARGET GENE. UGT1A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A1 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31377] Another function of GAM189 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a1 (UGT1A1, Accession NP_000454.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT1A1.

[31378] Udp glycosyltransferase 1 family, polypeptide a10 (UGT1A10, Accession NP_061948.1) is another GAM189 target gene, herein designated TARGET GENE. UGT1A10

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A10 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31379] Another function of GAM189 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a10 (UGT1A10, Accession NP_061948.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT1A10.

[31380] Udp glycosyltransferase 1 family, polypeptide a4 (UGT1A4, Accession NP_009051.1) is another GAM189 target gene, herein designated TARGET GENE. UGT1A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A4 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM189 RNA, herein designated

GAM RNA, also designated SEQ ID:246.

[31381] Another function of GAM189 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a4 (UGT1A4, Accession NP_009051.1), a gene which is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds. and therefore may be associated with Gilbert's syndrome, crigler- najjar. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Gilbert's syndrome, crigler- najjar, and of other diseases and clinical conditions associated with UGT1A4.

[31382] The function of UGT1A4 has been established by previous studies. By screening a liver cDNA library with a probe to a conserved transferase C- terminal sequence, followed by 5- prime RACE, Ritter et al. (1991) obtained cDNAs encoding UGT1A1 and UGT1A4, which they termed HUGBR1 and HUGBR2, respectively. The deduced 534- amino acid UGT1A4 protein shares 66% sequence similarity with UGT1A1 in the N terminus, which contains potential N-linked glycosylation sites, and complete identity after codon 287. Northern blot analysis revealed expression of a 2.6- kb transcript in liver. Unlike UGT1A1, expression of UGT1A4 is normal in type I Crigler- Najjar syndrome

(OMIM Ref. No. 218800). Functional analysis showed that UGT1A4 has glucuronidating activity although, in a review of the UGTs, Tukey and Strassburg (2000) found that UGT1A4 activity with bilirubin is rather modest compared to that of UGT1A1. UGT1A4 is relatively active with amines, steroids, and sapogenins. By Northern blot analysis, Ritter et al. (1992) determined that UGT1A4, then termed UGT1D, is expressed at lower levels than UGT1A1 in liver. By Southern blot analysis, Ritter et al. (1992) determined that all of the UGT1A genes map to the same locus on chromosome 2.

[31383]

[31384] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31385] Ritter, J. K.; Chen, F.; Sheen, Y. Y.; Tran, H. M.; Kimura, S.; Yeatman, M. T.; Owens, I. S. : A novel complex locus UGT1 encodes human bilirubin, phenol, and other UDP- glucuronosyltransferase isozymes with identical carboxyl termini. J. Biol. Chem. 267: 3257- 3261, 1992. ; and

[31386] Tukey, R. H.; Strassburg, C. P. : Human UDP- glucuronosyltransferases: metabolism, expression, and disease. Annu. Rev. Pharm. Toxicol. 40: 581- 616, 2000.

[31387] Further studies establishing the function and utilities of UGT1A4 are found in John Hopkins OMIM database record ID 606429, and in cited publications listed in Table 5, which are hereby incorporated by reference.Udp glycosyltransferase 1 family, polypeptide a6 (UGT1A6, Accession NP_001063.1) is another GAM189 target gene, herein designated TARGET GENE. UGT1A6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A6 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31388] Another function of GAM189 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a6 (UGT1A6, Accession NP_001063.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT1A6.

[31389] Udp glycosyltransferase 1 family, polypeptide a8 (UGT1A8, Accession NP_061949.3) is another GAM189 target gene, herein designated TARGET GENE. UGT1A8

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A8 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31390] Another function of GAM189 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a8 (UGT1A8, Accession NP_061949.3), a gene which is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT1A8.

[31391] The function of UGT1A8 has been established by previous studies. By screening colon cDNA libraries with UGT- specific primers, Mojarrabi and Mackenzie (1998) detected and sequenced UGT1A1, UGT1A3 (OMIM Ref. No. 606428), UGT1A4 (OMIM Ref. No. 606429), UGT1A6 (OMIM Ref. No. 606431), UGT1A8, UGT1A9 (OMIM Ref. No. 606434), and UGT1A10 (OMIM Ref. No. 606435). Of

these forms, only UGT1A8 and UGT1A10 are expressed predominantly in colon; the others are found in liver and other extrahepatic tissues. Sequence analysis predicted that the catalytically active form of UGT1A8 has lys132, thr202, and met212, instead of arg, ala, and leu, respectively, at these positions. Western blot analysis showed expression of a 56- kD protein that is most active towards hydroxylated metabolites of carcinogenic coumarins. RT-PCR analysis revealed expression in colon but not in liver, kidney, and several other tissues. Mojarrabi and Mackenzie (1998) suggested that UGT1A8 may be of particular importance in the glucuronidation of drugs given orally or as suppositories as well as in the elimination of ingested dietary mutagens and toxins. No 2 tissues contain the same identical complement of UGT proteins. This observation suggests that the functional properties of the proteins may have evolved to meet the unique challenges necessary for glucuronidation in different tissues. This is best represented by the extrahepatic expression of UGT1A7, UGT1A8, and UGT1A10, all 3 of which are found in different tissues of the intestinal tract. With the high concentration of UGTs in the intestinal tract, these proteins may play an important role in first- pass

metabolism, and thus alterations in function resulting from pharmacogenetic differences may influence systemic drug levels and therapeutic outcome. Huang et al. (2002) identified 4 genotypes at the UGT1A8 locus in 69 individuals. Their results indicated that the functional properties of the proteins encoded by UGT1A8*1 and UGT1A8*2 differ significantly in catalytic potential from UGT1A8*3.

[31392]

[31393] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31394] Huang, Y.- H.; Galijatovic, A.; Nguyen, N.; Geske, D.; Beaton, D.; Green, J.; Green, M.; Peters, W. H.; Tukey, R. H. : Identification and functional characterization of UDP-glucuronosyltransferases UGT1A8*1, UGT1A8*2 and UGT1A8*3. Pharmacogenetics 12: 287- 297, 2002. ; and

[31395] Mojarrabi, B.; Mackenzie, P. I. : Characterization of two UDP glucuronosyltransferases that are predominantly expressed in human colon. Biochem. Biophys. Res. Commun. 247: 704- 709, 199.

[31396] Further studies establishing the function and utilities of UGT1A8 are found in John Hopkins OMIM database record ID 606433, and in cited publications listed in Table 5,

which are hereby incorporated by reference.Udp glycosyltransferase 1 family, polypeptide a9 (UGT1A9, Accession NP_066307.1) is another GAM189 target gene, herein designated TARGET GENE. UGT1A9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A9 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31397] Another function of GAM189 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a9 (UGT1A9, Accession NP_066307.1), a gene which is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT1A9.

[31398] The function of UGT1A9 has been established by previous studies. By screening a liver cDNA library with a UGT1A6 (OMIM Ref. No. 606431) probe, Wooster et al. (1991) iso-

lated a cDNA encoding UGT1A9, which they termed HLUGP4. The deduced 531- amino acid protein shares 67% overall sequence identity with UGT1A1 but only 38% in the N terminus. Western blot analysis showed expression of a 56- kD protein. Functional analysis indicated that, like UGT1A6, UGT1A9 is most active towards halogenated phenols with higher UGT1A9 activity with simple phenols. Findlay et al. (2000) reported that the predominant thyroid hormone released from the thyroid gland, T4, and the inactive rat T3 were glucuronidated by cloned expressed bilirubin UGT1A1 and also phenol UGT1A9. Results from Crigler- Najjar (see OMIM Ref. No. 218800) microsomal samples indicated that UGT1A1 was the main contributor to thyroid hormone glucuronidation in the liver, with rat T3 being the preferential substrate. In kidney microsomes, thyroid hormone glucuronidation was more complex, suggesting that more than just the UGT1A9 isoform may be involved. Bioactive T3 was not significantly glucuronidated by these isoforms and other UGTs, and sulfotransferases may have been involved.

[31399]

[31400] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[31401] Wooster, R.; Sutherland, L.; Ebner, T.; Clarke, D.; Da Cruz e Silva, O.; Burchell, B. : Cloning and stable expression of a new member of the human liver phenol/bilirubin:UDP-glucuronosyltransferase cDNA family. Biochem. J. 278: 465- 469, 1991. ; and

[31402] Findlay, K. A. B.; Kaptein, E.; Visser, T. J.; Burchell, B. : Characterization of the uridine diphosphate- glucurono-syltransferase- catalyzing thyroid hormone glucuronida-tion in man. J. C.

[31403] Further studies establishing the function and utilities of UGT1A9 are found in John Hopkins OMIM database record ID 606434, and in cited publications listed in Table 5, which are hereby incorporated by reference.Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS, Ac-cession NP_000364.1) is another GAM189 target gene, herein designated TARGET GENE. UMPS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UMPS, corresponding to a target bind-ing site such as BINDING SITE I, BINDING SITE II or BIND-ING SITE III of Fig.8. Table 4 illustrates the complementar-ity of the nucleotide sequences of UMPS BINDING SITE,

designated SEQ ID:2144, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31404] Another function of GAM189 is therefore inhibition of Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS, Accession NP_000364.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UMPS.

[31405] Unc-84 homolog a (c. elegans) (UNC84B, Accession XP_039332.1) is another GAM189 target gene, herein designated TARGET GENE. UNC84B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UNC84B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UNC84B BINDING SITE, designated SEQ ID:13541, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31406] Another function of GAM189 is therefore inhibition of Unc-84 homolog a (c. elegans) (UNC84B, Accession XP_039332.1) . Accordingly, utilities of GAM189 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC84B.

[31407] Unc-84 homolog a (c. elegans) (UNC84B, Accession NP_056189.1) is another GAM189 target gene, herein designated TARGET GENE. UNC84B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UNC84B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UNC84B BINDING SITE, designated SEQ ID:13541, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31408] Another function of GAM189 is therefore inhibition of Unc-84 homolog a (c. elegans) (UNC84B, Accession NP_056189.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC84B.

[31409] URG4 (Accession NP_060390.2) is another GAM189 target gene, herein designated TARGET GENE. URG4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by URG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of URG4 BINDING SITE, designated SEQ ID:6788, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31410] Another function of GAM189 is therefore inhibition of URG4 (Accession NP_060390.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with URG4.

[31411] Ubiquitin specific protease 22 (USP22, Accession XP_042698.2) is another GAM189 target gene, herein designated TARGET GENE. USP22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by USP22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of USP22 BINDING SITE, designated SEQ ID:11288, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31412] Another function of GAM189 is therefore inhibition of Ubiquitin specific protease 22 (USP22, Accession XP_042698.2) . Accordingly, utilities of GAM189 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with USP22.

[31413] VDU1 (Accession NP_055832.2) is another GAM189 target gene, herein designated TARGET GENE. VDU1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VDU1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VDU1 BINDING SITE, designated SEQ ID:3187, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31414] Another function of GAM189 is therefore inhibition of VDU1 (Accession NP_055832.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VDU1.

[31415] Vent-like homeobox 2 (VENTX2, Accession NP_055283.1) is another GAM189 target gene, herein designated TARGET GENE. VENTX2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VENTX2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of VENTX2 BINDING SITE, designated SEQ ID:19331, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31416] Another function of GAM189 is therefore inhibition of Vent-like homeobox 2 (VENTX2, Accession NP_055283.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VENTX2.

[31417] Von hippel-lindau syndrome (VHL, Accession NP_000542.1) is another GAM189 target gene, herein designated TARGET GENE. VHL BINDING SITE1 and VHL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by VHL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VHL BINDING SITE1 and VHL BINDING SITE2, designated SEQ ID:3873 and SEQ ID:8786 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31418] Another function of GAM189 is therefore inhibition of Von hippel-lindau syndrome (VHL, Accession NP_000542.1), a

gene which may control rna stability through the selective degradation of rna- bound proteins. and therefore is associated with Von hippel- lindau disease. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Von hippel- lindau disease, and of other diseases and clinical conditions associated with VHL.

[31419] The function of VHL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Vasoactive intestinal peptide receptor 2 (VIPR2, Accession NP_003373.2) is another GAM189 target gene, herein designated TARGET GENE. VIPR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VIPR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VIPR2 BINDING SITE, designated SEQ ID:7754, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31420] Another function of GAM189 is therefore inhibition of Vasoactive intestinal peptide receptor 2 (VIPR2, Accession NP_003373.2) . Accordingly, utilities of GAM189 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with VIPR2.

[31421] VPS39 (Accession XP_031720.2) is another GAM189 target gene, herein designated TARGET GENE. VPS39 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VPS39, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VPS39 BINDING SITE, designated SEQ ID:18246, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31422] Another function of GAM189 is therefore inhibition of VPS39 (Accession XP_031720.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS39.

[31423] Vesicle transport through interaction with t-snares homolog 1a (yeast) (VTI1A, Accession NP_660207.1) is another GAM189 target gene, herein designated TARGET GENE. VTI1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VTI1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of VTI1A BINDING SITE, designated SEQ ID:2313, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31424] Another function of GAM189 is therefore inhibition of Vesicle transport through interaction with t-snares homolog 1a (yeast) (VTI1A, Accession NP_660207.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VTI1A.

[31425] Williams beuren syndrome chromosome region 18 (WBSCR18, Accession NP_115693.2) is another GAM189 target gene, herein designated TARGET GENE. WBSCR18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WBSCR18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR18 BINDING SITE, designated SEQ ID:2152, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31426] Another function of GAM189 is therefore inhibition of Williams beuren syndrome chromosome region 18

(WBSCR18, Accession NP_115693.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WB-SCR18.

[31427] Wd repeat domain 6 (WDR6, Accession NP_439891.1) is another GAM189 target gene, herein designated TARGET GENE. WDR6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by WDR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WDR6 BINDING SITE, designated SEQ ID:12628, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31428] Another function of GAM189 is therefore inhibition of Wd repeat domain 6 (WDR6, Accession NP_439891.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDR6.

[31429] Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_579889.1) is another GAM189 target gene, herein designated TARGET GENE. WHSC1 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WHSC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE, designated SEQ ID:9245, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31430] Another function of GAM189 is therefore inhibition of Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_579889.1), a gene which binds covalently to and repairs g/t mismatches. and therefore may be associated with Wolf- hirschhorn syndrome. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of Wolf- hirschhorn syndrome, and of other diseases and clinical conditions associated with WHSC1.

[31431] The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Wingless-type mmtv integration site family, member 5a (WNT5A, Accession NP_003383.1) is another GAM189 target gene, herein designated TARGET GENE. WNT5A BINDING SITE is a target binding site found in the

5` untranslated region of mRNA encoded by WNT5A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WNT5A BINDING SITE, designated SEQ ID:10269, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31432] Another function of GAM189 is therefore inhibition of Wingless-type mmtv integration site family, member 5a (WNT5A, Accession NP_003383.1), a gene which is a ligand for members of the frizzled family of seven transmembrane receptors and is probablely a developmental protein. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT5A.

[31433] The function of WNT5A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1) is another GAM189 target gene, herein designated TARGET GENE. XRCC2 BINDING SITE1 through XRCC2 BINDING SITE3 are target binding sites found in

untranslated regions of mRNA encoded by XRCC2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of XRCC2 BINDING SITE1 through XRCC2 BINDING SITE3, designated SEQ ID:10148, SEQ ID:12605 and SEQ ID:9688 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31434] Another function of GAM189 is therefore inhibition of X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1), a gene which involves in the homologous recombination repair (hrr) pathway of double- stranded dna. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XRCC2.

[31435] The function of XRCC2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.V-yes-1 yamaguchi sarcoma viral oncogene homolog 1 (YES1, Accession NP_005424.1) is another GAM189 target gene, herein designated TARGET GENE. YES1 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by YES1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of YES1 BINDING SITE, designated SEQ ID:16112, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31436] Another function of GAM189 is therefore inhibition of V-yes-1 yamaguchi sarcoma viral oncogene homolog 1 (YES1, Accession NP_005424.1), a gene which is a putative protein- tyrosine kinase. Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YES1.

[31437] The function of YES1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.ZAP (Accession NP_064504.2) is another GAM189 target gene, herein designated TARGET GENE. ZAP BINDING SITE1 and ZAP BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ZAP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of ZAP BINDING SITE1 and ZAP BINDING SITE2, designated SEQ ID:508 and SEQ ID:3071 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31438] Another function of GAM189 is therefore inhibition of ZAP (Accession NP_064504.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAP.

[31439] ZFP30 (Accession NP_055713.1) is another GAM189 target gene, herein designated TARGET GENE. ZFP30 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZFP30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP30 BINDING SITE, designated SEQ ID:9331, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31440] Another function of GAM189 is therefore inhibition of ZFP30 (Accession NP_055713.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP30.

[31441] ZFP42 (Accession NP_777560.1) is another GAM189 target gene, herein designated TARGET GENE. ZFP42 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZFP42, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP42 BINDING SITE, designated SEQ ID:10587, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31442] Another function of GAM189 is therefore inhibition of ZFP42 (Accession NP_777560.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP42.

[31443] Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_060667.1) is another GAM189 target gene, herein designated TARGET GENE. ZFP64 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP64, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP64 BINDING SITE, designated SEQ ID:15043, to the nucleotide

sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31444] Another function of GAM189 is therefore inhibition of Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_060667.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP64.

[31445] Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_071371.2) is another GAM189 target gene, herein designated TARGET GENE. ZFP64 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP64, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP64 BINDING SITE, designated SEQ ID:15043, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31446] Another function of GAM189 is therefore inhibition of Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_071371.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP64.

[31447] ZFYVE26 (Accession XP_031077.1) is another GAM189 target gene, herein designated TARGET GENE. ZFYVE26 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZFYVE26, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFYVE26 BINDING SITE, designated SEQ ID:12160, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31448] Another function of GAM189 is therefore inhibition of ZFYVE26 (Accession XP_031077.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFYVE26.

[31449] ZMYND17 (Accession NP_848546.1) is another GAM189 target gene, herein designated TARGET GENE. ZMYND17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZMYND17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZMYND17 BINDING SITE, designated SEQ ID:456, to the

nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31450] Another function of GAM189 is therefore inhibition of ZMYND17 (Accession NP_848546.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZMYND17.

[31451] Zinc finger protein 18 (kox 11) (ZNF18, Accession XP_085596.2) is another GAM189 target gene, herein designated TARGET GENE. ZNF18 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZNF18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF18 BINDING SITE, designated SEQ ID:19151, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31452] Another function of GAM189 is therefore inhibition of Zinc finger protein 18 (kox 11) (ZNF18, Accession XP_085596.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF18.

[31453] Zinc finger protein 253 (ZNF253, Accession NP_066385.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF253 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF253, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF253 BINDING SITE, designated SEQ ID:19746, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31454] Another function of GAM189 is therefore inhibition of Zinc finger protein 253 (ZNF253, Accession NP_066385.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF253.

[31455] Zinc finger protein 264 (ZNF264, Accession NP_003408.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF264 BINDING SITE1 and ZNF264 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ZNF264, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of ZNF264 BINDING SITE1 and ZNF264 BINDING SITE2, designated SEQ ID:3319 and SEQ ID:9147 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31456] Another function of GAM189 is therefore inhibition of Zinc finger protein 264 (ZNF264, Accession NP_003408.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF264.

[31457] Zinc finger protein 273 (ZNF273, Accession XP_088082.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF273 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF273, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF273 BINDING SITE, designated SEQ ID:18868, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31458] Another function of GAM189 is therefore inhibition of Zinc finger protein 273 (ZNF273, Accession XP_088082.1) .

Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF273.

[31459] Zinc finger protein 281 (ZNF281, Accession NP_036614.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF281 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF281, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF281 BINDING SITE, designated SEQ ID:16434, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31460] Another function of GAM189 is therefore inhibition of Zinc finger protein 281 (ZNF281, Accession NP_036614.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF281.

[31461] Zinc finger protein 289, id1 regulated (ZNF289, Accession NP_115765.2) is another GAM189 target gene, herein designated TARGET GENE. ZNF289 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by ZNF289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF289 BINDING SITE, designated SEQ ID:13159, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31462] Another function of GAM189 is therefore inhibition of Zinc finger protein 289, id1 regulated (ZNF289, Accession NP_115765.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF289.

[31463] Zinc finger protein 305 (ZNF305, Accession NP_055539.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF305 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF305, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF305 BINDING SITE, designated SEQ ID:18505, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31464] Another function of GAM189 is therefore inhibition of Zinc finger protein 305 (ZNF305, Accession NP_055539.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF305.

[31465] Zinc finger protein 334 (ZNF334, Accession NP_060572.2) is another GAM189 target gene, herein designated TARGET GENE. ZNF334 BINDING SITE1 and ZNF334 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ZNF334, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF334 BINDING SITE1 and ZNF334 BINDING SITE2, designated SEQ ID:9628 and SEQ ID:5064 respectively, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31466] Another function of GAM189 is therefore inhibition of Zinc finger protein 334 (ZNF334, Accession NP_060572.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF334.

[31467] Zinc finger protein 339 (ZNF339, Accession NP_067043.1)

is another GAM189 target gene, herein designated TARGET GENE. ZNF339 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF339, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF339 BINDING SITE, designated SEQ ID:1729, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31468] Another function of GAM189 is therefore inhibition of Zinc finger protein 339 (ZNF339, Accession NP_067043.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF339.

[31469] Zinc finger protein 345 (ZNF345, Accession NP_003410.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF345 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF345, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF345 BINDING SITE, designated SEQ ID:1011, to the nucleotide sequence of GAM189 RNA,

herein designated GAM RNA, also designated SEQ ID:246.

[31470] Another function of GAM189 is therefore inhibition of Zinc finger protein 345 (ZNF345, Accession NP_003410.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF345.

[31471] Zinc finger protein 398 (ZNF398, Accession NP_065832.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF398 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ZNF398, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF398 BINDING SITE, designated SEQ ID:8530, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31472] Another function of GAM189 is therefore inhibition of Zinc finger protein 398 (ZNF398, Accession NP_065832.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF398.

[31473] ZNF409 (Accession NP_055709.1) is another GAM189 tar-

get gene, herein designated TARGET GENE. ZNF409 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZNF409, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF409 BINDING SITE, designated SEQ ID:2388, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31474] Another function of GAM189 is therefore inhibition of ZNF409 (Accession NP_055709.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF409.

[31475] ZNF431 (Accession XP_086098.2) is another GAM189 target gene, herein designated TARGET GENE. ZNF431 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF431, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF431 BINDING SITE, designated SEQ ID:8477, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA,

also designated SEQ ID:246.

[31476] Another function of GAM189 is therefore inhibition of ZNF431 (Accession XP_086098.2) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF431.

[31477] ZNF432 (Accession NP_055465.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF432 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF432, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF432 BINDING SITE, designated SEQ ID:5065, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31478] Another function of GAM189 is therefore inhibition of ZNF432 (Accession NP_055465.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF432.

[31479] ZNF440 (Accession NP_689570.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF440 BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by ZNF440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF440 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31480] Another function of GAM189 is therefore inhibition of ZNF440 (Accession NP_689570.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF440.

[31481] Zinc finger protein 70 (cos17) (ZNF70, Accession NP_068735.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF70 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZNF70, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF70 BINDING SITE, designated SEQ ID:17076, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31482] Another function of GAM189 is therefore inhibition of Zinc finger protein 70 (cos17) (ZNF70, Accession NP_068735.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF70.

[31483] Zinc finger protein 70 (cos17) (ZNF70, Accession NP_852101.1) is another GAM189 target gene, herein designated TARGET GENE. ZNF70 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZNF70, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF70 BINDING SITE, designated SEQ ID:17076, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31484] Another function of GAM189 is therefore inhibition of Zinc finger protein 70 (cos17) (ZNF70, Accession NP_852101.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF70.

[31485] Zinc finger protein 74 (cos52) (ZNF74, Accession NP_003417.1) is another GAM189 target gene, herein

designated TARGET GENE. ZNF74 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZNF74, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF74 BINDING SITE, designated SEQ ID:12340, to the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, also designated SEQ ID:246.

[31486] Another function of GAM189 is therefore inhibition of Zinc finger protein 74 (cos52) (ZNF74, Accession NP_003417.1) . Accordingly, utilities of GAM189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF74.

[31487]

[31488] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 190 (GAM190), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[31489] GAM190 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM190 was detected is described hereinabove with reference to Figs. 8-15.

[31490] GAM190 gene, herein designated GAM GENE, and GAM190 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[31491] GAM190 gene encodes a GAM190 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM190 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM190 precursor RNA is designated SEQ ID:99, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:99 is located at position 151667587 relative to chromosome 3.

[31492] GAM190 precursor RNA folds onto itself, forming GAM190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[31493] GAM190 precursor RNA folds onto itself, forming GAM190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[31494] Nucleotide sequence of GAM190 precursor RNA, designated SEQ-ID: 99, and a schematic representation of a predicted secondary folding of GAM190 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[31495] An enzyme complex designated DICER COMPLEX, `dices` the GAM190 folded precursor RNA into GAM190 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM190 RNA is desig-

nated SEQ ID:289, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[31496] GAM190 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM190 target RNA, herein designated GAM TARGET RNA. GAM190 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[31497] GAM190 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM190 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM190 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM190 RNA may have a different number of target

binding sites in untranslated regions of a GAM190 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[31498] The complementary binding of GAM190 RNA, herein designated GAM RNA, to target binding sites on GAM190 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM190 target RNA into GAM190 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[31499] It is appreciated that GAM190 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM190 target genes. The mRNA of each one of this plurality of GAM190 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM190 RNA, herein designated GAM RNA, and which when bound by GAM190 RNA causes inhibition of translation of respective one or more GAM190 target proteins.

[31500] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM190 gene, herein designated GAM GENE, on one or more GAM190 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[31501] It is appreciated that specific functions and accordingly utilities of GAM190 correlate with, and may be deduced from, the identity of the target genes which GAM190 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[31502]

[31503]

[31504] Atp-binding cassette, sub-family c (cftr/mrp), member 3 (ABCC3, Accession NP_064422.1) is a GAM190 target gene, herein designated TARGET GENE. ABCC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABCC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCC3 BINDING SITE, designated SEQ ID:1929, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31505] A function of GAM190 is therefore inhibition of Atp-binding cassette, sub-family c (cftr/mrp), member 3 (ABCC3, Accession NP_064422.1), a gene which may act as an inducible transporter in the biliary and intestinal excretion of organic anions. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC3.

[31506] The function of ABCC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Acidic repeat containing (ACRC, Accession NP_443189.1) is another GAM190 target gene, herein

designated TARGET GENE. ACRC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ACRC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRC BINDING SITE, designated SEQ ID:16426, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31507] Another function of GAM190 is therefore inhibition of Acidic repeat containing (ACRC, Accession NP_443189.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRC.

[31508] Adenylate cyclase 1 (brain) (ADCY1, Accession NP_066939.1) is another GAM190 target gene, herein designated TARGET GENE. ADCY1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADCY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY1 BINDING SITE, designated SEQ ID:16609, to the

nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31509] Another function of GAM190 is therefore inhibition of Adenylate cyclase 1 (brain) (ADCY1, Accession NP_066939.1), a gene which a calmodulin- sensitive adenylyl cyclase. it may play a role in memory acquisition and learning. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY1.

[31510] The function of ADCY1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type iii) (AGL, Accession NP_000636.1) is another GAM190 target gene, herein designated TARGET GENE. AGL BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by AGL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGL BINDING SITE, designated SEQ ID:9569, to the nucleotide

sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31511] Another function of GAM190 is therefore inhibition of Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type iii) (AGL, Accession NP_000636.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGL.

[31512] AGS3 (Accession NP_056412.1) is another GAM190 target gene, herein designated TARGET GENE. AGS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AGS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGS3 BINDING SITE, designated SEQ ID:16761, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31513] Another function of GAM190 is therefore inhibition of AGS3 (Accession NP_056412.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGS3.

[31514] Ankyrin-like with transmembrane domains 1 (ANKTM1, Accession NP_015628.1) is another GAM190 target gene, herein designated TARGET GENE. ANKTM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ANKTM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANKTM1 BINDING SITE, designated SEQ ID:10754, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31515] Another function of GAM190 is therefore inhibition of Ankyrin-like with transmembrane domains 1 (ANKTM1, Accession NP_015628.1), a gene which attaches integral membrane proteins to cytoskeletal elements. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKTM1.

[31516] The function of ANKTM1 has been established by previous studies. A set of transformation- sensitive proteins that are expressed by normal fibroblasts but are specifically repressed after oncogenic transformation has emerged from studies of tumor virus- transformed fibroblasts. To

identify proteins that are lost during the establishment of the transformed phenotype of a tumor cell, Schenker and Trueb (1998) prepared a subtracted cDNA library with mRNA from normal human fibroblasts and from their matched SV40- transformed counterparts. They identified more than 40 clones that showed a dramatic reduction in their relative expression after oncogenic transformation, including a partial cDNA encoding a novel ankyrin- like protein, which has been named ANKTM1. ANKTM1 gene expression was consistently downregulated in a variety of cell lines derived from spontaneous mesenchymal tumors. By screening a human lung fibroblast cDNA library with the partial ANKTM1 cDNA, followed by 5- prime RACE, Jaquemar et al. (1999) isolated the complete ANKTM1 coding sequence. The deduced 1,119- amino acid ANKTM1 protein has a calculated molecular mass of 127.4 kD; the authors called it p120. ANKTM1 protein from fibroblast and liposarcoma cell extracts migrated as a 130-kD polypeptide on Western blots. The predicted ANKTM1 protein can be divided into 2 parts, an N- terminal portion that is related to the cytoskeletal protein ankyrin (see OMIM Ref. No. ANK1; 182900) and a C- terminal portion that is related to transmembrane proteins. The N- termi-

nal region contains eighteen 33- amino acid repeats, 15 of which share 21 to 52% sequence identity with the consensus motif derived from the repeats of ankyrin- like proteins and 3 of which share only partial similarity with the consensus repeat sequence. The C- terminal region contains 7 hydrophobic segments, 6 of which are putative transmembrane domains and 1 of which may enter the lipid bilayer only partially, possibly as a pore loop structure. ANKTM1 is predicted to assume a type II membrane orientation, with the N terminus located cytoplasmically. The overall structure of ANKTM1 is reminiscent of TRP- like proteins (e.g., TRPC7; 603749), which function as store- operated calcium channels. ANKTM1 contains 5 potential N- glycosylation sites, but 3 are situated cytoplasmically and are unlikely to be used. ANKTM1 does not contain an N- terminal signal peptide. Northern blot analysis detected a 4.6- kb ANKTM1 transcript in human fibroblasts. ANKTM1 expression was not observed in SV40- transformed fibroblasts or in cell lines derived from the following spontaneous mesenchymal tumors: 4 rhabdomyosarcomas, 2 fibrosarcomas, 1 osteosarcoma, and 1 chondrosarcoma. ANKTM1 was expressed in cells from a liposarcoma and in 1 of 2 leiomyosarcoma cell lines.

Northern blot analysis did not detect ANKTM1 expression in any of several adult or fetal human tissues. However, RT- PCR of RNA from a 12- week- old human embryo showed an extremely low level of ANKTM1 expression. Overexpression of recombinant ANKTM1 protein in eukaryotic cells appeared to interfere with normal growth. Jaquemar et al. (1999) suggested that ANKTM1 may play a direct or indirect role in signal transduction and growth control. By FISH, Jaquemar et al. (1999) mapped the ANKTM1 gene to 8q13.

[31517]

[31518] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31519] Jaquemar, D.; Schenker, T.; Trueb, B. : An ankyrin- like protein with transmembrane domains is specifically lost after oncogenic transformation of human fibroblasts. J. Biol. Chem. 274: 7325- 7333, 1999. ; and

[31520] Schenker, T.; Trueb, B. : Down- regulated proteins of mesenchymal tumor cells. Exp. Cell Res. 239: 161- 168, 1998.

[31521] Further studies establishing the function and utilities of ANKTM1 are found in John Hopkins OMIM database record

ID 604775, and in cited publications listed in Table 5, which are hereby incorporated by reference.Annexin a10 (ANXA10, Accession NP_009124.1) is another GAM190 target gene, herein designated TARGET GENE. ANXA10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ANXA10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANXA10 BINDING SITE, designated SEQ ID:6862, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31522] Another function of GAM190 is therefore inhibition of Annexin a10 (ANXA10, Accession NP_009124.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANXA10.

[31523] Rho gtpase activating protein 6 (ARHGAP6, Accession NP_001165.1) is another GAM190 target gene, herein designated TARGET GENE. ARHGAP6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ARHGAP6, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP6 BINDING SITE, designated SEQ ID:2102, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31524] Another function of GAM190 is therefore inhibition of Rho gtpase activating protein 6 (ARHGAP6, Accession NP_001165.1), a gene which activates the rho- type GTPases by converting them to an inactive GTP- bound state. and therefore may be associated with Skin defects syndrome. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of Skin defects syndrome., and of other diseases and clinical conditions associated with ARHGAP6.

[31525] The function of ARHGAP6 has been established by previous studies. In a search for the genetic defect in microphthalmia with linear skin defects syndrome (MLS; 309801), Schaefer et al. (1997) trapped exons from 14 overlapping cosmids from the 500- kb MLS critical region in Xp22.3. Using exon connection followed by cDNA library screening, they identified a 2.4- kb contig of cDNA clones spanning 170 kb of genomic sequence in the MLS deletion region. Northern analysis of this cDNA detected a prominent

transcript of approximately 4.2 kb and a less abundant transcript of approximately 6 kb in all tissues examined, with additional transcripts in skeletal muscle. Sequence analysis revealed a coding region of 601 amino acids contained in 12 exons, with a splice variant isoform of 495 amino acids. The predicted protein sequence of the gene, symbolized ARHGAP6, contains homology to the GTPase-activating (GAP) domain of the Rho- GAP family of proteins (e.g., 300023), which has been implicated in the regulation of actin polymerization at the plasma membrane in several cellular processes. Schaefer et al. (1997) discussed reasons for thinking that a defect in the Rho pathway may play a role in the pathogenesis of MLS syndrome. Prakash et al. (2000) investigated the function of ARHGAP6 by generating Arhgap6 null mice and also by in vitro expression studies. Surprisingly, loss of the rhoGAP function of Arhgap6 did not cause any detectable phenotypic or behavioral abnormalities in the mutant mice. Transfected mammalian cells expressing ARHGAP6 lost their actin stress fibers, retracted from the growth surface, and extended thin, branching processes resembling filopodia. The ARHGAP6 protein colocalized with actin filaments through an N- terminal domain and recruited fila-

mentous actin into the growing processes. Mutation of a conserved arginine residue in the rhoGAP domain prevented the loss of stress fibers but had little effect on process outgrowth. The authors concluded that ARHGAP6 has 2 independent functions: one as a GAP with specificity for RhoA and the other as a cytoskeletal protein that promotes actin remodeling.

[31526]

[31527] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31528] Prakash, S. K.; Paylor, R.; Jenna, S.; Lamarche- Vane, N.; Armstrong, D. L.; Xu, B.; Mancini, M. A.; Zoghbi, H. Y. : Functional analysis of ARHGAP6, a novel GTPase- activating protein for RhoA. Hum. Molec. Genet. 9: 477- 488, 2000. ; and

[31529] Schaefer, L.; Prakash, S.; Zoghbi, H. Y. : Cloning and characterization of a novel rho- type GTPase- activating protein gene (ARHGAP6) from the critical region for microphthalmia with li.

[31530] Further studies establishing the function and utilities of ARHGAP6 are found in John Hopkins OMIM database record ID 300118, and in cited publications listed in Table

5, which are hereby incorporated by reference.Rho guanine nucleotide exchange factor (gef) 7 (ARHGEF7, Accession NP_003890.1) is another GAM190 target gene, herein designated TARGET GENE. ARHGEF7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ARHGEF7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGEF7 BINDING SITE, designated SEQ ID:3061, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31531] Another function of GAM190 is therefore inhibition of Rho guanine nucleotide exchange factor (gef) 7 (ARHGEF7, Accession NP_003890.1), a gene which acts as a rac1 guanine nucleotide exchange factor (gef) and can induce membrane ruffling. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF7.

[31532] The function of ARHGEF7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.2.Atpase, class vi, type 11b (ATP11B, Accession

XP_087254.2) is another GAM190 target gene, herein designated TARGET GENE. ATP11B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP11B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP11B BINDING SITE, designated SEQ ID:10635, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31533] Another function of GAM190 is therefore inhibition of Atpase, class vi, type 11b (ATP11B, Accession XP_087254.2), a gene which is phosphorylated in their intermediate state, drives uphill transport of ions across membranes. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP11B.

[31534] The function of ATP11B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Atpase, h+ transporting, lysosomal 13kda, v1 subunit g isoform 2 (ATP6V1G2, Accession NP_612139.1) is another GAM190 target gene, herein designated TAR-

GET GENE. ATP6V1G2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ATP6V1G2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP6V1G2 BINDING SITE, designated SEQ ID:1415, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31535] Another function of GAM190 is therefore inhibition of Atpase, h+ transporting, lysosomal 13kda, v1 subunit g isoform 2 (ATP6V1G2, Accession NP_612139.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V1G2.

[31536] Atpase, h+ transporting, lysosomal 13kda, v1 subunit g isoform 2 (ATP6V1G2, Accession NP_569730.1) is another GAM190 target gene, herein designated TARGET GENE. ATP6V1G2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ATP6V1G2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of ATP6V1G2 BINDING SITE, designated SEQ ID:1415, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31537] Another function of GAM190 is therefore inhibition of Atpase, h+ transporting, lysosomal 13kda, v1 subunit g isoform 2 (ATP6V1G2, Accession NP_569730.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V1G2.

[31538] Atpase, cu++ transporting, beta polypeptide (wilson disease) (ATP7B, Accession NP_000044.1) is another GAM190 target gene, herein designated TARGET GENE. ATP7B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP7B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP7B BINDING SITE, designated SEQ ID:1270, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31539] Another function of GAM190 is therefore inhibition of Atpase, cu++ transporting, beta polypeptide (wilson dis-

ease) (ATP7B, Accession NP_000044.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7B.

[31540] Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5, Accession NP_004767.1) is another GAM190 target gene, herein designated TARGET GENE. B4GALT5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B4GALT5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B4GALT5 BINDING SITE, designated SEQ ID:2973, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31541] Another function of GAM190 is therefore inhibition of Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5, Accession NP_004767.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT5.

[31542] Bromodomain adjacent to zinc finger domain, 2a (BAZ2A, Accession NP_038477.1) is another GAM190 target gene,

herein designated TARGET GENE. BAZ2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BAZ2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAZ2A BINDING SITE, designated SEQ ID:6467, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31543] Another function of GAM190 is therefore inhibition of Bromodomain adjacent to zinc finger domain, 2a (BAZ2A, Accession NP_038477.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAZ2A.

[31544] C14orf132 (Accession NP_064600.1) is another GAM190 target gene, herein designated TARGET GENE. C14orf132 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf132 BINDING SITE, designated SEQ ID:10053, to the nucleotide sequence of GAM190 RNA, herein designated

GAM RNA, also designated SEQ ID:289.

[31545] Another function of GAM190 is therefore inhibition of C14orf132 (Accession NP_064600.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf132.

[31546] C1q and tumor necrosis factor related protein 5 (C1QTNF5, Accession NP_056460.1) is another GAM190 target gene, herein designated TARGET GENE. C1QTNF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1QTNF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1QTNF5 BINDING SITE, designated SEQ ID:19062, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31547] Another function of GAM190 is therefore inhibition of C1q and tumor necrosis factor related protein 5 (C1QTNF5, Accession NP_056460.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QTNF5.

[31548] Carbohydrate kinase-like (CARKL, Accession

NP_037408.1) is another GAM190 target gene, herein designated TARGET GENE. CARKL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CARKL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CARKL BINDING SITE, designated SEQ ID:13528, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31549] Another function of GAM190 is therefore inhibition of Carbohydrate kinase-like (CARKL, Accession NP_037408.1), a gene which is a putative carbohydrate kinase and may be a modifier for the cystinosis phenotype. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARKL.

[31550] The function of CARKL has been established by previous studies. Touchman et al. (2000) sequenced 200 kb surrounding the gene encoding cystinosin (CTNS; 606272), which is mutated in nephropathic cystinosis (OMIM Ref. No. 219800), on chromosome 17p13. They found that genomic sequence in this region matched known ESTs. Us-

ing PCR primers to amplify a human fetal kidney cDNA library, the authors cloned a cDNA, which they designated CARKL (carbohydrate kinase- like), encoding a deduced 478- amino acid protein. The CARKL protein contains motifs showing weak similarity to 2 domains of the FGGY family of carbohydrate kinases. It does not appear to contain a signal sequence, suggesting that it is localized in the cytoplasm. Northern blot analysis detected expression of a 3.9- kb CARKL transcript predominantly in liver, kidney, and pancreas, with weaker expression in heart, placenta, brain, and lung. Additionally, a 2.7- kb transcript was detected in liver and, to a lesser extent, in heart. By sequence analysis, Touchman et al. (2000) determined that the CARKL gene maps within the telomeric end of a 57- kb segment on 17p13 that is commonly deleted in cystinosis. They hypothesized that CARKL may be a modifier for the cystinosis phenotype.

[31551]

[31552] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31553] Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro, V. V.; McDowell, G.; Shotelersuk, V.; Bouffard, G.

G.; Beckstrom- Sternberg, S. M.; Gahl, W. A.; Green, E. D. : The genomic region encompassing the nephropathic cystinosis gene (CTNS): complete sequencing of a 200- kb segment and discovery of a novel gene within the common cystinosis- causing deletion. Genome Res. 10: 165-173, 2000. ; and

[31554] Phornphutkul, C.; Anikster, Y.; Huizing, M.; Braun, P.; Brodie, C.; Chou, J. Y.; Gahl, W. A. : The promoter of a lysosomal membrane transporter gene, CTNS, binds Sp-1, shares sequences.

[31555] Further studies establishing the function and utilities of CARKL are found in John Hopkins OMIM database record ID 605060, and in cited publications listed in Table 5, which are hereby incorporated by reference.CAS1 (Accession NP_075051.2) is another GAM190 target gene, herein designated TARGET GENE. CAS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAS1 BINDING SITE, designated SEQ ID:16002, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:289.

[31556] Another function of GAM190 is therefore inhibition of CAS1 (Accession NP_075051.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAS1.

[31557] Cyclin f (CCNF, Accession NP_001752.1) is another GAM190 target gene, herein designated TARGET GENE. CCNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCNF BINDING SITE, designated SEQ ID:2161, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31558] Another function of GAM190 is therefore inhibition of Cyclin f (CCNF, Accession NP_001752.1), a gene which likely to be involved in the control of the cell cycle during s phase and g2. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNF.

[31559] The function of CCNF and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM130.1.Chemokine (c-c motif) receptor 2 (CCR2, Accession NP_000638.1) is another GAM190 target gene, herein designated TARGET GENE. CCR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CCR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCR2 BINDING SITE, designated SEQ ID:8836, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31560] Another function of GAM190 is therefore inhibition of Chemokine (c-c motif) receptor 2 (CCR2, Accession NP_000638.1), a gene which binds chemokines and transduces a signal by increasing the intracellular calcium ions level. and therefore may be associated with Hiv- 1 infection. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of Hiv- 1 infection, and of other diseases and clinical conditions associated with CCR2.

[31561] The function of CCR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM175.1.Cd209 antigen (CD209, Accession NP_066978.1) is another GAM190 target gene, herein designated TARGET GENE. CD209 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD209, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD209 BINDING SITE, designated SEQ ID:1357, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31562] Another function of GAM190 is therefore inhibition of Cd209 antigen (CD209, Accession NP_066978.1), a gene which may play an important role in the CD4- independent association of HIV with cells. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD209.

[31563] The function of CD209 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Cd4 antigen (p55) (CD4, Accession NP_000607.1) is another GAM190 target gene, herein designated TARGET GENE. CD4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by CD4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD4 BINDING SITE, designated SEQ ID:4243, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31564] Another function of GAM190 is therefore inhibition of Cd4 antigen (p55) (CD4, Accession NP_000607.1), a gene which is T- cell surface glycoprotein and has role in cell-cell interactions and may act in signal transduction and therefore may be associated with Infectious and immune-mediated diseases. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of Infectious and immune- mediated diseases, and of other diseases and clinical conditions associated with CD4.

[31565] The function of CD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Cdc14 cell division cycle 14 homolog a (s. cerevisiae) (CDC14A, Accession NP_003663.2) is another GAM190 target gene, herein designated TARGET GENE. CDC14A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA

encoded by CDC14A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC14A BINDING SITE, designated SEQ ID:12880, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31566] Another function of GAM190 is therefore inhibition of Cdc14 cell division cycle 14 homolog a (s. cerevisiae) (CDC14A, Accession NP_003663.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC14A.

[31567] Centaurin, delta 2 (CENTD2, Accession NP_056057.1) is another GAM190 target gene, herein designated TARGET GENE. CENTD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CENTD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENTD2 BINDING SITE, designated SEQ ID:5185, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA,

also designated SEQ ID:289.

[31568] Another function of GAM190 is therefore inhibition of Centaurin, delta 2 (CENTD2, Accession NP_056057.1), a gene which involved in cell signaling/communication. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENTD2.

[31569] The function of CENTD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Centaurin, delta 2 (CENTD2, Accession NP_631920.1) is another GAM190 target gene, herein designated TARGET GENE. CENTD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CENTD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENTD2 BINDING SITE, designated SEQ ID:5185, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31570] Another function of GAM190 is therefore inhibition of Centaurin, delta 2 (CENTD2, Accession NP_631920.1), a

gene which involved in cell signaling/communication. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENTD2.

[31571] The function of CENTD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Chloride channel 6 (CLCN6, Accession NP_068504.1) is another GAM190 target gene, herein designated TARGET GENE. CLCN6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLCN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLCN6 BINDING SITE, designated SEQ ID:15103, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31572] Another function of GAM190 is therefore inhibition of Chloride channel 6 (CLCN6, Accession NP_068504.1), a gene which is a voltage- gated chloride channel. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with CLCN6.

[31573] The function of CLCN6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Chloride channel 6 (CLCN6, Accession NP_068503.1) is another GAM190 target gene, herein designated TARGET GENE. CLCN6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLCN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLCN6 BINDING SITE, designated SEQ ID:15103, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31574] Another function of GAM190 is therefore inhibition of Chloride channel 6 (CLCN6, Accession NP_068503.1), a gene which is a voltage- gated chloride channel. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN6.

[31575] The function of CLCN6 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM40.1.Chloride channel 6 (CLCN6, Accession NP_001277.1) is another GAM190 target gene, herein designated TARGET GENE. CLCN6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLCN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLCN6 BINDING SITE, designated SEQ ID:15103, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31576] Another function of GAM190 is therefore inhibition of Chloride channel 6 (CLCN6, Accession NP_001277.1), a gene which is a voltage- gated chloride channel. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN6.

[31577] The function of CLCN6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Chloride channel 6 (CLCN6, Accession NP_068505.1) is another GAM190 target gene, herein

designated TARGET GENE. CLCN6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLCN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLCN6 BINDING SITE, designated SEQ ID:15103, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31578] Another function of GAM190 is therefore inhibition of Chloride channel 6 (CLCN6, Accession NP_068505.1), a gene which is a voltage- gated chloride channel. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN6.

[31579] The function of CLCN6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9 (CLECSF9, Accession NP_055173.1) is another GAM190 target gene, herein designated TARGET GENE. CLECSF9 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by CLECSF9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLECSF9 BINDING SITE, designated SEQ ID:15211, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31580] Another function of GAM190 is therefore inhibition of C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9 (CLECSF9, Accession NP_055173.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLECSF9.

[31581] Clock homolog (mouse) (CLOCK, Accession NP_004889.1) is another GAM190 target gene, herein designated TARGET GENE. CLOCK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLOCK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLOCK BINDING SITE, designated SEQ ID:16410, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ

ID:289.

[31582] Another function of GAM190 is therefore inhibition of Clock homolog (mouse) (CLOCK, Accession NP_004889.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLOCK.

[31583] Carboxypeptidase a1 (pancreatic) (CPA1, Accession NP_001859.1) is another GAM190 target gene, herein designated TARGET GENE. CPA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPA1 BINDING SITE, designated SEQ ID:8808, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31584] Another function of GAM190 is therefore inhibition of Carboxypeptidase a1 (pancreatic) (CPA1, Accession NP_001859.1), a gene which is a monomeric pancreatic metalloprotease. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPA1.

[31585] The function of CPA1 has been established by previous

studies. Carboxypeptidase A (EC 3.4.2.1) is a pancreatic exopeptidase. Three different forms of human pancreatic procarboxypeptidase A have been isolated. The A1 and A2 (OMIM Ref. No. 600688) forms are monomeric proteins with different biochemical properties. Honey et al. (1984, 1986) found that an 8.6- kb human DNA fragment (detected by means of a rat cDNA probe for CPA) cosegregated with chromosome 7. The assignment was narrowed by demonstration of absence of the human DNA fragment in cells with a deletion of 7q22- qter. By studying mouse-hamster hybrid cells, Honey et al. (1986) assigned the CPA gene to mouse chromosome 6. Trypsin (OMIM Ref. No. 276000) is also on human 7q22- qter and on mouse 6. Stewart et al. (1990) concluded from multipoint linkage analysis with established chromosome 7 markers that the most likely location of carboxypeptidase is 7q31- qter. It lies distal to cystic fibrosis at a distance of approximately 12 cM Carboxypeptidase A1 is one of the genes whose expression in the pancreas was demonstrated by Velculescu et al. (1995) with a novel method for serial analysis of gene expression (SAGE). The method allowed the quantitative and simultaneous analysis of a large number of transcripts. To demonstrate the strategy, short diag-

nostic sequence tags (SSTs) were isolated from pancreas, concatenated, and cloned. Manual sequencing of 1,000 tags revealed a gene expression pattern characteristic of pancreas. New pancreatic transcripts corresponding to novel tags were also identified. SAGE is based on 2 principles: first, that a short nucleotide sequence tag (9 to 10 bp) contained sufficient information to uniquely identify a transcript; and second, that concatenation of SSTs allows the efficient analysis of transcripts in a serial manner by the sequencing of multiple tags within a single clone. Using SAGE, Velculescu et al. (1995) found that procarboxypeptidase A1 was the gene represented by the tag found most frequently in the pancreatic transcripts (7.6%). The authors suggested that SAGE should allow a direct readout of expression in any given cell type or tissue. They envisioned a major application to be the comparison of gene expression patterns in various developmental and disease states. Any laboratory with the capability to perform PCR and manual sequencing could perform SAGE for this purpose. Adaptation of this technique to an automated sequencer would allow the analysis of over 1,000 transcripts in a single 3- hour run

[31586]

[31587] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31588] Honey, N. K.; Sakaguchi, A. Y.; Lalley, P. A.; Quinto, C.; Rutter, W. J.; Naylor, S. L. : Assignment of the gene for carboxypeptidase A to human chromosome 7q22- qter and to mouse chromosome 6. Hum. Genet. 72: 27- 31, 1986. ; and

[31589] Velculescu, V. E.; Zhang, L.; Vogelstein, B.; Kinzler, K. W. : Serial analysis of gene expression. Science 270: 484- 487, 1995.

[31590] Further studies establishing the function and utilities of CPA1 are found in John Hopkins OMIM database record ID 114850, and in cited publications listed in Table 5, which are hereby incorporated by reference.Carboxypeptidase a5 (CPA5, Accession NP_525124.2) is another GAM190 target gene, herein designated TARGET GENE. CPA5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPA5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPA5 BINDING SITE, designated SEQ ID:16798, to the nucleotide se-

quence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31591] Another function of GAM190 is therefore inhibition of Carboxypeptidase a5 (CPA5, Accession NP_525124.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPA5.

[31592] Copine iii (CPNE3, Accession NP_003900.1) is another GAM190 target gene, herein designated TARGET GENE. CPNE3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPNE3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPNE3 BINDING SITE, designated SEQ ID:16717, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31593] Another function of GAM190 is therefore inhibition of Copine iii (CPNE3, Accession NP_003900.1), a gene which may function in membrane traffiking. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPNE3.

[31594] The function of CPNE3 has been established by previous

studies. By screening human brain cDNAs for the potential to encode proteins larger than 50 kD, Ishikawa et al. (1998) identified a CPNE3 cDNA, which they called KIAA0636. The deduced 537- amino acid CPNE3 protein is 65.7% identical to CPNE1. By SDS- PAGE, the in vitro transcribed/translated product of the CPNE3 cDNA had a molecular mass of 65 kD. RT- PCR detected CPNE3 expression in all human tissues examined By immunoprecipitation and kinase assays, Caudell et al. (2000) serendipitously identified a 60- kD protein identical to CPNE3. CPNE3 contains 2 N- terminal C2 domains, like CPNE1, CPNE6 (OMIM Ref. No. 605688), and CPNE7 (OMIM Ref. No. 605689), but these 4 copines have divergent C termini. CPNE3 is 63%, 52%, and 47% identical to CPNE1, CPNE6, and CPNE7, respectively. Northern blot analysis revealed ubiquitous expression of a 5.0- kb transcript. Biochemical analysis showed that CPNE3 appears to possess endogenous kinase activity, although it lacks a classic kinase domain. CPNE3 is phosphorylated on both serine and threonine residues but not on tyrosine residues.

[31595]

[31596] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[31597] Creutz, C. E.; Tomsig, J. L.; Snyder, S. L.; Gautier, M.- C.; Skouri, F.; Beisson, J.; Cohen, J. : The copines, a novel class of C2 domain- containing, calcium- dependent, phospholipid- binding proteins conserved from Paramecium to humans. J. Biol. Chem. 273: 1393- 1402, 1998. ; and

[31598] Caudell, E. G.; Caudell, J. J.; Tang, C.- H.; Yu, T.- K.; Frederick, M. J.; Grimm, E. A. : Characterization of human copine III as a phosphoprotein with associated kinase activity. Biochem.

[31599] Further studies establishing the function and utilities of CPNE3 are found in John Hopkins OMIM database record ID 604207, and in cited publications listed in Table 5, which are hereby incorporated by reference.Crystallin, zeta (quinone reductase)-like 1 (CRYZL1, Accession NP_005102.2) is another GAM190 target gene, herein designated TARGET GENE. CRYZL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRYZL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

CRYZL1 BINDING SITE, designated SEQ ID:7391, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31600] Another function of GAM190 is therefore inhibition of Crystallin, zeta (quinone reductase)-like 1 (CRYZL1, Accession NP_005102.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRYZL1.

[31601] Crystallin, zeta (quinone reductase)-like 1 (CRYZL1, Accession NP_665857.1) is another GAM190 target gene, herein designated TARGET GENE. CRYZL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRYZL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRYZL1 BINDING SITE, designated SEQ ID:7391, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31602] Another function of GAM190 is therefore inhibition of Crystallin, zeta (quinone reductase)-like 1 (CRYZL1, Accession NP_665857.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with CRYZL1.

[31603] Digeorge syndrome critical region gene 2 (DGCR2, Accession NP_005128.1) is another GAM190 target gene, herein designated TARGET GENE. DGCR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DGCR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DGCR2 BINDING SITE, designated SEQ ID:16760, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31604] Another function of GAM190 is therefore inhibition of Digeorge syndrome critical region gene 2 (DGCR2, Accession NP_005128.1), a gene which is putative adhesion receptor and intervenes in cell- cell or cell- matrix interactions and therefore may be associated with Digeorge syndrome . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of Digeorge syndrome ., and of other diseases and clinical conditions associated with DGCR2.

[31605] The function of DGCR2 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM84.1.DKFZp313G1735 (Accession XP_087728.2) is another GAM190 target gene, herein designated TARGET GENE. DKFZp313G1735 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp313G1735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp313G1735 BINDING SITE, designated SEQ ID:13429, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31606] Another function of GAM190 is therefore inhibition of DKFZp313G1735 (Accession XP_087728.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp313G1735.

[31607] DKFZP434E2135 (Accession NP_110431.1) is another GAM190 target gene, herein designated TARGET GENE. DKFZP434E2135 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434E2135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434E2135 BINDING SITE, designated SEQ ID:14814, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31608] Another function of GAM190 is therefore inhibition of DKFZP434E2135 (Accession NP_110431.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434E2135.

[31609] DKFZp434L142 (Accession NP_057697.1) is another GAM190 target gene, herein designated TARGET GENE. DKFZp434L142 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434L142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434L142 BINDING SITE, designated SEQ ID:14147, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31610] Another function of GAM190 is therefore inhibition of DKFZp434L142 (Accession NP_057697.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434L142.

[31611] DKFZP586D0919 (Accession NP_056248.1) is another GAM190 target gene, herein designated TARGET GENE. DKFZP586D0919 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586D0919, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586D0919 BINDING SITE, designated SEQ ID:19113, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31612] Another function of GAM190 is therefore inhibition of DKFZP586D0919 (Accession NP_056248.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586D0919.

[31613] DKFZP727G051 (Accession XP_045308.2) is another GAM190 target gene, herein designated TARGET GENE.

DKFZP727G051 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP727G051, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP727G051 BINDING SITE, designated SEQ ID:12451, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31614] Another function of GAM190 is therefore inhibition of DKFZP727G051 (Accession XP_045308.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP727G051.

[31615] DKFZP727M111 (Accession NP_056355.2) is another GAM190 target gene, herein designated TARGET GENE. DKFZP727M111 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP727M111, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP727M111 BINDING SITE, designated SEQ ID:12399, to the nucleotide sequence of

GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31616] Another function of GAM190 is therefore inhibition of DKFZP727M111 (Accession NP_056355.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP727M111.

[31617] DPF3 (Accession NP_036206.1) is another GAM190 target gene, herein designated TARGET GENE. DPF3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DPF3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DPF3 BINDING SITE, designated SEQ ID:14462, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31618] Another function of GAM190 is therefore inhibition of DPF3 (Accession NP_036206.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPF3.

[31619] E2IG5 (Accession NP_055182.2) is another GAM190 target gene, herein designated TARGET GENE. E2IG5 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by E2IG5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of E2IG5 BINDING SITE, designated SEQ ID:3520, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31620] Another function of GAM190 is therefore inhibition of E2IG5 (Accession NP_055182.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with E2IG5.

[31621] Extra spindle poles like 1 (s. cerevisiae) (ESPL1, Accession NP_036423.1) is another GAM190 target gene, herein designated TARGET GENE. ESPL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ESPL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ESPL1 BINDING SITE, designated SEQ ID:7872, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31622] Another function of GAM190 is therefore inhibition of Ex-

tra spindle poles like 1 (s. cerevisiae) (ESPL1, Accession NP_036423.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESPL1.

[31623] Ets variant gene 1 (ETV1, Accession NP_004947.2) is another GAM190 target gene, herein designated TARGET GENE. ETV1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ETV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ETV1 BINDING SITE, designated SEQ ID:18488, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31624] Another function of GAM190 is therefore inhibition of Ets variant gene 1 (ETV1, Accession NP_004947.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ETV1.

[31625] Exostoses (multiple)-like 2 (EXTL2, Accession NP_001430.1) is another GAM190 target gene, herein designated TARGET GENE. EXTL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by EXTL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EXTL2 BINDING SITE, designated SEQ ID:3245, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31626] Another function of GAM190 is therefore inhibition of Exostoses (multiple)-like 2 (EXTL2, Accession NP_001430.1), a gene which is homologous to the EXT and EXTL genes. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EXTL2.

[31627] The function of EXTL2 has been established by previous studies. In patients with multiple exostoses, mutations in 2 different genes have been found: EXT1 (OMIM Ref. No. 133700) on 8q and EXT2 (OMIM Ref. No. 133701) on 11p. In addition, linkage has demonstrated a third locus, EXT3 (OMIM Ref. No. 600209), on 19p as the site of mutations causing multiple exostoses. The family of EXT genes was extended by the identification of an EXT- like gene (EXTL1; 601738) showing a high degree of homology with the EXT genes. Wuyts et al. (1997) described a second EXT- like gene, EXTL2, that is homologous to the EXT and

EXTL genes. EXTL2 was found to consist of 5 exons encoding a ubiquitously expressed 330- amino acid protein. In addition, a putative pseudogene, EXTL2P, was identified. Saito et al. (1998) also cloned an EXTL2 cDNA, which they called EXTR2. By Northern blot analysis, they detected a 3.4- kb transcript in all tissues tested except leukocyte, where the gene was hardly transcribed. Its expression was relatively constant among tissues, but was weak in liver, lung, and thymus. By fluorescence in situ hybridization, Wuyts et al. (1997) mapped the EXTL2 gene to 1p12- p11 and the EXTL2 pseudogene to 2q24- q31. By somatic cell hybrid and radiation hybrid analyses, Saito et al. (1998) mapped the EXTL2 gene to chromosome 1p21. Wuyts and Van Hul (2000) cloned mouse Extl2, which has the same genomic structure as the human gene, encodes a protein identical in size, and has a sequence that is 87% identical to the human sequence. By radiation hybrid analysis, they mapped the mouse gene to chromosome 3.

[31628]

[31629] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31630] Wuyts, W.; Van Hul, W.; Hendrickx, J.; Speleman, F.; Wauters, J.; De Boulle, K.; Van Roy, N.; Van Agtmael, T.; Bossuyt, P.; Willems, P. J. : Identification and characterization of a novel member of the EXT gene family, EXTL2. Europ. J. Hum. Genet. 5: 382- 389, 1997. ; and

[31631] Wuyts, W.; Van Hul, W. : Characterization and genomic localization of the mouse Extl2 gene. Cytogenet. Cell Genet. 89: 185- 188, 2000.

[31632] Further studies establishing the function and utilities of EXTL2 are found in John Hopkins OMIM database record ID 602411, and in cited publications listed in Table 5, which are hereby incorporated by reference.FLJ00007 (Accession NP_258260.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ00007 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ00007, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ00007 BINDING SITE, designated SEQ ID:9436, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31633] Another function of GAM190 is therefore inhibition of

FLJ00007 (Accession NP_258260.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00007.

[31634] FLJ12425 (Accession XP_098290.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ12425 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12425, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12425 BINDING SITE, designated SEQ ID:16869, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31635] Another function of GAM190 is therefore inhibition of FLJ12425 (Accession XP_098290.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12425.

[31636] FLJ13114 (Accession NP_078817.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ13114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13114, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13114 BINDING SITE, designated SEQ ID:6552, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31637] Another function of GAM190 is therefore inhibition of FLJ13114 (Accession NP_078817.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13114.

[31638] FLJ13744 (Accession NP_079287.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ13744 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13744, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13744 BINDING SITE, designated SEQ ID:5728, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31639] Another function of GAM190 is therefore inhibition of FLJ13744 (Accession NP_079287.1) . Accordingly, utilities

of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13744.

[31640] FLJ13962 (Accession NP_079138.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ13962 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13962, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13962 BINDING SITE, designated SEQ ID:3592, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31641] Another function of GAM190 is therefore inhibition of FLJ13962 (Accession NP_079138.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13962.

[31642] FLJ14779 (Accession NP_116227.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ14779 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14779, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14779 BINDING SITE, designated SEQ ID:10085, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31643] Another function of GAM190 is therefore inhibition of FLJ14779 (Accession NP_116227.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14779.

[31644] FLJ20035 (Accession NP_060101.2) is another GAM190 target gene, herein designated TARGET GENE. FLJ20035 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20035, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20035 BINDING SITE, designated SEQ ID:7692, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31645] Another function of GAM190 is therefore inhibition of FLJ20035 (Accession NP_060101.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20035.

[31646] FLJ20189 (Accession NP_060174.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ20189 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20189, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20189 BINDING SITE, designated SEQ ID:6742, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31647] Another function of GAM190 is therefore inhibition of FLJ20189 (Accession NP_060174.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20189.

[31648] FLJ20618 (Accession NP_060373.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ20618 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20618, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ20618 BINDING SITE, designated SEQ ID:6968, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31649] Another function of GAM190 is therefore inhibition of FLJ20618 (Accession NP_060373.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20618.

[31650] FLJ21687 (Accession NP_079135.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ21687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21687 BINDING SITE, designated SEQ ID:11614, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31651] Another function of GAM190 is therefore inhibition of FLJ21687 (Accession NP_079135.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ21687.

[31652] FLJ22688 (Accession NP_079405.2) is another GAM190 target gene, herein designated TARGET GENE. FLJ22688 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22688, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22688 BINDING SITE, designated SEQ ID:18629, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31653] Another function of GAM190 is therefore inhibition of FLJ22688 (Accession NP_079405.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22688.

[31654] FLJ22955 (Accession NP_079095.2) is another GAM190 target gene, herein designated TARGET GENE. FLJ22955 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22955, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ22955 BINDING SITE, designated SEQ ID:11826, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31655] Another function of GAM190 is therefore inhibition of FLJ22955 (Accession NP_079095.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22955.

[31656] FLJ23235 (Accession NP_079219.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ23235 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23235 BINDING SITE, designated SEQ ID:2723, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31657] Another function of GAM190 is therefore inhibition of FLJ23235 (Accession NP_079219.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23235.

[31658] FLJ30046 (Accession NP_653196.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ30046 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30046, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30046 BINDING SITE, designated SEQ ID:2890, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31659] Another function of GAM190 is therefore inhibition of FLJ30046 (Accession NP_653196.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30046.

[31660] FLJ33318 (Accession NP_694961.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ33318 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33318 BINDING SITE, designated SEQ ID:5940, to the

nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31661] Another function of GAM190 is therefore inhibition of FLJ33318 (Accession NP_694961.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33318.

[31662] FLJ33708 (Accession NP_775946.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ33708 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33708 BINDING SITE, designated SEQ ID:7549, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31663] Another function of GAM190 is therefore inhibition of FLJ33708 (Accession NP_775946.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33708.

[31664] FLJ38865 (Accession NP_689907.1) is another GAM190

target gene, herein designated TARGET GENE. FLJ38865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38865 BINDING SITE, designated SEQ ID:17233, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31665] Another function of GAM190 is therefore inhibition of FLJ38865 (Accession NP_689907.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38865.

[31666] FLJ39378 (Accession NP_847884.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ39378 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39378, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39378 BINDING SITE, designated SEQ ID:15804, to the nucleotide sequence of GAM190 RNA, herein designated

GAM RNA, also designated SEQ ID:289.

[31667] Another function of GAM190 is therefore inhibition of FLJ39378 (Accession NP_847884.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39378.

[31668] FLJ39873 (Accession NP_776160.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ39873 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39873, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39873 BINDING SITE, designated SEQ ID:16670, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31669] Another function of GAM190 is therefore inhibition of FLJ39873 (Accession NP_776160.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39873.

[31670] FLJ40597 (Accession NP_689828.1) is another GAM190 target gene, herein designated TARGET GENE. FLJ40597

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ40597, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ40597 BINDING SITE, designated SEQ ID:10738, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31671] Another function of GAM190 is therefore inhibition of FLJ40597 (Accession NP_689828.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ40597.

[31672] Forkhead box o1a (rhabdomyosarcoma) (FOXO1A, Accession NP_002006.2) is another GAM190 target gene, herein designated TARGET GENE. FOXO1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOXO1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXO1A BINDING SITE, designated SEQ ID:9586, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA,

also designated SEQ ID:289.

[31673] Another function of GAM190 is therefore inhibition of Forkhead box o1a (rhabdomyosarcoma) (FOXO1A, Accession NP_002006.2), a gene which is a probable transcription factor. and therefore may be associated with Alveolar rhabdomyosarcoma- 2. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of Alveolar rhabdomyosarcoma- 2., and of other diseases and clinical conditions associated with FOXO1A.

[31674] The function of FOXO1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Fyve and coiled-coil domain containing 1 (FYCO1, Accession NP_078789.1) is another GAM190 target gene, herein designated TARGET GENE. FYCO1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FYCO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FYCO1 BINDING SITE, designated SEQ ID:17030, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31675] Another function of GAM190 is therefore inhibition of Fyve and coiled-coil domain containing 1 (FYCO1, Accession NP_078789.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FYCO1.

[31676] Growth arrest-specific 2 like 1 (GAS2L1, Accession NP_006469.2) is another GAM190 target gene, herein designated TARGET GENE. GAS2L1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by GAS2L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAS2L1 BINDING SITE, designated SEQ ID:11278, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31677] Another function of GAM190 is therefore inhibition of Growth arrest-specific 2 like 1 (GAS2L1, Accession NP_006469.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAS2L1.

[31678] GMPPA (Accession NP_037467.1) is another GAM190 target gene, herein designated TARGET GENE. GMPPA BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GMPPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GMPPA BINDING SITE, designated SEQ ID:709, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31679] Another function of GAM190 is therefore inhibition of GMPPA (Accession NP_037467.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GMPPA.

[31680] G protein-coupled receptor 56 (GPR56, Accession NP_005673.2) is another GAM190 target gene, herein designated TARGET GENE. GPR56 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR56, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR56 BINDING SITE, designated SEQ ID:5394, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31681] Another function of GAM190 is therefore inhibition of G

protein-coupled receptor 56 (GPR56, Accession NP_005673.2), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR56.

[31682] The function of GPR56 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Glutamate receptor, ionotropic, n-methyl-d-aspartate 3a (GRIN3A, Accession NP_597702.1) is another GAM190 target gene, herein designated TARGET GENE. GRIN3A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRIN3A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRIN3A BINDING SITE, designated SEQ ID:14895, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31683] Another function of GAM190 is therefore inhibition of Glutamate receptor, ionotropic, n-methyl-d-aspartate 3a

(GRIN3A, Accession NP_597702.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIN3A.

[31684] Histone deacetylase 6 (HDAC6, Accession NP_006035.2) is another GAM190 target gene, herein designated TARGET GENE. HDAC6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HDAC6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HDAC6 BINDING SITE, designated SEQ ID:11395, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31685] Another function of GAM190 is therefore inhibition of Histone deacetylase 6 (HDAC6, Accession NP_006035.2), a gene which plays an important role in transcriptional regulation, cell cycle progression and developmental events (by similarity). Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HDAC6.

[31686] The function of HDAC6 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM146.1.HECA (Accession NP_057301.1) is another GAM190 target gene, herein designated TARGET GENE. HECA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HECA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HECA BINDING SITE, designated SEQ ID:13430, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31687] Another function of GAM190 is therefore inhibition of HECA (Accession NP_057301.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HECA.

[31688] Human immunodeficiency virus type i enhancer binding protein 2 (HIVEP2, Accession NP_006725.2) is another GAM190 target gene, herein designated TARGET GENE. HIVEP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HIVEP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of HIVEP2 BINDING SITE, designated SEQ ID:3062, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31689] Another function of GAM190 is therefore inhibition of Human immunodeficiency virus type i enhancer binding protein 2 (HIVEP2, Accession NP_006725.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIVEP2.

[31690] Heat shock 70kda protein 4 (HSPA4, Accession XP_114482.1) is another GAM190 target gene, herein designated TARGET GENE. HSPA4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSPA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPA4 BINDING SITE, designated SEQ ID:10608, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31691] Another function of GAM190 is therefore inhibition of Heat shock 70kda protein 4 (HSPA4, Accession

XP_114482.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPA4.

[31692] Islet amyloid polypeptide (IAPP, Accession NP_000406.1) is another GAM190 target gene, herein designated TARGET GENE. IAPP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IAPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IAPP BINDING SITE, designated SEQ ID:10420, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31693] Another function of GAM190 is therefore inhibition of Islet amyloid polypeptide (IAPP, Accession NP_000406.1), a gene which selectively inhibits insulin- stimulated glucose utilization and glycogen deposition and therefore may be associated with Type ii diabetes . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of Type ii diabetes ., and of other diseases and clinical conditions associated with IAPP.

[31694] The function of IAPP has been established by previous studies. IAPP has cysteine residues in positions 2 and 7, a

feature found in all known calcitonin gene- related peptides (OMIM Ref. No. 114130). IAPP shows 46% amino acid sequence homology with CGRP II (OMIM Ref. No. 114160). Since IAPP has been demonstrated immunochemically in normal beta cells of several mammals, it probably has an important role in respect to pancreatic islet function. Cooper et al. (1988) presented evidence that the 37-amino acid peptide may be a hormone present in normal individuals; hence, 'diabetes- associated peptide' is an inappropriate designation. Cooper et al. (1988) synthesized whole amylin by using solid- phase techniques, with formation of the disulfide linkage by oxidation in dilute aqueous solution and recovery of the peptide by lyophilization. The effects of amylin on glucose metabolism were studied by 2 in vitro preparations: isolated rat soleus muscle strips and isolated rat adipocytes. In skeletal muscle, amylin resulted in a marked decrease in insulin- stimulated glycogen synthesis with resulting reduction in insulin- stimulated glucose uptake. In muscle, amylin resulted in a failure of response to the concentration of insulin required to stimulate glucose uptake half- maximally in untreated muscles. No effects were observed in isolated adipocytes. Amylin may be a factor in

the etiology of the insulin resistance in type II diabetes mellitus. A correlation has been observed between the extent of islet amyloid deposition and the clinical severity of type II diabetes. Mosselman et al. (1988) isolated and partially characterized the human IAPP gene. By hybridization to DNA from human- rodent somatic cell hybrids, Mosselman et al. (1988) demonstrated that the IAPP gene is located on 12pter- q14. Because of the striking parallelism in the genetic constitution of chromosomes 11 and 12, suggesting an ancient tetraploidization, the mapping of this calcitonin- related gene to 12 is of interest; 2 calcitonin genes are located on 11p. The amyloid in amyloid-producing medullary carcinoma of the thyroid, a feature of multiple endocrine neoplasia type II (OMIM Ref. No. 171400), is derived from calcitonin. Sanke et al. (1988) showed that the islet amyloid polypeptide is derived from an 89- amino acid precursor by proteolytic processing. The processed peptide, 37- amino acids long, is bracketed at its NH(2) and COOH termini by lys- arg and gly-lys- arg, respectively. The data indicated that this amyloid peptide is generated by proteolytic processing similar to that for proinsulin and other islet prohormones and also that the peptide may be carboxyamidated. Mosselman et

al. (1989) found that 2 exons, which are approximately 5 kb apart, encode the 89- amino acid pre- pro- IAPP. A putative signal sequence at the amino- terminus of the precursor suggested that IAPP is a secreted protein. From the DNA sequence of a partial cDNA clone and a phage lambda genomic clone of the coding region of the amylin gene, Roberts et al. (1989) concluded that this peptide is synthesized as a precursor peptide called proamylin. The sequences of the genes for amylin and the calcitonin gene- related peptides show strong similarity, especially in their 5- prime coding regions, where these peptides have a conserved intramolecular disulfide bridge, and also in their 3- prime coding regions, where the presence of a glycine codon strongly suggests that the carboxyl- terminal residue, like that of CGRP, is amidated. In a study of the biologic activity of amylin synthesized with or without the disulfide bridge and/or amidation, Roberts et al. (1989) demonstrated that both features are necessary for full biologic activity, thereby confirming the functional importance of those regions of the molecule that have been conserved at both protein and genetic levels.

[31695] Animal model experiments lend further support to the function of IAPP. Janson et al. (1996) created homozygous

transgenic mice with a high level of expression of human IAPP. Male transgenic mice spontaneously developed diabetes mellitus by 8 weeks of age, which was associated with selective beta- cell death and impaired insulin secretion. Approximately 20% of female transgenic mice spontaneously developed diabetes at 30+ weeks of age when beta- cell degeneration and both amorphous and amyloid deposits of IAPP were present. Large deposits of IAPP- derived amyloid did not appear to be important to the cytotoxicity, but early, small amorphous intra- and extracellular aggregates of human IAPP were consistently present at the time of beta- cell death and therefore may be the most cytotoxic form of IAPP.

[31696] It is appreciated that the abovementioned animal model for IAPP is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[31697] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31698] Cooper, G. J.; Willis, A. C.; Clark, A.; Turner, R. C.; Sim, R. B.; Reid, K. B. : Purification and characterization of a peptide from amyloid- rich pancreases of type 2 diabetic pa-

tients. Proc. Nat. Acad. Sci. 84: 8628- 8632, 1987. ; and

[31699] Cooper, G. J. S.; Leighton, B.; Dimitriadis, G. D.; Parry-Billings, M.; Kowalchuk, J. M.; Howland, K.; Rothbard, J. B.; Willis, A. C.; Reid, K. B. M. : Amylin found in amyloid deposits.

[31700] Further studies establishing the function and utilities of IAPP are found in John Hopkins OMIM database record ID 147940, and in cited publications listed in Table 5, which are hereby incorporated by reference.Interleukin 10 receptor, alpha (IL10RA, Accession NP_001549.1) is another GAM190 target gene, herein designated TARGET GENE. IL10RA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL10RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL10RA BINDING SITE, designated SEQ ID:2291, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31701] Another function of GAM190 is therefore inhibition of Interleukin 10 receptor, alpha (IL10RA, Accession NP_001549.1), a gene which is a receptor for il- 10. Accordingly, utilities of GAM190 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with IL10RA.

[31702] The function of IL10RA has been established by previous studies. Interleukin- 10 (OMIM Ref. No. 124092) is a cytokine produced by B cells, T helper cells, and cells of the monocyte/macrophage lineage that exhibits diverse activities on different cell lines. Tan et al. (1993) showed that the protein can be enzymatically iodinated to high specific radioactivity with retention of biologic activity. The radiolabeled ligand was found to bind specifically to its receptor in several mouse and human cell lines. For both mouse and human cell lines examined, there appeared to be at most only a few hundred IL10 receptors per cell. Mouse IL10 was capable of blocking binding of human IL10 to mouse but not human cells. Ho et al. (1993) found that mouse il- 10r is structurally related to interferon receptors. Since IL- 10 inhibits macrophage activation by interferon- gamma, a possible implication of this relationship is interaction of IL- 10R and IFN- gamma- R or their signaling pathways. Liu et al. (1994) assigned the IL10R gene to chromosome 11 by analysis of DNAs from human/hamster hybrid cell lines. Taniyama et al. (1995) regionalized the assignment to 11q23.3 by fluorescence in situ

hybridization.

[31703]

[31704] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31705] Ho, A. S. Y.; Liu, Y.; Khan, T. A.; Hsu, D.- H.; Bazan, J. F.; Moore, K. W. : A receptor for interleukin 10 is related to interferon receptors. Proc. Nat. Acad. Sci. 90: 11267- 11271, 1993. ; and

[31706] Liu, Y.; Wei, S. H.- Y.; Ho, A. S.- Y.; de Waal Malefyt, R.; Moore, K. W. : Expression cloning and characterization of a human Il- 10 receptor. J. Immun. 152: 1821- 1829, 1994.

[31707] Further studies establishing the function and utilities of IL10RA are found in John Hopkins OMIM database record ID 146933, and in cited publications listed in Table 5, which are hereby incorporated by reference.Interleukin 18 receptor 1 (IL18R1, Accession NP_003846.1) is another GAM190 target gene, herein designated TARGET GENE. IL18R1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL18R1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of IL18R1 BINDING SITE, designated SEQ ID:10177, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31708] Another function of GAM190 is therefore inhibition of Interleukin 18 receptor 1 (IL18R1, Accession NP_003846.1), a gene which is required for dorsal- ventral embryonic polarity and promotes heterophilic cellular adhesion. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL18R1.

[31709] The function of IL18R1 has been established by previous studies. Using a YAC template known to contain IL1R1 (OMIM Ref. No. 147810), Parnet et al. (1996) cloned by PCR with degenerate primers what was thought to be a member of the interleukin- 1 receptor family, which they called IL1 receptor- related protein (OMIM Ref. No. IL1RRP). The gene encodes a 541- amino acid protein. Although the sequence was similar to that of IL1Rs, the extracellular portion failed to bind IL1A (OMIM Ref. No. 147760), IL1B (OMIM Ref. No. 147720), or IL1RN (OMIM Ref. No. 147679). When the cytoplasmic domain was fused to mouse IL1 extracellular and transmembrane por-

tions, it activated NF- kappa- B (OMIM Ref. No. 164011) in response to IL1. Northern blot analysis revealed that IL1RRP is expressed in lung, leukocytes, spleen, liver, thymus, prostate, small intestine, colon, placenta, and heart, and is absent from brain, skeletal muscle, pancreas, and kidney. Torigoe et al. (1997) purified human IL18R, symbolized IL18R1, by selecting a Hodgkin disease cell line, L428, that was the best binder in IL18 (OMIM Ref. No. 600953) binding assays. The binding of radiolabeled IL18 was inhibited by IL18 but not by IL1B, with which it has 15% amino acid homology but no functional resemblance. The authors raised a monoclonal antibody against L428 cells and used it to purify IL18R from solubilized cells after wheat germ lectin chromatography. They found that the internal amino acid sequence matched that of IL1RRP. When expressed in COS- 1 cells, the cDNA of IL1RRP conferred IL18 binding properties and the ability to activate NF- kappa- B in response to IL18 but not IL1B.

[31710]

[31711] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31712] Dale, M.; Nicklin, M. J. : Interleukin- 1 receptor cluster:

gene organization of IL1R2, IL1R1, IL1RL2 (IL- 1Rrp2), IL1RL1 (T1/ST2), and IL18R1 (IL- 1Rrp) on human chromosome 2q. Genomics 57: 177- 179, 1999. ; and

[31713] Parnet, P.; Garka, K. E.; Bonnert, T. P.; Dower, S. K.; Sims, J. E. : IL- 1Rrp is a novel receptor- like molecule similar to the type I interleukin- 1 receptor and its homologues T1/ST2 an.

[31714] Further studies establishing the function and utilities of IL18R1 are found in John Hopkins OMIM database record ID 604494, and in cited publications listed in Table 5, which are hereby incorporated by reference.Insulin receptor-related receptor (INSRR, Accession XP_043563.2) is another GAM190 target gene, herein designated TARGET GENE. INSRR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by INSRR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INSRR BINDING SITE, designated SEQ ID:19916, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31715] Another function of GAM190 is therefore inhibition of In-

sulin receptor-related receptor (INSRR, Accession XP_043563.2), a gene which phosphorylates the insulin receptor substrates irs- 1 and irs- 2. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INSRR.

[31716] The function of INSRR has been established by previous studies. Shier and Watt (1989) isolated genomic DNA that appeared to encode a novel receptor that was structurally as similar to the insulin receptor (OMIM Ref. No. 147670) and the IGF1 receptor (OMIM Ref. No. 147370) as the last two are to each other. This similarity suggested that the insulin receptor- related receptor (IRR) mediates the action of a ligand that is identical or very similar to insulin, IGF1, or IGF2. Kurachi et al. (1992) isolated IRR cDNA from rat brain and examined the expression of IRR mRNA in a variety of rat tissues. They demonstrated that, in contrast to the wide distribution of the insulin receptor and the IGF1 receptor mRNAs, the IRR mRNA is expressed preferentially in the kidney, which indicates that it has unique functions as a member of the insulin receptor family. Using genomic DNA encoding part of IRR in Southern blot analysis of DNA from human- mouse cell hybrids, Shier et al. (1990) assigned the INSRR gene to human chromo-

some 1. By radiation hybrid analysis, Whitmore et al. (1999) mapped the gene to chromosome 1q21- q23

[31717]

[31718] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31719] Shier, P.; Willard, H. F.; Watt, V. M. : Localization of the insulin receptor- related receptor gene to human chromosome 1. Cytogenet. Cell Genet. 54: 80- 81, 1990. ; and

[31720] Whitmore, T. E.; Maurer, M. F.; Day, H. L.; Jelmberg, A. C.; Dasovich, M. M.; Sundborg, L. M.; Burkhead, S. K.; Heipel, M. D.; Madden, K. L.; Kramer, J. M.; Kuijper, J. L.; Xu, W. F.; Ja.

[31721] Further studies establishing the function and utilities of INSRR are found in John Hopkins OMIM database record ID 147671, and in cited publications listed in Table 5, which are hereby incorporated by reference.Insulin receptor substrate 2 (IRS2, Accession XP_007095.5) is another GAM190 target gene, herein designated TARGET GENE. IRS2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IRS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of IRS2 BINDING SITE, designated SEQ ID:13393, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31722] Another function of GAM190 is therefore inhibition of Insulin receptor substrate 2 (IRS2, Accession XP_007095.5), a gene which may mediate the control of various cellular processes by insulin. and therefore may be associated with Diabetes, type ii, susceptibility to. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of Diabetes, type ii, susceptibility to, and of other diseases and clinical conditions associated with IRS2.

[31723] The function of IRS2 has been established by previous studies. The protein IRS1 (OMIM Ref. No. 147545) acts as an interface between signaling proteins with Src homology- 2 domains (SH2 proteins) and the receptors for insulin (INS; 176730), IGF2 (OMIM Ref. No. 147470), growth hormone (GH1; 139250), several interleukins (IL4, 147780; IL9, 146931; IL13, 147683), and other cytokines. It regulates gene expression and stimulates mitogenesis and appears to mediate insulin/IGF1- stimulated glucose transport. Thus, the finding that survival of the homozygous Irs1 knockout mouse with only mild resistance to

hypertension was surprising. This dilemma was provisionally resolved by the discovery by Sun et al. (1995) of a second IRS signaling protein in mouse. They purified and cloned a likely candidate from mouse myeloid progenitor cells and, because of its resemblance to IRS1, they designated it IRS2. Alignment of the sequences of IRS2 and IRS1 demonstrated a highly conserved N terminus containing a pleckstrin- homology domain and a phosphotyrosine-binding (PTB) domain, and a poorly conserved C terminus containing several tyrosine phosphorylation motifs. IRS2 is expressed in many cells, including tissues from the homozygous IRS1 knockout mouse. Sun et al. (1995) suggested that IRS2 may be essential for signaling by several receptor systems. Mammarella et al. (2000) genotyped 193 Italian patients with type II diabetes (OMIM Ref. No. 125853) and 206 control subjects for the IRS2 G1057D polymorphism (600797.0001). They found evidence for a strong association between type II diabetes and the polymorphism, which appears to be protective against type II diabetes in a codominant fashion

[31724] Animal model experiments lend further support to the function of IRS2. Tobe et al. (2001) observed that Irs2-deficient mice (Kubota et al. (2000)) showed increased

adiposity with increased serum leptin level, suggesting leptin resistance before the mice developed diabetes. Using oligonucleotide microarray and Northern blot analyses to analyze gene expression, Tobe et al. (2001) detected increased expression of SREBP1, a downstream target of insulin, in Irs2- deficient mouse liver. Using high dose leptin administration, They provided evidence that leptin resistance in Irs2- deficient mice is causally related to SREBP1 gene induction. The authors concluded that Irs2 gene disruption results in leptin resistance, causing SREBP1 gene induction, obesity, fatty liver, and diabetes

[31725] It is appreciated that the abovementioned animal model for IRS2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[31726] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31727] Sun, X. J.; Wang, L.- M.; Zhang, Y.; Yenush, L.; Myers, M. G., Jr.; Glasheen, E.; Lane, W. S.; Pierce, J. H.; White, M. F. : Role of IRS- 2 in insulin and cytokine signalling. Nature 377: 173- 177, 1995. ; and

[31728] Tobe, K.; Suzuki, R.; Aoyama, M.; Yamauchi, T.; Kamon, J.;

Kubota, N.; Terauchi, Y.; Matsui, J.; Akanuma, Y.; Kimura, S.; Tanaka, J.; Abe, M.; Ohsumi, J.; Nagai, R.; Kadowaki, T. : Incre.

[31729] Further studies establishing the function and utilities of IRS2 are found in John Hopkins OMIM database record ID 600797, and in cited publications listed in Table 5, which are hereby incorporated by reference.Inter-alpha (globulin) inhibitor, h1 polypeptide (ITIH1, Accession NP_002206.1) is another GAM190 target gene, herein designated TARGET GENE. ITIH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITIH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITIH1 BINDING SITE, designated SEQ ID:16797, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31730] Another function of GAM190 is therefore inhibition of Inter-alpha (globulin) inhibitor, h1 polypeptide (ITIH1, Accession NP_002206.1), a gene which may act as a carrier of hyaluronan in serum or as a binding protein between hyaluronan and other matrix protein. Accordingly, utilities

of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITIH1.

[31731] The function of ITIH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Potassium channel, subfamily k, member 5 (KCNK5, Accession NP_003731.1) is another GAM190 target gene, herein designated TARGET GENE. KCNK5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KCNK5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNK5 BINDING SITE, designated SEQ ID:14350, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31732] Another function of GAM190 is therefore inhibition of Potassium channel, subfamily k, member 5 (KCNK5, Accession NP_003731.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK5.

[31733] KEO4 (Accession NP_006450.1) is another GAM190 target gene, herein designated TARGET GENE. KEO4 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KEO4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KEO4 BINDING SITE, designated SEQ ID:12625, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31734] Another function of GAM190 is therefore inhibition of KEO4 (Accession NP_006450.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KEO4.

[31735] KIAA0179 (Accession XP_035973.4) is another GAM190 target gene, herein designated TARGET GENE. KIAA0179 BINDING SITE1 and KIAA0179 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0179, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0179 BINDING SITE1 and KIAA0179 BINDING SITE2, designated SEQ ID:16659 and SEQ ID:5898 respectively, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:289.

[31736] Another function of GAM190 is therefore inhibition of KIAA0179 (Accession XP_035973.4) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0179.

[31737] KIAA1001 (Accession NP_055775.1) is another GAM190 target gene, herein designated TARGET GENE. KIAA1001 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1001 BINDING SITE, designated SEQ ID:2770, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31738] Another function of GAM190 is therefore inhibition of KIAA1001 (Accession NP_055775.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1001.

[31739] KIAA1007 (Accession NP_057368.1) is another GAM190 target gene, herein designated TARGET GENE. KIAA1007

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1007, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1007 BINDING SITE, designated SEQ ID:17180, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31740] Another function of GAM190 is therefore inhibition of KIAA1007 (Accession NP_057368.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1007.

[31741] KIAA1025 (Accession XP_034056.6) is another GAM190 target gene, herein designated TARGET GENE. KIAA1025 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1025, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1025 BINDING SITE, designated SEQ ID:11253, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31742] Another function of GAM190 is therefore inhibition of KIAA1025 (Accession XP_034056.6) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1025.

[31743] KIAA1200 (Accession XP_031054.4) is another GAM190 target gene, herein designated TARGET GENE. KIAA1200 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1200, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1200 BINDING SITE, designated SEQ ID:8002, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31744] Another function of GAM190 is therefore inhibition of KIAA1200 (Accession XP_031054.4) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1200.

[31745] KIAA1432 (Accession XP_039698.3) is another GAM190 target gene, herein designated TARGET GENE. KIAA1432 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by KIAA1432, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1432 BINDING SITE, designated SEQ ID:20070, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31746] Another function of GAM190 is therefore inhibition of KIAA1432 (Accession XP_039698.3) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1432.

[31747] KIAA1613 (Accession XP_035946.3) is another GAM190 target gene, herein designated TARGET GENE. KIAA1613 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1613, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1613 BINDING SITE, designated SEQ ID:8531, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31748] Another function of GAM190 is therefore inhibition of

KIAA1613 (Accession XP_035946.3) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1613.

[31749] KIAA1813 (Accession XP_046743.2) is another GAM190 target gene, herein designated TARGET GENE. KIAA1813 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1813 BINDING SITE, designated SEQ ID:13394, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31750] Another function of GAM190 is therefore inhibition of KIAA1813 (Accession XP_046743.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1813.

[31751] KIAA1894 (Accession XP_058025.2) is another GAM190 target gene, herein designated TARGET GENE. KIAA1894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1894, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1894 BINDING SITE, designated SEQ ID:7357, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31752] Another function of GAM190 is therefore inhibition of KIAA1894 (Accession XP_058025.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1894.

[31753] KIAA1999 (Accession XP_114447.2) is another GAM190 target gene, herein designated TARGET GENE. KIAA1999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1999 BINDING SITE, designated SEQ ID:4798, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31754] Another function of GAM190 is therefore inhibition of KIAA1999 (Accession XP_114447.2) . Accordingly, utilities

of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1999.

[31755] KIAA2028 (Accession XP_059415.2) is another GAM190 target gene, herein designated TARGET GENE. KIAA2028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA2028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA2028 BINDING SITE, designated SEQ ID:7392, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31756] Another function of GAM190 is therefore inhibition of KIAA2028 (Accession XP_059415.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2028.

[31757] LCHN (Accession XP_098615.2) is another GAM190 target gene, herein designated TARGET GENE. LCHN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCHN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCHN BINDING SITE, designated SEQ ID:13962, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31758] Another function of GAM190 is therefore inhibition of LCHN (Accession XP_098615.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCHN.

[31759] Lim homeobox protein 3 (LHX3, Accession NP_055379.1) is another GAM190 target gene, herein designated TARGET GENE. LHX3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LHX3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LHX3 BINDING SITE, designated SEQ ID:17614, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31760] Another function of GAM190 is therefore inhibition of Lim homeobox protein 3 (LHX3, Accession NP_055379.1) . Accordingly, utilities of GAM190 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with LHX3.

[31761] Lim homeobox protein 3 (LHX3, Accession NP_835258.1) is another GAM190 target gene, herein designated TARGET GENE. LHX3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LHX3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LHX3 BINDING SITE, designated SEQ ID:17614, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31762] Another function of GAM190 is therefore inhibition of Lim homeobox protein 3 (LHX3, Accession NP_835258.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHX3.

[31763] LOC112868 (Accession XP_053402.1) is another GAM190 target gene, herein designated TARGET GENE. LOC112868 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112868, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112868 BINDING SITE, designated SEQ ID:19114, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31764] Another function of GAM190 is therefore inhibition of LOC112868 (Accession XP_053402.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112868.

[31765] LOC122282 (Accession XP_063046.4) is another GAM190 target gene, herein designated TARGET GENE. LOC122282 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC122282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC122282 BINDING SITE, designated SEQ ID:3932, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31766] Another function of GAM190 is therefore inhibition of LOC122282 (Accession XP_063046.4) . Accordingly, utilities of GAM190 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC122282.

[31767] LOC130074 (Accession XP_072228.2) is another GAM190 target gene, herein designated TARGET GENE. LOC130074 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC130074, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130074 BINDING SITE, designated SEQ ID:12021, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31768] Another function of GAM190 is therefore inhibition of LOC130074 (Accession XP_072228.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130074.

[31769] LOC130951 (Accession NP_620159.2) is another GAM190 target gene, herein designated TARGET GENE. LOC130951 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC130951, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC130951 BINDING SITE, designated SEQ ID:12589, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31770] Another function of GAM190 is therefore inhibition of LOC130951 (Accession NP_620159.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130951.

[31771] LOC145820 (Accession XP_085246.1) is another GAM190 target gene, herein designated TARGET GENE. LOC145820 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145820, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145820 BINDING SITE, designated SEQ ID:17550, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31772] Another function of GAM190 is therefore inhibition of LOC145820 (Accession XP_085246.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC145820.

[31773] LOC146895 (Accession XP_097120.1) is another GAM190 target gene, herein designated TARGET GENE. LOC146895 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146895, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146895 BINDING SITE, designated SEQ ID:17975, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31774] Another function of GAM190 is therefore inhibition of LOC146895 (Accession XP_097120.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146895.

[31775] LOC150138 (Accession XP_086789.1) is another GAM190 target gene, herein designated TARGET GENE. LOC150138 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC150138 BINDING SITE, designated SEQ ID:16139, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31776] Another function of GAM190 is therefore inhibition of LOC150138 (Accession XP_086789.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150138.

[31777] LOC150933 (Accession XP_097971.1) is another GAM190 target gene, herein designated TARGET GENE. LOC150933 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150933, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150933 BINDING SITE, designated SEQ ID:802, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31778] Another function of GAM190 is therefore inhibition of LOC150933 (Accession XP_097971.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150933.

[31779] LOC151979 (Accession XP_087354.5) is another GAM190 target gene, herein designated TARGET GENE. LOC151979 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151979, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151979 BINDING SITE, designated SEQ ID:2273, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31780] Another function of GAM190 is therefore inhibition of LOC151979 (Accession XP_087354.5) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151979.

[31781] LOC157556 (Accession XP_098783.1) is another GAM190 target gene, herein designated TARGET GENE. LOC157556 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC157556, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157556 BINDING SITE, designated SEQ ID:13070, to

the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31782] Another function of GAM190 is therefore inhibition of LOC157556 (Accession XP_098783.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157556.

[31783] LOC168474 (Accession XP_095122.3) is another GAM190 target gene, herein designated TARGET GENE. LOC168474 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC168474, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC168474 BINDING SITE, designated SEQ ID:1886, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31784] Another function of GAM190 is therefore inhibition of LOC168474 (Accession XP_095122.3) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168474.

[31785] LOC196264 (Accession XP_113683.1) is another GAM190

target gene, herein designated TARGET GENE. LOC196264 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196264, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196264 BINDING SITE, designated SEQ ID:2140, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31786] Another function of GAM190 is therefore inhibition of LOC196264 (Accession XP_113683.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196264.

[31787] LOC201229 (Accession XP_113925.1) is another GAM190 target gene, herein designated TARGET GENE. LOC201229 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201229, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201229 BINDING SITE, designated SEQ ID:8606, to the nucleotide sequence of GAM190 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:289.

[31788] Another function of GAM190 is therefore inhibition of LOC201229 (Accession XP_113925.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201229.

[31789] LOC203107 (Accession XP_300975.1) is another GAM190 target gene, herein designated TARGET GENE. LOC203107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC203107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC203107 BINDING SITE, designated SEQ ID:3628, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31790] Another function of GAM190 is therefore inhibition of LOC203107 (Accession XP_300975.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203107.

[31791] LOC222160 (Accession XP_168431.1) is another GAM190 target gene, herein designated TARGET GENE. LOC222160

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222160, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222160 BINDING SITE, designated SEQ ID:4845, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31792] Another function of GAM190 is therefore inhibition of LOC222160 (Accession XP_168431.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222160.

[31793] LOC253782 (Accession XP_171023.1) is another GAM190 target gene, herein designated TARGET GENE. LOC253782 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253782, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253782 BINDING SITE, designated SEQ ID:10609, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31794] Another function of GAM190 is therefore inhibition of LOC253782 (Accession XP_171023.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253782.

[31795] LOC255167 (Accession XP_173156.1) is another GAM190 target gene, herein designated TARGET GENE. LOC255167 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC255167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255167 BINDING SITE, designated SEQ ID:8769, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31796] Another function of GAM190 is therefore inhibition of LOC255167 (Accession XP_173156.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255167.

[31797] LOC256374 (Accession XP_170597.1) is another GAM190 target gene, herein designated TARGET GENE. LOC256374 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC256374, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256374 BINDING SITE, designated SEQ ID:4774, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31798] Another function of GAM190 is therefore inhibition of LOC256374 (Accession XP_170597.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256374.

[31799] LOC283107 (Accession XP_210889.1) is another GAM190 target gene, herein designated TARGET GENE. LOC283107 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283107 BINDING SITE, designated SEQ ID:19787, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31800] Another function of GAM190 is therefore inhibition of

LOC283107 (Accession XP_210889.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283107.

[31801] LOC283143 (Accession XP_210920.1) is another GAM190 target gene, herein designated TARGET GENE. LOC283143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283143 BINDING SITE, designated SEQ ID:8033, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31802] Another function of GAM190 is therefore inhibition of LOC283143 (Accession XP_210920.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283143.

[31803] LOC283244 (Accession XP_208583.2) is another GAM190 target gene, herein designated TARGET GENE. LOC283244 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283244, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283244 BINDING SITE, designated SEQ ID:11642, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31804] Another function of GAM190 is therefore inhibition of LOC283244 (Accession XP_208583.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283244.

[31805] LOC283331 (Accession XP_210977.1) is another GAM190 target gene, herein designated TARGET GENE. LOC283331 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283331, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283331 BINDING SITE, designated SEQ ID:19234, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31806] Another function of GAM190 is therefore inhibition of LOC283331 (Accession XP_210977.1) . Accordingly, utili-

ties of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283331.

[31807] LOC283352 (Accession XP_210989.1) is another GAM190 target gene, herein designated TARGET GENE. LOC283352 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283352, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283352 BINDING SITE, designated SEQ ID:11381, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31808] Another function of GAM190 is therefore inhibition of LOC283352 (Accession XP_210989.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283352.

[31809] LOC283582 (Accession XP_211119.1) is another GAM190 target gene, herein designated TARGET GENE. LOC283582 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283582, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283582 BINDING SITE, designated SEQ ID:19719, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31810] Another function of GAM190 is therefore inhibition of LOC283582 (Accession XP_211119.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283582.

[31811] LOC283624 (Accession XP_211126.1) is another GAM190 target gene, herein designated TARGET GENE. LOC283624 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283624, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283624 BINDING SITE, designated SEQ ID:3276, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31812] Another function of GAM190 is therefore inhibition of LOC283624 (Accession XP_211126.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283624.

[31813] LOC283911 (Accession XP_211259.2) is another GAM190 target gene, herein designated TARGET GENE. LOC283911 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283911, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283911 BINDING SITE, designated SEQ ID:5990, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31814] Another function of GAM190 is therefore inhibition of LOC283911 (Accession XP_211259.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283911.

[31815] LOC284019 (Accession XP_211302.1) is another GAM190 target gene, herein designated TARGET GENE. LOC284019 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284019, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC284019 BINDING SITE, designated SEQ ID:17779, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31816] Another function of GAM190 is therefore inhibition of LOC284019 (Accession XP_211302.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284019.

[31817] LOC284145 (Accession XP_211353.1) is another GAM190 target gene, herein designated TARGET GENE. LOC284145 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284145, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284145 BINDING SITE, designated SEQ ID:4876, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31818] Another function of GAM190 is therefore inhibition of LOC284145 (Accession XP_211353.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284145.

[31819] LOC284260 (Accession XP_211408.1) is another GAM190 target gene, herein designated TARGET GENE. LOC284260 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284260, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284260 BINDING SITE, designated SEQ ID:9975, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31820] Another function of GAM190 is therefore inhibition of LOC284260 (Accession XP_211408.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284260.

[31821] LOC284665 (Accession XP_211581.1) is another GAM190 target gene, herein designated TARGET GENE. LOC284665 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284665, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC284665 BINDING SITE, designated SEQ ID:9976, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31822] Another function of GAM190 is therefore inhibition of LOC284665 (Accession XP_211581.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284665.

[31823] LOC284678 (Accession XP_209318.1) is another GAM190 target gene, herein designated TARGET GENE. LOC284678 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284678, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284678 BINDING SITE, designated SEQ ID:10939, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31824] Another function of GAM190 is therefore inhibition of LOC284678 (Accession XP_209318.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284678.

[31825] LOC284719 (Accession XP_211601.1) is another GAM190 target gene, herein designated TARGET GENE. LOC284719 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284719 BINDING SITE, designated SEQ ID:9623, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31826] Another function of GAM190 is therefore inhibition of LOC284719 (Accession XP_211601.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284719.

[31827] LOC284995 (Accession XP_211729.1) is another GAM190 target gene, herein designated TARGET GENE. LOC284995 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284995, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284995 BINDING SITE, designated SEQ ID:17855, to

the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31828] Another function of GAM190 is therefore inhibition of LOC284995 (Accession XP_211729.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284995.

[31829] LOC285009 (Accession XP_209435.1) is another GAM190 target gene, herein designated TARGET GENE. LOC285009 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285009, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285009 BINDING SITE, designated SEQ ID:13385, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31830] Another function of GAM190 is therefore inhibition of LOC285009 (Accession XP_209435.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285009.

[31831] LOC285023 (Accession XP_211737.1) is another GAM190

target gene, herein designated TARGET GENE. LOC285023 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285023, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285023 BINDING SITE, designated SEQ ID:6445, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31832] Another function of GAM190 is therefore inhibition of LOC285023 (Accession XP_211737.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285023.

[31833] LOC285026 (Accession XP_209440.1) is another GAM190 target gene, herein designated TARGET GENE. LOC285026 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285026, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285026 BINDING SITE, designated SEQ ID:4367, to the nucleotide sequence of GAM190 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:289.

[31834] Another function of GAM190 is therefore inhibition of LOC285026 (Accession XP_209440.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285026.

[31835] LOC285402 (Accession XP_211884.1) is another GAM190 target gene, herein designated TARGET GENE. LOC285402 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285402, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285402 BINDING SITE, designated SEQ ID:12287, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31836] Another function of GAM190 is therefore inhibition of LOC285402 (Accession XP_211884.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285402.

[31837] LOC285531 (Accession XP_211929.1) is another GAM190 target gene, herein designated TARGET GENE. LOC285531

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285531, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285531 BINDING SITE, designated SEQ ID:7733, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31838] Another function of GAM190 is therefore inhibition of LOC285531 (Accession XP_211929.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285531.

[31839] LOC285703 (Accession XP_209728.1) is another GAM190 target gene, herein designated TARGET GENE. LOC285703 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285703, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285703 BINDING SITE, designated SEQ ID:11785, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31840] Another function of GAM190 is therefore inhibition of LOC285703 (Accession XP_209728.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285703.

[31841] LOC285733 (Accession XP_212006.1) is another GAM190 target gene, herein designated TARGET GENE. LOC285733 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285733, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285733 BINDING SITE, designated SEQ ID:12713, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31842] Another function of GAM190 is therefore inhibition of LOC285733 (Accession XP_212006.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285733.

[31843] LOC285945 (Accession XP_212092.1) is another GAM190 target gene, herein designated TARGET GENE. LOC285945 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC285945, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285945 BINDING SITE, designated SEQ ID:1977, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31844] Another function of GAM190 is therefore inhibition of LOC285945 (Accession XP_212092.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285945.

[31845] LOC286030 (Accession XP_209868.1) is another GAM190 target gene, herein designated TARGET GENE. LOC286030 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286030, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286030 BINDING SITE, designated SEQ ID:3883, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31846] Another function of GAM190 is therefore inhibition of

LOC286030 (Accession XP_209868.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286030.

[31847] LOC338616 (Accession XP_294666.1) is another GAM190 target gene, herein designated TARGET GENE. LOC338616 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338616, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338616 BINDING SITE, designated SEQ ID:10009, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31848] Another function of GAM190 is therefore inhibition of LOC338616 (Accession XP_294666.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338616.

[31849] LOC338866 (Accession XP_294736.1) is another GAM190 target gene, herein designated TARGET GENE. LOC338866 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338866, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338866 BINDING SITE, designated SEQ ID:10133, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31850] Another function of GAM190 is therefore inhibition of LOC338866 (Accession XP_294736.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338866.

[31851] LOC339273 (Accession XP_294893.1) is another GAM190 target gene, herein designated TARGET GENE. LOC339273 BINDING SITE1 and LOC339273 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339273, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339273 BINDING SITE1 and LOC339273 BINDING SITE2, designated SEQ ID:7171 and SEQ ID:1143 respectively, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31852] Another function of GAM190 is therefore inhibition of LOC339273 (Accession XP_294893.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339273.

[31853] LOC339545 (Accession XP_290946.1) is another GAM190 target gene, herein designated TARGET GENE. LOC339545 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339545, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339545 BINDING SITE, designated SEQ ID:18173, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31854] Another function of GAM190 is therefore inhibition of LOC339545 (Accession XP_290946.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339545.

[31855] LOC339553 (Accession XP_290949.1) is another GAM190 target gene, herein designated TARGET GENE. LOC339553 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC339553, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339553 BINDING SITE, designated SEQ ID:18173, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31856] Another function of GAM190 is therefore inhibition of LOC339553 (Accession XP_290949.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339553.

[31857] LOC339694 (Accession XP_295035.1) is another GAM190 target gene, herein designated TARGET GENE. LOC339694 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339694, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339694 BINDING SITE, designated SEQ ID:1952, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31858] Another function of GAM190 is therefore inhibition of

LOC339694 (Accession XP_295035.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339694.

[31859] LOC339859 (Accession XP_295088.1) is another GAM190 target gene, herein designated TARGET GENE. LOC339859 BINDING SITE1 and LOC339859 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339859, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339859 BINDING SITE1 and LOC339859 BINDING SITE2, designated SEQ ID:12990 and SEQ ID:15811 respectively, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31860] Another function of GAM190 is therefore inhibition of LOC339859 (Accession XP_295088.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339859.

[31861] LOC339874 (Accession XP_295090.1) is another GAM190 target gene, herein designated TARGET GENE. LOC339874

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339874, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339874 BINDING SITE, designated SEQ ID:1545, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31862] Another function of GAM190 is therefore inhibition of LOC339874 (Accession XP_295090.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339874.

[31863] LOC339987 (Accession XP_295123.1) is another GAM190 target gene, herein designated TARGET GENE. LOC339987 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339987, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339987 BINDING SITE, designated SEQ ID:18833, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31864] Another function of GAM190 is therefore inhibition of LOC339987 (Accession XP_295123.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339987.

[31865] LOC348326 (Accession XP_300696.1) is another GAM190 target gene, herein designated TARGET GENE. LOC348326 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348326, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348326 BINDING SITE, designated SEQ ID:18880, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31866] Another function of GAM190 is therefore inhibition of LOC348326 (Accession XP_300696.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348326.

[31867] LOC348445 (Accession XP_300738.1) is another GAM190 target gene, herein designated TARGET GENE. LOC348445 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC348445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348445 BINDING SITE, designated SEQ ID:18880, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31868] Another function of GAM190 is therefore inhibition of LOC348445 (Accession XP_300738.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348445.

[31869] LOC348492 (Accession XP_300758.1) is another GAM190 target gene, herein designated TARGET GENE. LOC348492 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348492, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348492 BINDING SITE, designated SEQ ID:6321, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31870] Another function of GAM190 is therefore inhibition of

LOC348492 (Accession XP_300758.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348492.

[31871] LOC348527 (Accession XP_300779.1) is another GAM190 target gene, herein designated TARGET GENE. LOC348527 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348527, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348527 BINDING SITE, designated SEQ ID:19269, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31872] Another function of GAM190 is therefore inhibition of LOC348527 (Accession XP_300779.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348527.

[31873] LOC348570 (Accession XP_290329.1) is another GAM190 target gene, herein designated TARGET GENE. LOC348570 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348570, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348570 BINDING SITE, designated SEQ ID:8957, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31874] Another function of GAM190 is therefore inhibition of LOC348570 (Accession XP_290329.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348570.

[31875] LOC348687 (Accession XP_302853.1) is another GAM190 target gene, herein designated TARGET GENE. LOC348687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348687 BINDING SITE, designated SEQ ID:18314, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31876] Another function of GAM190 is therefore inhibition of LOC348687 (Accession XP_302853.1) . Accordingly, utili-

ties of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348687.

[31877] LOC348808 (Accession XP_302893.1) is another GAM190 target gene, herein designated TARGET GENE. LOC348808 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348808, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348808 BINDING SITE, designated SEQ ID:9714, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31878] Another function of GAM190 is therefore inhibition of LOC348808 (Accession XP_302893.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348808.

[31879] LOC348835 (Accession XP_302902.1) is another GAM190 target gene, herein designated TARGET GENE. LOC348835 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348835, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348835 BINDING SITE, designated SEQ ID:3838, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31880] Another function of GAM190 is therefore inhibition of LOC348835 (Accession XP_302902.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348835.

[31881] LOC349251 (Accession XP_300251.1) is another GAM190 target gene, herein designated TARGET GENE. LOC349251 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349251, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349251 BINDING SITE, designated SEQ ID:13594, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31882] Another function of GAM190 is therefore inhibition of LOC349251 (Accession XP_300251.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC349251.

[31883] LOC349408 (Accession XP_303044.1) is another GAM190 target gene, herein designated TARGET GENE. LOC349408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349408 BINDING SITE, designated SEQ ID:19652, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31884] Another function of GAM190 is therefore inhibition of LOC349408 (Accession XP_303044.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349408.

[31885] LOC51619 (Accession NP_057067.1) is another GAM190 target gene, herein designated TARGET GENE. LOC51619 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51619, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of LOC51619 BINDING SITE, designated SEQ ID:4728, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31886] Another function of GAM190 is therefore inhibition of LOC51619 (Accession NP_057067.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51619.

[31887] LOC57209 (Accession XP_290488.1) is another GAM190 target gene, herein designated TARGET GENE. LOC57209 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC57209, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC57209 BINDING SITE, designated SEQ ID:19313, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31888] Another function of GAM190 is therefore inhibition of LOC57209 (Accession XP_290488.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC57209.

[31889] LOC65121 (Accession NP_075389.1) is another GAM190 target gene, herein designated TARGET GENE. LOC65121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC65121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC65121 BINDING SITE, designated SEQ ID:18173, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31890] Another function of GAM190 is therefore inhibition of LOC65121 (Accession NP_075389.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC65121.

[31891] LOC65122 (Accession NP_075390.1) is another GAM190 target gene, herein designated TARGET GENE. LOC65122 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC65122, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

LOC65122 BINDING SITE, designated SEQ ID:18173, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31892] Another function of GAM190 is therefore inhibition of LOC65122 (Accession NP_075390.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC65122.

[31893] LOC90170 (Accession XP_029589.1) is another GAM190 target gene, herein designated TARGET GENE. LOC90170 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC90170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90170 BINDING SITE, designated SEQ ID:16015, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31894] Another function of GAM190 is therefore inhibition of LOC90170 (Accession XP_029589.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90170.

[31895] LOC90750 (Accession XP_033868.1) is another GAM190 target gene, herein designated TARGET GENE. LOC90750 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90750, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90750 BINDING SITE, designated SEQ ID:3453, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31896] Another function of GAM190 is therefore inhibition of LOC90750 (Accession XP_033868.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90750.

[31897] LOC91250 (Accession XP_037135.1) is another GAM190 target gene, herein designated TARGET GENE. LOC91250 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91250, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91250 BINDING SITE, designated SEQ ID:4751, to the

nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31898] Another function of GAM190 is therefore inhibition of LOC91250 (Accession XP_037135.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91250.

[31899] LOC92249 (Accession XP_043814.1) is another GAM190 target gene, herein designated TARGET GENE. LOC92249 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92249, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92249 BINDING SITE, designated SEQ ID:14921, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31900] Another function of GAM190 is therefore inhibition of LOC92249 (Accession XP_043814.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92249.

[31901] Low density lipoprotein-related protein 1b (deleted in tu-

mors) (LRP1B, Accession NP_061027.1) is another GAM190 target gene, herein designated TARGET GENE. LRP1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LRP1B BINDING SITE, designated SEQ ID:12085, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31902] Another function of GAM190 is therefore inhibition of Low density lipoprotein-related protein 1b (deleted in tumors) (LRP1B, Accession NP_061027.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP1B.

[31903] Low density lipoprotein receptor-related protein 4 (LRP4, Accession XP_035037.2) is another GAM190 target gene, herein designated TARGET GENE. LRP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LRP4 BINDING SITE,

designated SEQ ID:16297, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31904] Another function of GAM190 is therefore inhibition of Low density lipoprotein receptor-related protein 4 (LRP4, Accession XP_035037.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP4.

[31905] Mitogen-activated protein kinase kinase kinase 13 (MAP3K13, Accession NP_004712.1) is another GAM190 target gene, herein designated TARGET GENE. MAP3K13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAP3K13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAP3K13 BINDING SITE, designated SEQ ID:9282, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31906] Another function of GAM190 is therefore inhibition of Mitogen-activated protein kinase kinase kinase 13 (MAP3K13, Accession NP_004712.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MAP3K13.

[31907] MAPKBP1 (Accession XP_031706.7) is another GAM190 target gene, herein designated TARGET GENE. MAPKBP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAPKBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPKBP1 BINDING SITE, designated SEQ ID:2864, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31908] Another function of GAM190 is therefore inhibition of MAPKBP1 (Accession XP_031706.7) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPKBP1.

[31909] Methyl-cpg binding domain protein 4 (MBD4, Accession NP_003916.1) is another GAM190 target gene, herein designated TARGET GENE. MBD4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MBD4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MBD4 BINDING SITE, designated SEQ ID:6949, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31910] Another function of GAM190 is therefore inhibition of Methyl-cpg binding domain protein 4 (MBD4, Accession NP_003916.1), a gene which are likely to be mediators of the effects of DNA methylation in mammalian cells. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBD4.

[31911] The function of MBD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.MGC13053 (Accession NP_116099.1) is another GAM190 target gene, herein designated TARGET GENE. MGC13053 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13053, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13053 BINDING SITE, designated SEQ ID:7515, to the nucleotide sequence of

GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31912] Another function of GAM190 is therefore inhibition of MGC13053 (Accession NP_116099.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13053.

[31913] MGC15438 (Accession NP_116263.2) is another GAM190 target gene, herein designated TARGET GENE. MGC15438 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC15438, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15438 BINDING SITE, designated SEQ ID:8619, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31914] Another function of GAM190 is therefore inhibition of MGC15438 (Accession NP_116263.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15438.

[31915] MGC17986 (Accession NP_705836.1) is another GAM190

target gene, herein designated TARGET GENE. MGC17986 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC17986, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC17986 BINDING SITE, designated SEQ ID:5825, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31916] Another function of GAM190 is therefore inhibition of MGC17986 (Accession NP_705836.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC17986.

[31917] MGC35304 (Accession NP_694987.1) is another GAM190 target gene, herein designated TARGET GENE. MGC35304 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35304, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35304 BINDING SITE, designated SEQ ID:17665, to the nucleotide sequence of GAM190 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:289.

[31918] Another function of GAM190 is therefore inhibition of MGC35304 (Accession NP_694987.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35304.

[31919] MGC45714 (Accession NP_689677.1) is another GAM190 target gene, herein designated TARGET GENE. MGC45714 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC45714, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC45714 BINDING SITE, designated SEQ ID:8478, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31920] Another function of GAM190 is therefore inhibition of MGC45714 (Accession NP_689677.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC45714.

[31921] MGC5466 (Accession NP_112184.1) is another GAM190 target gene, herein designated TARGET GENE. MGC5466

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC5466, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC5466 BINDING SITE, designated SEQ ID:3145, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31922] Another function of GAM190 is therefore inhibition of MGC5466 (Accession NP_112184.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5466.

[31923] MLC1SA (Accession NP_002466.1) is another GAM190 target gene, herein designated TARGET GENE. MLC1SA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MLC1SA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLC1SA BINDING SITE, designated SEQ ID:4844, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31924] Another function of GAM190 is therefore inhibition of MLC1SA (Accession NP_002466.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLC1SA.

[31925] Myelin oligodendrocyte glycoprotein (MOG, Accession NP_002424.1) is another GAM190 target gene, herein designated TARGET GENE. MOG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MOG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MOG BINDING SITE, designated SEQ ID:6547, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31926] Another function of GAM190 is therefore inhibition of Myelin oligodendrocyte glycoprotein (MOG, Accession NP_002424.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOG.

[31927] MORF4L2 (Accession NP_036418.1) is another GAM190 target gene, herein designated TARGET GENE. MORF4L2 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MORF4L2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MORF4L2 BINDING SITE, designated SEQ ID:17588, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31928] Another function of GAM190 is therefore inhibition of MORF4L2 (Accession NP_036418.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MORF4L2.

[31929] M-phase phosphoprotein 9 (MPHOSPH9, Accession NP_073619.1) is another GAM190 target gene, herein designated TARGET GENE. MPHOSPH9 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MPHOSPH9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPHOSPH9 BINDING SITE, designated SEQ ID:8003, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31930] Another function of GAM190 is therefore inhibition of M-phase phosphoprotein 9 (MPHOSPH9, Accession NP_073619.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPHOSPH9.

[31931] Male-specific lethal 3-like 1 (drosophila) (MSL3L1, Accession NP_523352.1) is another GAM190 target gene, herein designated TARGET GENE. MSL3L1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MSL3L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MSL3L1 BINDING SITE, designated SEQ ID:17050, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31932] Another function of GAM190 is therefore inhibition of Male-specific lethal 3-like 1 (drosophila) (MSL3L1, Accession NP_523352.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSL3L1.

[31933] Metallothionein 1f (functional) (MT1F, Accession NP_005940.1) is another GAM190 target gene, herein

designated TARGET GENE. MT1F BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MT1F, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MT1F BINDING SITE, designated SEQ ID:17234, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31934] Another function of GAM190 is therefore inhibition of Metallothionein 1f (functional) (MT1F, Accession NP_005940.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MT1F.

[31935] Metallothionein 1g (MT1G, Accession NP_005941.1) is another GAM190 target gene, herein designated TARGET GENE. MT1G BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MT1G, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MT1G BINDING SITE, designated SEQ ID:4199, to the nucleotide sequence of GAM190 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:289.

[31936] Another function of GAM190 is therefore inhibition of Metallothionein 1g (MT1G, Accession NP_005941.1), a gene which is active in metal homeostasis and protects against heavy- metal toxicity. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MT1G.

[31937] The function of MT1G has been established by previous studies. See 156350. Karin et al. (1984), West et al. (1990), and others have mapped the locus containing the MT1 gene family to chromosome 16q13. Foster et al. (1988) described the structure of the human MT1G gene. They showed that the MT1G gene promoter is not cell type- specific. However, they also found that, while the gene was expressed in certain hepatoma- derived cell lines in response to heavy metals (but not to dexamethasone), a lymphoblastoid cell line did not express MT1G, suggesting to them that MT1G gene expression is regulated differentially and in a cell- specific manner. They also found that the MT1G promoter is 5 times more active than the MT1F (OMIM Ref. No. 156352) promoter in transient transfection studies.

[31938]

[31939] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31940] Karin, M.; Eddy, R. L.; Henry, W. M.; Haley, L. L.; Byers, M. G.; Shows, T. B. : Human metallothionein genes are clustered on chromosome 16. Proc. Nat. Acad. Sci. 81: 5494-5498, 1984. ; and

[31941] West, A. K.; Stallings, R.; Hildebrand, C. E.; Chiu, R.; Karin, M.; Richards, R. I. : Human metallothionein genes: structure of the functional locus at 16q13. Genomics 8: 513-518, 1990.

[31942] Further studies establishing the function and utilities of MT1G are found in John Hopkins OMIM database record ID 156353, and in cited publications listed in Table 5, which are hereby incorporated by reference.Metallothionein 1h (MT1H, Accession NP_005942.1) is another GAM190 target gene, herein designated TARGET GENE. MT1H BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MT1H, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MT1H BINDING SITE, designated SEQ ID:6444, to the nucleotide se-

quence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31943] Another function of GAM190 is therefore inhibition of Metallothionein 1h (MT1H, Accession NP_005942.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MT1H.

[31944] Metallothionein 1l (MT1L, Accession NP_002441.2) is another GAM190 target gene, herein designated TARGET GENE. MT1L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MT1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MT1L BINDING SITE, designated SEQ ID:17203, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31945] Another function of GAM190 is therefore inhibition of Metallothionein 1l (MT1L, Accession NP_002441.2), a gene which plays a role in zinc and copper homeostasis during development. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MT1L.

[31946] The function of MT1L has been established by previous studies. See 156350. Karin et al. (1984), West et al. (1990), and others have mapped the locus containing the MT1 gene family to chromosome 16q13.

[31947]

[31948] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31949] Karin, M.; Eddy, R. L.; Henry, W. M.; Haley, L. L.; Byers, M. G.; Shows, T. B. : Human metallothionein genes are clustered on chromosome 16. Proc. Nat. Acad. Sci. 81: 5494-5498, 1984. ; and

[31950] West, A. K.; Stallings, R.; Hildebrand, C. E.; Chiu, R.; Karin, M.; Richards, R. I. : Human metallothionein genes: structure of the functional locus at 16q13. Genomics 8: 513-518, 1990.

[31951] Further studies establishing the function and utilities of MT1L are found in John Hopkins OMIM database record ID 156358, and in cited publications listed in Table 5, which are hereby incorporated by reference.Metallothionein 1x (MT1X, Accession NP_005943.1) is another GAM190 target gene, herein designated TARGET GENE. MT1X BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by MT1X, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MT1X BINDING SITE, designated SEQ ID:7997, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31952] Another function of GAM190 is therefore inhibition of Metallothionein 1x (MT1X, Accession NP_005943.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MT1X.

[31953] Myosin viia and rab interacting protein (MYRIP, Accession NP_056275.1) is another GAM190 target gene, herein designated TARGET GENE. MYRIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYRIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYRIP BINDING SITE, designated SEQ ID:14896, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31954] Another function of GAM190 is therefore inhibition of Myosin viia and rab interacting protein (MYRIP, Accession NP_056275.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYRIP.

[31955] NALP2 (Accession NP_060322.1) is another GAM190 target gene, herein designated TARGET GENE. NALP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NALP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NALP2 BINDING SITE, designated SEQ ID:2364, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31956] Another function of GAM190 is therefore inhibition of NALP2 (Accession NP_060322.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NALP2.

[31957] Nck adaptor protein 1 (NCK1, Accession NP_006144.1) is another GAM190 target gene, herein designated TARGET GENE. NCK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCK1,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCK1 BINDING SITE, designated SEQ ID:17015, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31958] Another function of GAM190 is therefore inhibition of Nck adaptor protein 1 (NCK1, Accession NP_006144.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCK1.

[31959] Nk3 transcription factor related, locus 1 (drosophila) (NKX3-1, Accession NP_006158.2) is another GAM190 target gene, herein designated TARGET GENE. NKX3-1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NKX3-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NKX3-1 BINDING SITE, designated SEQ ID:8119, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31960] Another function of GAM190 is therefore inhibition of Nk3

transcription factor related, locus 1 (drosophila) (NKX3-1, Accession NP_006158.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NKX3-1.

[31961] Neuroligin 1 (NLGN1, Accession NP_055747.1) is another GAM190 target gene, herein designated TARGET GENE. NLGN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NLGN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NLGN1 BINDING SITE, designated SEQ ID:8186, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31962] Another function of GAM190 is therefore inhibition of Neuroligin 1 (NLGN1, Accession NP_055747.1), a gene which may trigger the de novo formation of presynaptic structure. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NLGN1.

[31963] The function of NLGN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM90.1.Notch homolog 1, translocation-associated (drosophila) (NOTCH1, Accession NP_060087.2) is another GAM190 target gene, herein designated TARGET GENE. NOTCH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOTCH1 BINDING SITE, designated SEQ ID:11588, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31964] Another function of GAM190 is therefore inhibition of Notch homolog 1, translocation-associated (drosophila) (NOTCH1, Accession NP_060087.2), a gene which is possibly involved in cell differentiation and lymphocyte function. and therefore may be associated with Neoplasia, a t-cell acute lymphoblastic leukemia. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of Neoplasia, a t- cell acute lymphoblastic leukemia., and of other diseases and clinical conditions associated with NOTCH1.

[31965] The function of NOTCH1 has been established by previous studies. Cytogenetic studies have shown that chromo-

some 7 band q34- q35, which contains the gene for the beta T- cell receptor (OMIM Ref. No. 186930), is a common site for translocation in T- cell neoplasms. In a translocation t(7;9)(q34;q34.3) found in a case of acute T-cell lymphoblastic leukemia, Ellisen et al. (1991) found that the locus on chromosome 9 contains a gene highly homologous to the Drosophila gene 'Notch.' Transcripts of the human gene, for which they proposed the name TAN1 (an acronym for translocation- associated Notch homolog), and its murine counterpart were demonstrated in many normal human fetal and adult mouse tissues but were most abundant in lymphoid tissues. In t(7;9)(q34;q34.3) translocations from 3 cases of acute T-cell lymphoblastic leukemia, Ellisen et al. (1991) found breakpoints within 100 bp of an intron in TAN1, resulting in truncation of TAN1 transcripts. They interpreted the observations to indicate that TAN1 is important for normal lymphocyte function and that alterations in TAN1 play a role in the pathogenesis of some T- cell neoplasms. Milner et al. (1994) found that at least 1 Notch homolog is expressed in human bone marrow CD34+ cells, a population enriched for hematopoietic precursors. On the basis of these findings, they suggested that members of the

Notch family, including TAN1, may be involved in mediating cell- fate decisions during hematopoiesis.

[31966] Animal model experiments lend further support to the function of NOTCH1. Huppert et al. (2000) mutated valine at position 1744 of the mouse Notch1 gene to glycine. This position is the site for proteolytic cleavage and is critical for Notch1 intracellular processing in tissue- culture cells. Huppert et al. (2000) generated homozygous animals carrying 2 germline mutations and compared these with mice who have 2 null alleles for Notch1 (Conlon et al., 1995). At embryonic day 8.5 to 10.5, homozygous embryos were detected at the expected mendelian frequency. Similar to the null alleles, embryo absorption was detected between embryonic day 10 and 12, and no homozygous embryos were recovered past embryonic day 12. These results suggested that efficient Notch processing is necessary for the early embryonic developmental aspects of Notch activity. RT- PCR and immunoprecipitation showed comparable amounts of Notch mRNA and protein, respectively, in the processing- deficient embryos and their heterozygous and wildtype littermates. The phenotypes associated with the single point mutation resembled the null Notch1 phenotype, but with slightly reduced

penetrance.

[31967] It is appreciated that the abovementioned animal model for NOTCH1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[31968] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31969] Ellisen, L. W.; Bird, J.; West, D. C.; Soreng, A. L.; Reynolds, T. C.; Smith, S. D.; Sklar, J. : TAN- 1, the human homolog of the Drosophila Notch gene, is broken by chromosomal translocations in T lymphoblastic neoplasms. Cell 66: 649- 661, 1991. ; and

[31970] Huppert, S. S.; Le, A.; Schroeter, E. H.; Mumm, J. S.; Saxena, M. T.; Milner, L. A.; Kopan, R. : Embryonic lethality in mice homozygous for a processing- deficient allele of Notch1. Natu.

[31971] Further studies establishing the function and utilities of NOTCH1 are found in John Hopkins OMIM database record ID 190198, and in cited publications listed in Table 5, which are hereby incorporated by reference.Nadph oxidase 1 (NOX1, Accession NP_039249.1) is another GAM190 target gene, herein designated TARGET GENE.

NOX1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NOX1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOX1 BINDING SITE, designated SEQ ID:8938, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31972] Another function of GAM190 is therefore inhibition of Nadph oxidase 1 (NOX1, Accession NP_039249.1), a gene which mediates the h+ currents of resting phagocytes and other tissues. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOX1.

[31973] The function of NOX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Nadph oxidase 1 (NOX1, Accession NP_039248.1) is another GAM190 target gene, herein designated TARGET GENE. NOX1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NOX1, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOX1 BINDING SITE, designated SEQ ID:8938, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31974] Another function of GAM190 is therefore inhibition of Nadph oxidase 1 (NOX1, Accession NP_039248.1), a gene which mediates the h+ currents of resting phagocytes and other tissues. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOX1.

[31975] The function of NOX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Nadph oxidase 1 (NOX1, Accession NP_008983.1) is another GAM190 target gene, herein designated TARGET GENE. NOX1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NOX1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOX1 BINDING SITE, designated SEQ ID:8938, to the nucleotide

sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31976] Another function of GAM190 is therefore inhibition of Nadph oxidase 1 (NOX1, Accession NP_008983.1), a gene which mediates the h+ currents of resting phagocytes and other tissues. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOX1.

[31977] The function of NOX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Neuronal pentraxin ii (NPTX2, Accession NP_002514.1) is another GAM190 target gene, herein designated TARGET GENE. NPTX2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPTX2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPTX2 BINDING SITE, designated SEQ ID:4797, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31978] Another function of GAM190 is therefore inhibition of Neuronal pentraxin ii (NPTX2, Accession NP_002514.1), a

gene which is likely to play role in the modification of cellular properties that underlie long- term plasticity. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTX2.

[31979] The function of NPTX2 has been established by previous studies. Pentraxins constitute a family of proteins that include C- reactive protein (CRP; 123260) and serum amyloid P protein (APCS; 104770). Hsu and Perin (1995) noted that the prototypic pentraxin, C- reactive protein, was first identified as a serum component that binds Streptococcus pneumoniae (Tillett and Francis, 1930 and Abernethy and Avery, 1941) and whose serum concentration increases up to 1,000- fold during an acute phase response. Pentraxins acquired their name from their ability to form pentameric (or decameric) complexes and have been characterized by their ability to bind numerous ligands. The latter property raises the possibility that these proteins may mediate a nonspecific uptake of bacteria and cell debris that may be associated with inflammation and immune responses. Schlimgen et al. (1995) identified a novel neuronal pentraxin in rat as a potential receptor mediating the uptake of the presynaptic snake venom

toxin taipoxin (see OMIM Ref. No. NPTX1, 602367). Based on the low identity to other pentraxins and the hypothesis that this neuronal pentraxin may mediate uptake of degraded synaptic material, Hsu and Perin (1995) sought to identify additional members of what they suspected represents a new family of pentraxins. They reported the cDNA and genomic sequences of a second neuronal pentraxin in humans, for which they proposed the name neuronal pentraxin II (NPTX2). They found that it shows 54% amino acid identity to rat neuronal pentraxin I, with 69% identity over the carboxy- terminal half of NP I, and is 88% identical to a sperm acrosomal pentraxin. Northern blot analysis demonstrated that NPTX2 message is present in brain, testis, pancreas, liver, heart, and skeletal muscle; thus, unlike NP I, NP II is not exclusively localized to neurons. Like NP I, NP II has potential N- linked glycosylation sites. The human NPTX2 gene is 11 kb long and contains 4 introns. By fluorescence in situ hybridization, Hsu and Perin (1995) mapped the NPTX2 gene to 7q21.3- q22.1.

[31980]

[31981] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31982] Hsu, Y.- C.; Perin, M. S. : Human neuronal pentraxin II (NPTX2): conservation, genomic structure, and chromosomal localization. Genomics 28: 220- 227, 1995. ; and

[31983] Schlimgen, A. K.; Helms, J. A.; Vogel, H.; Perin, M. S. : Neuronal pentraxin, a secreted protein with homology to acute phase proteins of the immune system. Neuron 14: 519- 526, 1995.

[31984] Further studies establishing the function and utilities of NPTX2 are found in John Hopkins OMIM database record ID 600750, and in cited publications listed in Table 5, which are hereby incorporated by reference.Neuronal pentraxin receptor (NPTXR, Accession NP_478058.1) is another GAM190 target gene, herein designated TARGET GENE. NPTXR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NPTXR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE, designated SEQ ID:13368, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31985] Another function of GAM190 is therefore inhibition of

Neuronal pentraxin receptor (NPTXR, Accession NP_478058.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR.

[31986] Neuronal pentraxin receptor (NPTXR, Accession NP_055108.2) is another GAM190 target gene, herein designated TARGET GENE. NPTXR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NPTXR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE, designated SEQ ID:13368, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31987] Another function of GAM190 is therefore inhibition of Neuronal pentraxin receptor (NPTXR, Accession NP_055108.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR.

[31988] Neuregulin 1 (NRG1, Accession NP_039252.1) is another GAM190 target gene, herein designated TARGET GENE. NRG1 BINDING SITE is a target binding site found in the 3`

untranslated region of multiple transcripts of mRNA encoded by NRG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRG1 BINDING SITE, designated SEQ ID:17541, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31989] Another function of GAM190 is therefore inhibition of Neuregulin 1 (NRG1, Accession NP_039252.1), a gene which is essential for neuronal development. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRG1.

[31990] The function of NRG1 has been established by previous studies. The NEU/ERBB2 protooncogene (OMIM Ref. No. 164870) encodes a molecule that is closely related to epidermal growth factor receptor (EGFR; 131550) but binds none of the ligands of this receptor. Originally, NEU was identified as a dominant transforming gene in tumors of the peripheral nervous system that were induced by transplacental treatment of rat embryos with N- ethylnitrosourea. The period of susceptibility of NEU to carcino-

genesis, i.e., midgestation, correlated with the timing of its expression in the nervous system. The existence of a NEU- specific ligand of endogenous nature activating NEU at a specific developmental stage was suggested. This ligand, known as heregulin (Holmes et al., 1992) or NEU differentiation factor, is a 44- kD glycoprotein that interacts with the NEU/ERBB2 receptor tyrosine kinase to increase its phosphorylation on tyrosine residues. Splice variants of heregulin, referred to as heregulin betas, have been described by Holmes et al. (1992).

[31991] Animal model experiments lend further support to the function of NRG1. Mice homozygous for disruptions of all NRG1 isoforms, all Ig- NRG1 isoforms, and all cytoplasmic tail- containing isoforms die at embryonic day 10.5 from cardiac defects. In particular, these mice die before significant expression of CRD- NRG1 isoforms, which predominate after midgestation. By histologic analyses, Wolpowitz et al. (2000) found that homozygous CRD- NRG1- deficient mice had normal neuronal trajectory and outgrowth, but that the projections defasciculated, branched abnormally, and failed to sustain peripheral neuromuscular synaptic development. Newborn mutants had immature skeletal muscle. Schwann cells were generated in the mu-

tants but failed to survive, consistent with the designation of NRG1 as a Schwann cell survival factor. Schwann cells in turn appeared to provide trophic support only after the nerve had entered its target field and had begun synapse formation.

[31992] It is appreciated that the abovementioned animal model for NRG1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[31993] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[31994] Holmes, W. E.; Sliwkowski, M. X.; Akita, R. W.; Henzel, W. J.; Lee, J.; Park, J. W.; Yansura, D.; Abadi, N.; Raab, H.; Lewis, G. D.; Shepard, H. M.; Kuang, W.- J.; Wood, W. I.; Goeddel, D. V.; Vandlen, R. L. : Identification of heregulin, a specific activator of p185(erbB2). Science 256: 1205-1210, 1992. ; and

[31995] Wolpowitz, D.; Mason, T. B. A.; Dietrich, P.; Mendelsohn, M.; Talmage, D. A.; Role, L. W. : Cysteine- rich domain isoforms of the neuregulin- 1 gene are required for maintenance of periph.

[31996] Further studies establishing the function and utilities of

NRG1 are found in John Hopkins OMIM database record ID 142445, and in cited publications listed in Table 5, which are hereby incorporated by reference.Neuregulin 1 (NRG1, Accession NP_039256.1) is another GAM190 target gene, herein designated TARGET GENE. NRG1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NRG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRG1 BINDING SITE, designated SEQ ID:17541, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[31997] Another function of GAM190 is therefore inhibition of Neuregulin 1 (NRG1, Accession NP_039256.1), a gene which is essential for neuronal development. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRG1.

[31998] The function of NRG1 has been established by previous studies. The NEU/ERBB2 protooncogene (OMIM Ref. No. 164870) encodes a molecule that is closely related to epidermal growth factor receptor (EGFR; 131550) but binds

none of the ligands of this receptor. Originally, NEU was identified as a dominant transforming gene in tumors of the peripheral nervous system that were induced by transplacental treatment of rat embryos with N- ethylnitrosourea. The period of susceptibility of NEU to carcinogenesis, i.e., midgestation, correlated with the timing of its expression in the nervous system. The existence of a NEU- specific ligand of endogenous nature activating NEU at a specific developmental stage was suggested. This ligand, known as heregulin (Holmes et al., 1992) or NEU differentiation factor, is a 44- kD glycoprotein that interacts with the NEU/ERBB2 receptor tyrosine kinase to increase its phosphorylation on tyrosine residues. Splice variants of heregulin, referred to as heregulin betas, have been described by Holmes et al. (1992).

[31999] Animal model experiments lend further support to the function of NRG1. Mice homozygous for disruptions of all NRG1 isoforms, all Ig- NRG1 isoforms, and all cytoplasmic tail- containing isoforms die at embryonic day 10.5 from cardiac defects. In particular, these mice die before significant expression of CRD- NRG1 isoforms, which predominate after midgestation. By histologic analyses, Wolpowitz et al. (2000) found that homozygous CRD- NRG1- defi-

cient mice had normal neuronal trajectory and outgrowth, but that the projections defasciculated, branched abnormally, and failed to sustain peripheral neuromuscular synaptic development. Newborn mutants had immature skeletal muscle. Schwann cells were generated in the mutants but failed to survive, consistent with the designation of NRG1 as a Schwann cell survival factor. Schwann cells in turn appeared to provide trophic support only after the nerve had entered its target field and had begun synapse formation.

[32000] It is appreciated that the abovementioned animal model for NRG1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[32001] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32002] Holmes, W. E.; Sliwkowski, M. X.; Akita, R. W.; Henzel, W. J.; Lee, J.; Park, J. W.; Yansura, D.; Abadi, N.; Raab, H.; Lewis, G. D.; Shepard, H. M.; Kuang, W.- J.; Wood, W. I.; Goeddel, D. V.; Vandlen, R. L. : Identification of heregulin, a specific activator of p185(erbB2). Science 256: 1205-1210, 1992. ; and

[32003] Wolpowitz, D.; Mason, T. B. A.; Dietrich, P.; Mendelsohn, M.; Talmage, D. A.; Role, L. W. : Cysteine- rich domain isoforms of the neuregulin- 1 gene are required for maintenance of periph.

[32004] Further studies establishing the function and utilities of NRG1 are found in John Hopkins OMIM database record ID 142445, and in cited publications listed in Table 5, which are hereby incorporated by reference.Neuregulin 1 (NRG1, Accession NP_039253.1) is another GAM190 target gene, herein designated TARGET GENE. NRG1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NRG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRG1 BINDING SITE, designated SEQ ID:17541, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32005] Another function of GAM190 is therefore inhibition of Neuregulin 1 (NRG1, Accession NP_039253.1), a gene which is essential for neuronal development. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with NRG1.

[32006] The function of NRG1 has been established by previous studies. The NEU/ERBB2 protooncogene (OMIM Ref. No. 164870) encodes a molecule that is closely related to epidermal growth factor receptor (EGFR; 131550) but binds none of the ligands of this receptor. Originally, NEU was identified as a dominant transforming gene in tumors of the peripheral nervous system that were induced by transplacental treatment of rat embryos with N- ethylnitrosourea. The period of susceptibility of NEU to carcinogenesis, i.e., midgestation, correlated with the timing of its expression in the nervous system. The existence of a NEU- specific ligand of endogenous nature activating NEU at a specific developmental stage was suggested. This ligand, known as heregulin (Holmes et al., 1992) or NEU differentiation factor, is a 44- kD glycoprotein that interacts with the NEU/ERBB2 receptor tyrosine kinase to increase its phosphorylation on tyrosine residues. Splice variants of heregulin, referred to as heregulin betas, have been described by Holmes et al. (1992).

[32007] Animal model experiments lend further support to the function of NRG1. Mice homozygous for disruptions of all NRG1 isoforms, all Ig- NRG1 isoforms, and all cytoplasmic

tail- containing isoforms die at embryonic day 10.5 from cardiac defects. In particular, these mice die before significant expression of CRD- NRG1 isoforms, which predominate after midgestation. By histologic analyses, Wolpowitz et al. (2000) found that homozygous CRD- NRG1- deficient mice had normal neuronal trajectory and outgrowth, but that the projections defasciculated, branched abnormally, and failed to sustain peripheral neuromuscular synaptic development. Newborn mutants had immature skeletal muscle. Schwann cells were generated in the mutants but failed to survive, consistent with the designation of NRG1 as a Schwann cell survival factor. Schwann cells in turn appeared to provide trophic support only after the nerve had entered its target field and had begun synapse formation.

[32008] It is appreciated that the abovementioned animal model for NRG1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[32009] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32010] Holmes, W. E.; Sliwkowski, M. X.; Akita, R. W.; Henzel, W.

J.; Lee, J.; Park, J. W.; Yansura, D.; Abadi, N.; Raab, H.; Lewis, G. D.; Shepard, H. M.; Kuang, W.- J.; Wood, W. I.; Goeddel, D. V.; Vandlen, R. L. : Identification of heregulin, a specific activator of p185(erbB2). Science 256: 1205-1210, 1992. ; and

[32011] Wolpowitz, D.; Mason, T. B. A.; Dietrich, P.; Mendelsohn, M.; Talmage, D. A.; Role, L. W. : Cysteine- rich domain isoforms of the neuregulin- 1 gene are required for maintenance of periph.

[32012] Further studies establishing the function and utilities of NRG1 are found in John Hopkins OMIM database record ID 142445, and in cited publications listed in Table 5, which are hereby incorporated by reference.Neurexin 3 (NRXN3, Accession NP_004787.2) is another GAM190 target gene, herein designated TARGET GENE. NRXN3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NRXN3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRXN3 BINDING SITE, designated SEQ ID:14089, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32013] Another function of GAM190 is therefore inhibition of Neurexin 3 (NRXN3, Accession NP_004787.2), a gene which may be involved in cell recognition, cell adhesion, and mediate intracellular signaling. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRXN3.

[32014] The function of NRXN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Neurexin 3 (NRXN3, Accession NP_620426.1) is another GAM190 target gene, herein designated TARGET GENE. NRXN3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NRXN3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRXN3 BINDING SITE, designated SEQ ID:14089, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32015] Another function of GAM190 is therefore inhibition of Neurexin 3 (NRXN3, Accession NP_620426.1), a gene which may be involved in cell recognition, cell adhesion,

and mediate intracellular signaling. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRXN3.

[32016] The function of NRXN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Oxidised low density lipoprotein (lectin-like) receptor 1 (OLR1, Accession NP_002534.1) is another GAM190 target gene, herein designated TARGET GENE. OLR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OLR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OLR1 BINDING SITE, designated SEQ ID:2011, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32017] Another function of GAM190 is therefore inhibition of Oxidised low density lipoprotein (lectin-like) receptor 1 (OLR1, Accession NP_002534.1), a gene which is involved in degradation of oxidized LDL by vascular endothelial cells. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with OLR1.

[32018] The function of OLR1 has been established by previous studies. Endothelial cell dysfunction or activation elicited by oxidatively modified low density lipoprotein (OMIM Ref. No. Ox- LDL) has been implicated in the pathogenesis of atherosclerosis. Vascular endothelial cells internalize and degrade Ox- LDL through a putative receptor- mediated pathway that does not involve macrophage scavenger receptors (see OMIM Ref. No. MSR1; 153622). To identify genes encoding Ox- LDL receptors, Sawamura et al. (1997) transfected mammalian cells with a cDNA expression library derived from bovine aortic endothelial cells and assayed for uptake of labeled Ox- LDL. They recovered a cDNA encoding an Ox- LDL receptor, which they designated lectin- like Ox- LDL receptor- 1 (LOX1). Immunofluorescence studies showed that bovine LOX1 is expressed on the cell surface. Sawamura et al. (1997) cloned a cDNA encoding the human homolog of LOX1 by screening a human lung cDNA library with the bovine LOX1 cDNA. Cells stably expressing human LOX1 showed uptake of labeled Ox- LDL. The predicted 273- amino acid human LOX1 protein is 72% identical to bovine LOX1. Its structure is similar to that of C- type lectins such as

CD94 (KLRD1) and NKR- P1 (KLRB1). Northern blot analysis revealed that human LOX1 is expressed as a 2.8- kb mRNA in various tissues, with the most abundant expression in placenta. Yamanaka et al. (1998) determined that LOX1 is expressed in vascular- rich organs but not in lymphocytes. Yamanaka et al. (1998) found that the LOX1 gene spans approximately 15 kb and consists of 6 exons. By fluorescence in situ hybridization, they mapped the gene to 12p12- p13, where genes of the natural killer cell receptors are clustered.

[32019]

[32020] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32021] Sawamura, T.; Kume, N.; Aoyama, T.; Moriwaki, H.; Hoshikawa, H.; Aiba, Y.; Tanaka, T.; Miwa, S.; Katsura, Y.; Kita, T.; Masaki, T. : An endothelial receptor for oxidized low- density lipoprotein. Nature 386: 73- 77, 1997. ; and

[32022] Yamanaka, S.; Zhang, X.- Y.; Miura, K.; Kim, S.; Iwao, H. : The human gene encoding the lectin- type oxidized LDL receptor (OLR1) is a novel member of the natural killer gene complex with.

[32023] Further studies establishing the function and utilities of

OLR1 are found in John Hopkins OMIM database record ID 602601, and in cited publications listed in Table 5, which are hereby incorporated by reference.Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663162.1) is another GAM190 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:18511, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32024] Another function of GAM190 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663162.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[32025] Oxysterol binding protein-like 3 (OSBPL3, Accession NP_056365.1) is another GAM190 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:18511, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32026] Another function of GAM190 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_056365.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[32027] Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663161.1) is another GAM190 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:18511, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32028] Another function of GAM190 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663161.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[32029] Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663164.1) is another GAM190 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:18511, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32030] Another function of GAM190 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663164.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[32031] Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663160.1) is another GAM190 target gene, herein

designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:18511, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32032] Another function of GAM190 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663160.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[32033] Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663163.1) is another GAM190 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:18511, to the nu-

cleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32034] Another function of GAM190 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663163.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[32035] Peptidyl arginine deiminase, type iii (PADI3, Accession NP_057317.1) is another GAM190 target gene, herein designated TARGET GENE. PADI3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PADI3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PADI3 BINDING SITE, designated SEQ ID:16411, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32036] Another function of GAM190 is therefore inhibition of Peptidyl arginine deiminase, type iii (PADI3, Accession NP_057317.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PADI3.

[32037] Putative homeodomain transcription factor 2 (PHTF2, Accession NP_065165.1) is another GAM190 target gene, herein designated TARGET GENE. PHTF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PHTF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PHTF2 BINDING SITE, designated SEQ ID:13802, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32038] Another function of GAM190 is therefore inhibition of Putative homeodomain transcription factor 2 (PHTF2, Accession NP_065165.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHTF2.

[32039] POLR3D (Accession NP_001713.1) is another GAM190 target gene, herein designated TARGET GENE. POLR3D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLR3D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLR3D

BINDING SITE, designated SEQ ID:17860, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32040] Another function of GAM190 is therefore inhibition of POLR3D (Accession NP_001713.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLR3D.

[32041] Peptidylprolyl isomerase a (cyclophilin a) (PPIA, Accession NP_066953.1) is another GAM190 target gene, herein designated TARGET GENE. PPIA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPIA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPIA BINDING SITE, designated SEQ ID:8957, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32042] Another function of GAM190 is therefore inhibition of Peptidylprolyl isomerase a (cyclophilin a) (PPIA, Accession NP_066953.1), a gene which is involved in protein folding and/or intracellular protein transport. Accordingly, utilities of GAM190 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with PPIA.

[32043] The function of PPIA has been established by previous studies. Cyclophilin is a specific high- affinity binding protein for the immunosuppressant agent cyclosporin A. Because of its dramatic effects on decreasing morbidity and increasing survival rates in human transplants, the molecular mechanism of immunosuppression by cyclosporin A has been a matter of much interest. Liu et al. (1990) cloned human cDNA for T- cell CYPH and constructed an expression vector under control of the tac promoter for efficient expression in E. coli. Cyclophilin A (also designated peptidyl- prolyl cis/trans isomerase A or PPIA) is a member of the immunophilin class of proteins that all possess peptidyl- prolyl cis/trans isomerase activity and, therefore, are believed to be involved in protein folding and/or intracellular protein transport. Luban et al. (1993) showed that cyclophilin A binds to the gag protein of human immunodeficiency virus type 1 (HIV- 1). This interaction can be inhibited by the immunosuppressant cyclosporin A and also by nonimmunosuppressive, cyclophilin A- binding cyclosporin A derivatives, which were also shown to exhibit potent anti- HIV- 1 activity. Thus,

cyclophilin A may have an essential function in HIV- 1 replication. Using a panel of somatic rodent/human cell hybrids and PCR technology, Willenbrink et al. (1995) mapped the cyclophilin gene (designated PPIA) on chromosome 7 and 4 pseudogenes (PPIP2, PPIP3, PPIP4, and PPIP6) to chromosomes 14, 10, 18, and 3, respectively. Using chromosome 7 and chromosome 10 deletion hybrid panels, they further localized the PPIA coding gene to 7p13- p11.2, as confirmed by fluorescence in situ hybridization (FISH) analysis, and a pseudogene (PPIP3) to the region 10q11.2- q23. Braaten et al. (1996) mapped the PPIA gene to 7p13 by FISH.

[32044]

[32045] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32046] Liu, J.; Albers, M. W.; Chen, C.- M.; Schreiber, S. L.; Walsh, C. T. : Cloning, expression, and purification of human cyclophilin in Escherichia coli and assessment of the catalytic role of cysteines by site- directed mutagenesis. Proc. Nat. Acad. Sci. 87: 2304- 2308, 1990. ; and

[32047] Willenbrink, W.; Halaschek, J.; Schuffenhauer, S.; Kunz, J.; Steinkasserer, A. : Cyclophilin A, the major intracellular

receptor for the immunosuppressant cyclosporin A, maps to chromosome.

[32048] Further studies establishing the function and utilities of PPIA are found in John Hopkins OMIM database record ID 123840, and in cited publications listed in Table 5, which are hereby incorporated by reference.Proteasome (prosome, macropain) 26s subunit, non-atpase, 5 (PSMD5, Accession NP_005038.1) is another GAM190 target gene, herein designated TARGET GENE. PSMD5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSMD5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSMD5 BINDING SITE, designated SEQ ID:8408, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32049] Another function of GAM190 is therefore inhibition of Proteasome (prosome, macropain) 26s subunit, non-atpase, 5 (PSMD5, Accession NP_005038.1), a gene which is the non- ATPase subunit 5 of the 26S proteasome (prosome macropain). Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with PSMD5.

[32050] The function of PSMD5 has been established by previous studies. The covalent attachment of ubiquitin to proteins produces substrates for the 26S ATP- dependent protease. This enzyme is composed of the multicatalytic protease, or proteasome, and a regulatory ATPase complex. Both the multicatalytic protease and the regulatory complex are multisubunit structures that associate in the presence of ATP to form the 26S enzyme. Deveraux et al. (1994) identified a 50- kD subunit of the regulatory complex, which they called subunit 5 (S5) based upon its relative mobility on SDS- polyacrylamide gels. Deveraux et al. (1995) demonstrated that 2 distinct subunits of the 26S protease migrate as 50- kD proteins, and thus, S5 represents 2 proteins, which the authors termed S5A (PSMD4; 601648) and S5B, also called PSMD5. Deveraux et al. (1995) sequenced peptides from the PSMD5 subunit of the human red blood cell 26S protease. Using the amino acid sequence, they isolated human cDNAs comprising a full-length PSMD5 cDNA. The deduced 505- amino acid PSMD5 protein is enriched in leucine residues, particularly in the N- terminal region. PSMD5 contains 9 dileucine repeats and a sequence, NPNY, similar to the tyrosine-

based motifs. Dileucine repeats and tyrosine- based motifs are thought to contribute to internalization and/or targeting. PSMD5 has a calculated molecular mass of 56 kD and focuses at pH 5.3 on 2- dimensional gels. Recombinant PSMD5 did not bind to ubiquitin polymers. By sequencing cDNAs randomly selected from a cDNA library derived from a human immature myeloid cell line, Nomura et al. (1994) isolated a partial cDNA encoding PSMD5, which they called KIAA0072. Northern blot analysis detected PSMD5 expression in a wide variety of human tissues, with the highest expression in lung and skeletal muscle. Deveraux et al. (1995) noted that the nucleotide sequence of the KIAA0072 cDNA is identical to the corresponding nucleotide sequence of the S5B cDNA.

[32051]

[32052] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32053] Deveraux, Q.; Jensen, C.; Rechsteiner, M. : Molecular cloning and expression of a 26 S protease subunit enriched in dileucine repeats. J. Biol. Chem. 270: 23726-23729, 1995. ; and

[32054] Deveraux, Q.; Ustrell, V.; Pickart, C.; Rechsteiner, M. : A 26

S protease subunit that binds ubiquitin conjugates. J. Biol. Chem. 269: 7059- 7061, 1994.

[32055] Further studies establishing the function and utilities of PSMD5 are found in John Hopkins OMIM database record ID 604452, and in cited publications listed in Table 5, which are hereby incorporated by reference.Prostaglandin-endoperoxide synthase 1 (prostaglandin g/h synthase and cyclooxygenase) (PTGS1, Accession NP_542158.1) is another GAM190 target gene, herein designated TARGET GENE. PTGS1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTGS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGS1 BINDING SITE, designated SEQ ID:9441, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32056] Another function of GAM190 is therefore inhibition of Prostaglandin-endoperoxide synthase 1 (prostaglandin g/h synthase and cyclooxygenase) (PTGS1, Accession NP_542158.1), a gene which may play an important role in regulating or promoting cell proliferation in some normal

and neoplastically transformed cells. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGS1.

[32057] The function of PTGS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Prostaglandin-endoperoxide synthase 1 (prostaglandin g/h synthase and cyclooxygenase) (PTGS1, Accession NP_000953.2) is another GAM190 target gene, herein designated TARGET GENE. PTGS1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTGS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGS1 BINDING SITE, designated SEQ ID:9441, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32058] Another function of GAM190 is therefore inhibition of Prostaglandin-endoperoxide synthase 1 (prostaglandin g/h synthase and cyclooxygenase) (PTGS1, Accession NP_000953.2), a gene which may play an important role in regulating or promoting cell proliferation in some normal

and neoplastically transformed cells. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGS1.

[32059] The function of PTGS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Arginine-glutamic acid dipeptide (re) repeats (RERE, Accession NP_036234.2) is another GAM190 target gene, herein designated TARGET GENE. RERE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RERE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RERE BINDING SITE, designated SEQ ID:16468, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32060] Another function of GAM190 is therefore inhibition of Arginine-glutamic acid dipeptide (re) repeats (RERE, Accession NP_036234.2), a gene which binds DRPLA and locates in the nucleus and therefore may be associated with Dentatorubral- pallidoluysian atrophy. Accordingly, utilities of GAM190 include diagnosis, prevention and treat-

ment of Dentatorubral- pallidoluysian atrophy, and of other diseases and clinical conditions associated with RERE.

[32061] The function of RERE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Regulating synaptic membrane exocytosis 2 (RIMS2, Accession NP_055492.1) is another GAM190 target gene, herein designated TARGET GENE. RIMS2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RIMS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RIMS2 BINDING SITE, designated SEQ ID:14112, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32062] Another function of GAM190 is therefore inhibition of Regulating synaptic membrane exocytosis 2 (RIMS2, Accession NP_055492.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIMS2.

[32063] SEMA6D (Accession NP_705872.1) is another GAM190 tar-

get gene, herein designated TARGET GENE. SEMA6D BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SEMA6D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEMA6D BINDING SITE, designated SEQ ID:13936, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32064] Another function of GAM190 is therefore inhibition of SEMA6D (Accession NP_705872.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA6D.

[32065] Solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, na+/h+, amiloride sensitive) (SLC9A1, Accession NP_003038.2) is another GAM190 target gene, herein designated TARGET GENE. SLC9A1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC9A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of SLC9A1 BINDING SITE, designated SEQ ID:7514, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32066] Another function of GAM190 is therefore inhibition of Solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, na+/h+, amiloride sensitive) (SLC9A1, Accession NP_003038.2), a gene which is involved in ph regulation to eliminate acids generated by active metabolism or to counter adverse environmental conditions. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC9A1.

[32067] The function of SLC9A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.SNX24 (Accession NP_054754.1) is another GAM190 target gene, herein designated TARGET GENE. SNX24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNX24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of SNX24 BINDING SITE, designated SEQ ID:12825, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32068] Another function of GAM190 is therefore inhibition of SNX24 (Accession NP_054754.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX24.

[32069] Suppressor of cytokine signaling 1 (SOCS1, Accession NP_003736.1) is another GAM190 target gene, herein designated TARGET GENE. SOCS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SOCS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SOCS1 BINDING SITE, designated SEQ ID:10166, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32070] Another function of GAM190 is therefore inhibition of Suppressor of cytokine signaling 1 (SOCS1, Accession NP_003736.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOCS1.

[32071] Spondin 1, (f-spondin) extracellular matrix protein (SPON1, Accession NP_006099.1) is another GAM190 target gene, herein designated TARGET GENE. SPON1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPON1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPON1 BINDING SITE, designated SEQ ID:13425, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32072] Another function of GAM190 is therefore inhibition of Spondin 1, (f-spondin) extracellular matrix protein (SPON1, Accession NP_006099.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPON1.

[32073] Sprouty homolog 3 (drosophila) (SPRY3, Accession NP_005831.1) is another GAM190 target gene, herein designated TARGET GENE. SPRY3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPRY3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of SPRY3 BINDING SITE, designated SEQ ID:14598, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32074] Another function of GAM190 is therefore inhibition of Sprouty homolog 3 (drosophila) (SPRY3, Accession NP_005831.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPRY3.

[32075] SSH-3 (Accession NP_060746.2) is another GAM190 target gene, herein designated TARGET GENE. SSH-3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SSH-3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SSH-3 BINDING SITE, designated SEQ ID:17604, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32076] Another function of GAM190 is therefore inhibition of SSH-3 (Accession NP_060746.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSH-3.

[32077] SSH-3 (Accession NP_060327.2) is another GAM190 target gene, herein designated TARGET GENE. SSH-3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SSH-3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SSH-3 BINDING SITE, designated SEQ ID:17604, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32078] Another function of GAM190 is therefore inhibition of SSH-3 (Accession NP_060327.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSH-3.

[32079] Suppressor of fused homolog (drosophila) (SUFU, Accession NP_057253.2) is another GAM190 target gene, herein designated TARGET GENE. SUFU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SUFU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SUFU BINDING SITE, designated SEQ ID:12371, to the nucleotide sequence of GAM190

RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32080] Another function of GAM190 is therefore inhibition of Suppressor of fused homolog (drosophila) (SUFU, Accession NP_057253.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUFU.

[32081] Srb7 suppressor of rna polymerase b homolog (yeast) (SURB7, Accession NP_004255.2) is another GAM190 target gene, herein designated TARGET GENE. SURB7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SURB7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SURB7 BINDING SITE, designated SEQ ID:3571, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32082] Another function of GAM190 is therefore inhibition of Srb7 suppressor of rna polymerase b homolog (yeast) (SURB7, Accession NP_004255.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURB7.

[32083] SUV39H2 (Accession NP_078946.1) is another GAM190 target gene, herein designated TARGET GENE. SUV39H2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SUV39H2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SUV39H2 BINDING SITE, designated SEQ ID:3837, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32084] Another function of GAM190 is therefore inhibition of SUV39H2 (Accession NP_078946.1), a gene which is involved in gene repression and the modification of position- effect- variegation. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUV39H2.

[32085] The function of SUV39H2 has been established by previous studies. O'Carroll et al. (2000) isolated and characterized a murine gene, Suv39h2, that encodes an H3 histone (see OMIM Ref. No. 601128) methyltransferase (OMIM Ref. No. HMTase) with 59% identity to Suv39h1 (OMIM Ref. No. 300254). Although both Suv39h loci displayed overlapping expression profiles during mouse embryogenesis,

Suv39h2 transcripts remained specifically expressed in adult testes. Immunolocalization of the Suv39h2 protein during spermatogenesis indicated enriched distribution at the heterochromatin from the leptotene to the round spermatid stage. Moreover, Suv39h2 specifically accumulated with chromatin of the sex chromosomes (XY body), which undergo transcriptional silencing during the first meiotic prophase. These data were consistent with redundant enzymatic roles for Suv39h1 and Suv39h2 during mouse development and suggested an additional function of the Suv39h2 HMTase in organizing meiotic heterochromatin that may even impart an epigenetic imprint to the male germline.

[32086] Animal model experiments lend further support to the function of SUV39H2. Peters et al. (2001) generated mice deficient for either Suv39h1 or Suv39h2. These animals displayed normal viability and fertility and did not exhibit apparent phenotypes. The authors subsequently intercrossed Suv39h1 - /- and Suv39h2 - /- mice to generate compound Suv39h mutants that were then used to derive Suv39h double- null mice (Suv39h1 - /- and Suv39h2 - /-). These mice displayed severely impaired viability and chromosomal instabilities that were associated with an in-

creased tumor risk and perturbed chromosome interactions during male meiosis. These data suggested a crucial role for pericentric H3 histone- lys9 methylation in protecting genome stability and defined the Suv39h HMTases as important epigenetic regulators for mammalian development.

[32087] It is appreciated that the abovementioned animal model for SUV39H2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[32088] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32089] O'Carroll, D.; Scherthan, H.; Peters, A. H. F. M.; Opravil, S.; Haynes, A. R.; Laible, G.; Rea, S.; Schmid, M.; Lebersorger, A.; Jerratsch, M.; Sattler, L.; Mattei, M. G.; Denny, P.; Brown, S. D. M.; Schweizer, D.; Jenuwein, T. : Isolation and characterization of Suv39h2, a second histone H3 methyltransferase gene that displays testis- specific expression. Molec. Cell. Biol. 20: 9423- 9433, 2000. ; and

[32090] Peters, A. H. F. M.; O'Carroll, D.; Scherthan, H.; Mechtler, K.; Sauer, S.; Schofer, C.; Weipoltshammer, K.; Pagani, M.; Lachner, M.; Kohlmaier, A.; Opravil, S.; Doyle, M.; Sibilia,

M.

[32091] Further studies establishing the function and utilities of SUV39H2 are found in John Hopkins OMIM database record ID 606503, and in cited publications listed in Table 5, which are hereby incorporated by reference.TPH2 (Accession NP_775489.1) is another GAM190 target gene, herein designated TARGET GENE. TPH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TPH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPH2 BINDING SITE, designated SEQ ID:11938, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32092] Another function of GAM190 is therefore inhibition of TPH2 (Accession NP_775489.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TPH2.

[32093] Trophinin (TRO, Accession NP_808223.1) is another GAM190 target gene, herein designated TARGET GENE. TRO BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA en-

coded by TRO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRO BINDING SITE, designated SEQ ID:7155, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32094] Another function of GAM190 is therefore inhibition of Trophinin (TRO, Accession NP_808223.1), a gene which functions as an adhesion molecule. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRO.

[32095] The function of TRO has been established by previous studies. The initial attachment of the trophoblast to the endometrial epithelium during implantation occurs via the apical cell membranes of the embryonic and maternal cells. Fukuda et al. (1995) found that cells from HT- H, a trophoblastic teratocarcinoma cell line, adhered efficiently to cells from SNG- M, an endometrial adenocarcinoma cell line. The adhesion was homophilic and cell type- specific, and occurred at the respective upper cell surfaces. To identify the adhesion molecules, the authors screened an HT- H expression library in COS- 1 cells. They found that expression of 2 distinct cDNAs, encoding trophinin

(cloned from trophoblastic cells) and tastin (OMIM Ref. No. 603872), was necessary for adhesion. The deduced 749-amino acid trophinin protein contains 69 tandem repeats of decapeptide sequences. In vitro translated trophinin has a molecular mass of 61 kD. Sequence and structural analyses revealed that trophinin is an intrinsic plasma membrane protein with 8 predicted transmembrane domains, an intracellular N- terminal region, and 3 hydrophilic regions exposed on the cell surface. COS- 1 cells expressing trophinin and tastin aggregated in suspension, and soluble peptides of the cell surface domain of trophinin bound to the cell surface of trophinin- expressing cells. Northern blot analysis detected trophinin expression as 3.5-, 7.5-, and 10- kb mRNAs in both HT- H and SNG- M cells. However, neither trophinin nor tastin was expressed in various other human cell types tested, with the exception of macrophages. Using immunofluorescence, Fukuda et al. (1995) detected strong expression of both genes in the trophectoderm surface of monkey blastocysts, as well as in human endometrial surface epithelium at a time consistent with that expected for the 'implantation window.' These authors suggested that trophinin and tastin might mediate the adhesion of the

blastocyst to the endometrial epithelium at the time of implantation. Using immunohistochemistry, Suzuki et al. (1999) determined that trophinin and bystin (OMIM Ref. No. 603871), a trophinin- and tastin- binding protein, were found in the placenta from the sixth week of pregnancy. Trophinin and bystin were localized in the cytoplasm of the syncytiotrophoblast in the chorionic villi and in endometrial decidual cells at the uteroplacental interface. After week 10, the levels of trophinin, tastin, and bystin decreased and then disappeared from placental villi.

[32096]

[32097] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32098] Fukuda, M. N.; Sato, T.; Nakayama, J.; Klier, G.; Mikami, M.; Aoki, D.; Nozawa, S. : Trophinin and tastin, a novel cell adhesion molecule complex with potential involvement in embryo implantation. Genes Dev. 9: 1199- 1210, 1995. ; and

[32099] Suzuki, N.; Nakayama, J.; Shih, I. M.; Aoki, D.; Nozawa, S.; Fukuda, M. N. : Expression of trophinin, tastin, and bystin by trophoblast and endometrial cells in human placenta.

Biol. Reprod.

[32100] Further studies establishing the function and utilities of TRO are found in John Hopkins OMIM database record ID 300132, and in cited publications listed in Table 5, which are hereby incorporated by reference.Trophinin (TRO, Accession NP_808226.1) is another GAM190 target gene, herein designated TARGET GENE. TRO BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRO BINDING SITE, designated SEQ ID:7155, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32101] Another function of GAM190 is therefore inhibition of Trophinin (TRO, Accession NP_808226.1), a gene which functions as an adhesion molecule. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRO.

[32102] The function of TRO has been established by previous studies. The initial attachment of the trophoblast to the endometrial epithelium during implantation occurs via the

apical cell membranes of the embryonic and maternal cells. Fukuda et al. (1995) found that cells from HT- H, a trophoblastic teratocarcinoma cell line, adhered efficiently to cells from SNG- M, an endometrial adenocarcinoma cell line. The adhesion was homophilic and cell type- specific, and occurred at the respective upper cell surfaces. To identify the adhesion molecules, the authors screened an HT- H expression library in COS- 1 cells. They found that expression of 2 distinct cDNAs, encoding trophinin (cloned from trophoblastic cells) and tastin (OMIM Ref. No. 603872), was necessary for adhesion. The deduced 749-amino acid trophinin protein contains 69 tandem repeats of decapeptide sequences. In vitro translated trophinin has a molecular mass of 61 kD. Sequence and structural analyses revealed that trophinin is an intrinsic plasma membrane protein with 8 predicted transmembrane domains, an intracellular N- terminal region, and 3 hydrophilic regions exposed on the cell surface. COS- 1 cells expressing trophinin and tastin aggregated in suspension, and soluble peptides of the cell surface domain of trophinin bound to the cell surface of trophinin- expressing cells. Northern blot analysis detected trophinin expression as 3.5-, 7.5-, and 10- kb mRNAs in both HT- H

and SNG- M cells. However, neither trophinin nor tastin was expressed in various other human cell types tested, with the exception of macrophages. Using immunofluorescence, Fukuda et al. (1995) detected strong expression of both genes in the trophectoderm surface of monkey blastocysts, as well as in human endometrial surface epithelium at a time consistent with that expected for the 'implantation window.' These authors suggested that trophinin and tastin might mediate the adhesion of the blastocyst to the endometrial epithelium at the time of implantation. Using immunohistochemistry, Suzuki et al. (1999) determined that trophinin and bystin (OMIM Ref. No. 603871), a trophinin- and tastin- binding protein, were found in the placenta from the sixth week of pregnancy. Trophinin and bystin were localized in the cytoplasm of the syncytiotrophoblast in the chorionic villi and in endometrial decidual cells at the uteroplacental interface. After week 10, the levels of trophinin, tastin, and bystin decreased and then disappeared from placental villi.

[32103]

[32104] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[32105] Fukuda, M. N.; Sato, T.; Nakayama, J.; Klier, G.; Mikami, M.; Aoki, D.; Nozawa, S. : Trophinin and tastin, a novel cell adhesion molecule complex with potential involvement in embryo implantation. Genes Dev. 9: 1199- 1210, 1995. ; and

[32106] Suzuki, N.; Nakayama, J.; Shih, I. M.; Aoki, D.; Nozawa, S.; Fukuda, M. N. : Expression of trophinin, tastin, and bystin by trophoblast and endometrial cells in human placenta. Biol. Reprod.

[32107] Further studies establishing the function and utilities of TRO are found in John Hopkins OMIM database record ID 300132, and in cited publications listed in Table 5, which are hereby incorporated by reference.Transient receptor potential cation channel, subfamily v, member 3 (TRPV3, Accession NP_659505.1) is another GAM190 target gene, herein designated TARGET GENE. TRPV3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPV3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV3 BINDING SITE, designated SEQ ID:668, to the nucleotide sequence of

GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32108] Another function of GAM190 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 3 (TRPV3, Accession NP_659505.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV3.

[32109] Ubiquilin 2 (UBQLN2, Accession NP_038472.2) is another GAM190 target gene, herein designated TARGET GENE. UBQLN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBQLN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBQLN2 BINDING SITE, designated SEQ ID:17562, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32110] Another function of GAM190 is therefore inhibition of Ubiquilin 2 (UBQLN2, Accession NP_038472.2), a gene which is involved in spindle pole body duplication with rad23. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with UBQLN2.

[32111] The function of UBQLN2 has been established by previous studies. By performing independent yeast 2- hybrid screens, Kleijnen et al. (2000) isolated cDNAs encoding PLIC1 (UBQLN1; 605046) and PLIC2, homologs of the mouse Plics (proteins linking integrin- associated protein (IAP; 601028) and cytoskeleton) and the yeast Dsk2 protein. The predicted 624- amino acid PLIC2 protein, also called UBQLN2, shares 72% amino acid identity with PLIC1. Two motifs are conserved in the mammalian PLICs and yeast Dsk2, an N- terminal ubiquitin (OMIM Ref. No. 191320)- like (UBL) domain and a C- terminal ubiquitin-associated (UBA) domain. Unlike ubiquitin, the UBL domain of the PLICs does not have a diglycine motif in its C terminus; the diglycine motif serves as a target site for cellular hydrolases that release ubiquitin from precursor fusion proteins. The absence of a GG sequence suggests that the UBL domain in the PLICs is an integral part of the open reading frame. The UBA domain is a loosely defined sequence motif present in multiple enzyme classes of the ubiquitination machinery. The most notable difference between the mammalian PLICs is the presence of a collagen- like motif in PLIC2 that is absent in PLIC1 and yeast

Dsk2. This domain is most homologous to the collagen- like oncoprotein of herpesvirus Saimiri, STP- C488, which is implicated in intracellular signaling via the RAS- RAF pathway (see OMIM Ref. No. 190020). The collagen- like domain of PLIC2 contains 8 PXGP motifs that are susceptible to cleavage by collagenase in vitro. Kleijnen et al (2000) showed that the human PLICs physically associate with both proteasomes and ubiquitin ligases in large complexes. Overexpression of PLICs interfered with the in vivo degradation of 2 unrelated ubiquitin- dependent proteasome substrates, p53 (OMIM Ref. No. 191170) and I- kappa- B- alpha (NFKBIA; 164008), but not a ubiquitin- independent substrate. These findings raised the possibility that the PLICs, and possibly related ubiquitin- like family members, may functionally link the ubiquitination machinery to the proteasome to affect in vivo protein degradation. By screening a human lung 2- hybrid cDNA library using a pGBT9- STCH (OMIM Ref. No. 601100) plasmid as bait, Kaye et al. (2000) isolated a cDNA encoding UBQLN2, which they termed CHAP1/DSK2. Mutation analysis determined that the C- terminal Sti1- like repeat sequence, but neither the N- terminal UBL domain nor the C- terminal UBA domain, is required for binding of

UBQLN2 to the ATPase domain of STCH.

[32112]

[32113] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32114] Kaye, F. J.; Shows, T. B. : Assignment of ubiquilin 2 (UBQLN2) to human chromosome xp11.23- p11.1 by GeneBridge radiation hybrids. Cytogenet. Cell Genet. 89: 116- 117, 2000. ; and

[32115] Kleijnen, M. F.; Shih, A. H.; Zhou, P.; Kumar, S.; Soccio, R. E.; Kedersha, N. L.; Gill, G.; Howley, P. M. : The hPLIC proteins may provide a link between the ubiquitination machinery.

[32116] Further studies establishing the function and utilities of UBQLN2 are found in John Hopkins OMIM database record ID 300264, and in cited publications listed in Table 5, which are hereby incorporated by reference.Unc-5 homolog b (c. elegans) (UNC5C, Accession NP_003719.2) is another GAM190 target gene, herein designated TARGET GENE. UNC5C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UNC5C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UNC5C BINDING SITE, designated SEQ ID:19876, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32117] Another function of GAM190 is therefore inhibition of Unc-5 homolog b (c. elegans) (UNC5C, Accession NP_003719.2), a gene which is a putative receptor for netrin, which is involved in axon guidance. Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC5C.

[32118] The function of UNC5C has been established by previous studies. Migration of neurons from proliferative zones to their functional sites is fundamental to the normal development of the central nervous system. Mice homozygous for the rostral cerebellar malformation (rcm) mutation exhibit cerebellar and midbrain defects, apparently as a result of abnormal neuronal migration. Ackerman et al. (1997) reported that in rcm- mutant mice, the cerebellum is smaller and has fewer folia than in wildtype, ectopic cerebellar cells are present in midbrain regions by 3 days after birth, and there are abnormalities in postnatal cere-

bellar- neuronal migration. The authors isolated cDNAs encoding the rcm protein (Rcm). Sequence analysis revealed that the predicted 931- amino acid mouse protein is a transmembrane protein that contains 2 immunoglobulin (Ig)- like domains and 2 type I thrombospondin (THBS1; 188060) motifs in the extracellular region. Ig and THBS1 domains are also found in the extracellular region of the C. elegans UNC5 transmembrane protein, and the C- terminal 865- amino acid region of Rcm is 30% identical to UNC5. Ackerman et al. (1997) stated that the UNC5 protein is essential for dorsal guidance of pioneer axons and for the movement of cells away from the netrin ligand. In the developing brain of vertebrates, netrin- 1 (OMIM Ref. No. 601614) plays a role in both cell migration and axonal guidance. Leonardo et al. (1997) demonstrated that Rcm binds netrin- 1 in vitro. Ackerman et al. (1997) concluded that Rcm and its ligand are important in critical migratory and/or cell- proliferation events during cerebellar development. Przyborski et al. (1998) found that disruption of the mouse rcm gene, also called the Unc5h3 gene, resulted in a failure of tangentially migrating granule cells to recognize the rostral boundary of the cerebellum. By searching an EST database for sequences related

to the Unc5h3 gene, Ackerman and Knowles (1998) identified a partial human fetal brain cDNA encoding UNC5C, the human Unc5h3 homolog. Using 5- prime RACE, they cloned a cDNA corresponding to the entire UNC5C coding region. The predicted 931- amino acid human protein has the overall domain structure of UNC5 family proteins, and is 97% identical to Unc5h3. Northern blot analysis revealed that the 9.5- kb UNC5 mRNA is expressed in brain and heart, and at low levels in kidney.

[32119]

[32120] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32121] Przyborski, S. A.; Knowles, B. B.; Ackerman, S. L. : Embryonic phenotype of Unc5h3 mutant mice suggests chemorepulsion during the formation of the rostral cerebellar boundary. Development 125: 41- 50, 1998. ; and

[32122] Ackerman, S. L.; Knowles, B. B. : Cloning and mapping of the UNC5C gene to human chromosome 4q21- q23. Genomics 52: 205- 208, 1998.

[32123] Further studies establishing the function and utilities of UNC5C are found in John Hopkins OMIM database record ID 603610, and in cited publications listed in Table 5,

which are hereby incorporated by reference.Reserved (WDR17, Accession NP_733828.2) is another GAM190 target gene, herein designated TARGET GENE. WDR17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WDR17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WDR17 BINDING SITE, designated SEQ ID:1039, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32124] Another function of GAM190 is therefore inhibition of Reserved (WDR17, Accession NP_733828.2) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDR17.

[32125] ZBTB2 (Accession NP_065912.1) is another GAM190 target gene, herein designated TARGET GENE. ZBTB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZBTB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZBTB2 BIND-

ING SITE, designated SEQ ID:12940, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32126] Another function of GAM190 is therefore inhibition of ZBTB2 (Accession NP_065912.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZBTB2.

[32127] Zinc finger protein 179 (ZNF179, Accession NP_009079.1) is another GAM190 target gene, herein designated TARGET GENE. ZNF179 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF179, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF179 BINDING SITE, designated SEQ ID:13355, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32128] Another function of GAM190 is therefore inhibition of Zinc finger protein 179 (ZNF179, Accession NP_009079.1), a gene which has zink finger and a member of the RING finger protein family of transcription factors. and therefore may be associated with Smith- magenis syndrome. Ac-

cordingly, utilities of GAM190 include diagnosis, prevention and treatment of Smith- magenis syndrome, and of other diseases and clinical conditions associated with ZNF179.

[32129] The function of ZNF179 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Zinc finger protein 213 (ZNF213, Accession XP_036493.1) is another GAM190 target gene, herein designated TARGET GENE. ZNF213 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF213, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF213 BINDING SITE, designated SEQ ID:6621, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32130] Another function of GAM190 is therefore inhibition of Zinc finger protein 213 (ZNF213, Accession XP_036493.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF213.

[32131] Zinc finger protein 264 (ZNF264, Accession NP_003408.1) is another GAM190 target gene, herein designated TARGET GENE. ZNF264 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF264, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF264 BINDING SITE, designated SEQ ID:15761, to the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, also designated SEQ ID:289.

[32132] Another function of GAM190 is therefore inhibition of Zinc finger protein 264 (ZNF264, Accession NP_003408.1) . Accordingly, utilities of GAM190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF264.

[32133]

[32134] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 191 (GAM191), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32135] GAM191 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM191 was detected is described hereinabove with reference to Figs. 8-15.

[32136] GAM191 gene, herein designated GAM GENE, and GAM191 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[32137] GAM191 gene encodes a GAM191 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM191 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM191 precursor RNA is designated SEQ ID:165, and is provided hereinbelow with reference to the sequence listing part.

[32138] GAM191 precursor RNA folds onto itself, forming GAM191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide

sequence of the second half thereof.

[32139] GAM191 precursor RNA folds onto itself, forming GAM191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[32140] Nucleotide sequence of GAM191 precursor RNA, designated SEQ-ID: 165, and a schematic representation of a predicted secondary folding of GAM191 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[32141] An enzyme complex designated DICER COMPLEX, `dices` the GAM191 folded precursor RNA into GAM191 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy

Group: C) nucleotide sequence of GAM191 RNA is designated SEQ ID:389, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[32142] GAM191 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM191 target RNA, herein designated GAM TARGET RNA. GAM191 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[32143] GAM191 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM191 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM191 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limit-

ing GAM191 RNA may have a different number of target binding sites in untranslated regions of a GAM191 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[32144] The complementary binding of GAM191 RNA, herein designated GAM RNA, to target binding sites on GAM191 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM191 target RNA into GAM191 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32145] It is appreciated that GAM191 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM191 target genes. The mRNA of each one of this plurality of GAM191 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM191 RNA, herein designated GAM RNA, and which when bound by GAM191 RNA causes inhibition of translation of respective one or more GAM191 target proteins.

[32146] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM191 gene, herein designated GAM GENE, on one or more GAM191 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32147] It is appreciated that specific functions and accordingly utilities of GAM191 correlate with, and may be deduced from, the identity of the target genes which GAM191 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32148]

[32149]

[32150] PRO1048 (Accession NM_018497.1) is a GAM191 target gene, herein designated TARGET GENE. PRO1048 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO1048, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO1048 BINDING SITE, designated SEQ ID:7282, to the nucleotide sequence of GAM191 RNA, herein designated GAM RNA, also designated SEQ ID:389.

[32151] A function of GAM191 is therefore inhibition of PRO1048 (Accession NM_018497.1) . Accordingly, utilities of GAM191 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1048.

[32152]

[32153] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 192 (GAM192), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32154] GAM192 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM192 was detected is described hereinabove with reference to Figs. 8-15.

[32155] GAM192 gene, herein designated GAM GENE, and GAM192 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[32156] GAM192 gene encodes a GAM192 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM192 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM192 precursor RNA is designated SEQ ID:70, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:70 is located at position 208634246 relative to chromosome 2.

[32157] GAM192 precursor RNA folds onto itself, forming GAM192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32158] GAM192 precursor RNA folds onto itself, forming GAM192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[32159] Nucleotide sequence of GAM192 precursor RNA, designated SEQ-ID: 70, and a schematic representation of a predicted secondary folding of GAM192 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[32160] An enzyme complex designated DICER COMPLEX, `dices` the GAM192 folded precursor RNA into GAM192 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM192 RNA is desig-

nated SEQ ID:393, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[32161] GAM192 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM192 target RNA, herein designated GAM TARGET RNA. GAM192 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[32162] GAM192 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM192 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM192 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM192 RNA may have a different number of target

binding sites in untranslated regions of a GAM192 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[32163] The complementary binding of GAM192 RNA, herein designated GAM RNA, to target binding sites on GAM192 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM192 target RNA into GAM192 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32164] It is appreciated that GAM192 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM192 target genes. The mRNA of each one of this plurality of GAM192 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM192 RNA, herein designated GAM RNA, and which when bound by GAM192 RNA causes inhibition of translation of respective one or more GAM192 target proteins.

[32165] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM192 gene, herein designated GAM GENE, on one or more GAM192 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32166] It is appreciated that specific functions and accordingly utilities of GAM192 correlate with, and may be deduced from, the identity of the target genes which GAM192 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32167]

[32168]

[32169] A kinase (prka) anchor protein 2 (AKAP2, Accession) is a GAM192 target gene, herein designated TARGET GENE. AKAP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AKAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKAP2 BINDING SITE, designated SEQ ID:7475, to the nucleotide sequence of GAM192 RNA, herein designated GAM RNA, also designated SEQ ID:393.

[32170] A function of GAM192 is therefore inhibition of A kinase (prka) anchor protein 2 (AKAP2, Accession), a gene which binds to regulatory subunit (rii) of protein kinase a. Accordingly, utilities of GAM192 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP2.

[32171] The function of AKAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.KIAA1336 (Accession NM_020779.1) is another GAM192 target gene, herein designated TARGET GENE. KIAA1336 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

KIAA1336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1336 BINDING SITE, designated SEQ ID:4284, to the nucleotide sequence of GAM192 RNA, herein designated GAM RNA, also designated SEQ ID:393.

[32172] Another function of GAM192 is therefore inhibition of KIAA1336 (Accession NM_020779.1) . Accordingly, utilities of GAM192 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1336.

[32173]

[32174] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 193 (GAM193), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32175] GAM193 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM193 was detected is described hereinabove with reference to Figs. 8-15.

[32176] GAM193 gene, herein designated GAM GENE, and

GAM193 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[32177] GAM193 gene encodes a GAM193 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM193 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM193 precursor RNA is designated SEQ ID:139, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:139 is located at position 362 relative to chromosome 7.

[32178] GAM193 precursor RNA folds onto itself, forming GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32179] GAM193 precursor RNA folds onto itself, forming GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[32180] Nucleotide sequence of GAM193 precursor RNA, designated SEQ-ID: 139, and a schematic representation of a predicted secondary folding of GAM193 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[32181] An enzyme complex designated DICER COMPLEX, `dices` the GAM193 folded precursor RNA into GAM193 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM193 RNA is designated SEQ ID:268, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[32182] GAM193 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM193 target RNA, herein designated GAM TARGET RNA. GAM193 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[32183] GAM193 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM193 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM193 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM193 RNA may have a different number of target binding sites in untranslated regions of a GAM193 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an

example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[32184] The complementary binding of GAM193 RNA, herein designated GAM RNA, to target binding sites on GAM193 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM193 target RNA into GAM193 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32185] It is appreciated that GAM193 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM193 target genes. The mRNA of each one of this plurality of GAM193 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM193 RNA, herein designated GAM RNA, and which when bound by GAM193 RNA causes inhibition of translation of respective one or more GAM193 target proteins.

[32186] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM193 gene, herein designated GAM GENE, on one or

more GAM193 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32187] It is appreciated that specific functions and accordingly utilities of GAM193 correlate with, and may be deduced from, the identity of the target genes which GAM193 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32188]

[32189]

[32190] AHRR (Accession NP_065782.1) is a GAM193 target gene, herein designated TARGET GENE. AHRR BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by AHRR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AHRR BINDING SITE, designated SEQ ID:2984, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32191] A function of GAM193 is therefore inhibition of AHRR (Accession NP_065782.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AHRR.

[32192] Aldo-keto reductase family 7, member a3 (aflatoxin aldehyde reductase) (AKR7A3, Accession NP_036199.1) is another GAM193 target gene, herein designated TARGET GENE. AKR7A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AKR7A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKR7A3 BINDING SITE, designated SEQ ID:11149, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32193] Another function of GAM193 is therefore inhibition of Aldo-keto reductase family 7, member a3 (aflatoxin aldehyde reductase) (AKR7A3, Accession NP_036199.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKR7A3.

[32194] Angiomotin like 1 (AMOTL1, Accession NP_570899.1) is another GAM193 target gene, herein designated TARGET GENE. AMOTL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AMOTL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMOTL1 BINDING SITE, designated SEQ ID:14975, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32195] Another function of GAM193 is therefore inhibition of Angiomotin like 1 (AMOTL1, Accession NP_570899.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMOTL1.

[32196] Bcl2-like 13 (apoptosis facilitator) (BCL2L13, Accession

NP_056182.1) is another GAM193 target gene, herein designated TARGET GENE. BCL2L13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCL2L13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCL2L13 BINDING SITE, designated SEQ ID:14529, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32197] Another function of GAM193 is therefore inhibition of Bcl2-like 13 (apoptosis facilitator) (BCL2L13, Accession NP_056182.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL2L13.

[32198] Chromosome 2 open reading frame 7 (C2orf7, Accession NP_115695.1) is another GAM193 target gene, herein designated TARGET GENE. C2orf7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C2orf7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C2orf7 BINDING SITE, designated

SEQ ID:11975, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32199] Another function of GAM193 is therefore inhibition of Chromosome 2 open reading frame 7 (C2orf7, Accession NP_115695.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C2orf7.

[32200] C4ST (Accession NP_060883.1) is another GAM193 target gene, herein designated TARGET GENE. C4ST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C4ST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C4ST BINDING SITE, designated SEQ ID:18004, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32201] Another function of GAM193 is therefore inhibition of C4ST (Accession NP_060883.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C4ST.

[32202] Calcium channel, voltage-dependent, beta 2 subunit

(CACNB2, Accession NP_000715.1) is another GAM193 target gene, herein designated TARGET GENE. CACNB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CACNB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CACNB2 BINDING SITE, designated SEQ ID:11254, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32203] Another function of GAM193 is therefore inhibition of Calcium channel, voltage-dependent, beta 2 subunit (CACNB2, Accession NP_000715.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNB2.

[32204] Calpain 2, (m/ii) large subunit (CAPN2, Accession NP_001739.1) is another GAM193 target gene, herein designated TARGET GENE. CAPN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAPN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of CAPN2 BINDING SITE, designated SEQ ID:4529, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32205] Another function of GAM193 is therefore inhibition of Calpain 2, (m/ii) large subunit (CAPN2, Accession NP_001739.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPN2.

[32206] Carboxypeptidase d (CPD, Accession NP_001295.2) is another GAM193 target gene, herein designated TARGET GENE. CPD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPD BINDING SITE, designated SEQ ID:7505, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32207] Another function of GAM193 is therefore inhibition of Carboxypeptidase d (CPD, Accession NP_001295.2), a gene which is a membrane- bound metalloprotease. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with CPD.

[32208] The function of CPD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.DKFZp434M0331 (Accession NP_060070.1) is another GAM193 target gene, herein designated TARGET GENE. DKFZp434M0331 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp434M0331, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434M0331 BINDING SITE, designated SEQ ID:16786, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32209] Another function of GAM193 is therefore inhibition of DKFZp434M0331 (Accession NP_060070.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434M0331.

[32210] Down syndrome critical region gene 1-like 1 (DSCR1L1, Accession NP_005813.1) is another GAM193 target gene, herein designated TARGET GENE. DSCR1L1 BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR1L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSCR1L1 BINDING SITE, designated SEQ ID:3399, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32211] Another function of GAM193 is therefore inhibition of Down syndrome critical region gene 1-like 1 (DSCR1L1, Accession NP_005813.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSCR1L1.

[32212] Ets variant gene 5 (ets-related molecule) (ETV5, Accession NP_004445.1) is another GAM193 target gene, herein designated TARGET GENE. ETV5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ETV5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ETV5 BINDING SITE, designated SEQ ID:10755, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ

ID:268.

[32213] Another function of GAM193 is therefore inhibition of Ets variant gene 5 (ets-related molecule) (ETV5, Accession NP_004445.1), a gene which DNA binding protein of the Ets oncoprotein family. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ETV5.

[32214] The function of ETV5 has been established by previous studies. See ETV1 (OMIM Ref. No. 600541), ETV4 (OMIM Ref. No. 600711), and ETV6 (OMIM Ref. No. 600618). Monte et al. (1994) isolated a human testis cDNA for ERM, a member of the Ets- related transcription factors. The 2.2- kb clone encoded a 510- amino acid putative protein which shares about 95% identity with the mouse genes Pea3 and Er81 in the 85- residue DNA- binding ETS do- main. ERM is about 85% identical with these proteins within the N- terminal acidic domain. Further, the protein was shown to bind to an oligonucleotide containing the consensus nucleotide core sequence GGAA recognized by the other Ets proteins. Monte et al. (1994) showed that ERM is widely expressed in human cell lines and tissues (except for normal lymphocytes) and is especially high in brain and placenta. In mouse tissues, Pea3 and Er81 mR-

NAs displayed restricted patterns of expression, whereas ERM was widely expressed in human tissues. Monte et al. (1996) showed that the human ERM gene contains 14 exons distributed over 65 kb of genomic DNA. The authors mapped the gene to 3q27- q29 by in situ hybridization. Protopopova et al. (1996) mapped the ERM gene, a transcription factor related to the ETS1 (OMIM Ref. No. 164720), to 3q28 by fluorescence in situ hybridization.

[32215]

[32216] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32217] Monte, D.; Baert, J. L.; Defossez, P. A.; de Launoit, Y.; Stehelin, D. : Molecular cloning and characterization of human ERM, a new member of the Ets family closely related to mouse PEA3 and ER81 transcription factors. Oncogene 9: 1397- 1406, 1994. ; and

[32218] Monte, D.; Coutte, L.; Dewitte, F.; Defossez, P.- A.; Le Coniat, M.; Stehelin, D.; Berger, R.; de Launoit, Y. : Genomic organization of the human ERM (ETV5) gene, a PEA3 group member of E.

[32219] Further studies establishing the function and utilities of ETV5 are found in John Hopkins OMIM database record ID

601600, and in cited publications listed in Table 5, which are hereby incorporated by reference.Formin homology 2 domain containing 2 (FHOD2, Accession XP_057927.2) is another GAM193 target gene, herein designated TARGET GENE. FHOD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHOD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FHOD2 BINDING SITE, designated SEQ ID:8919, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32220] Another function of GAM193 is therefore inhibition of Formin homology 2 domain containing 2 (FHOD2, Accession XP_057927.2) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHOD2.

[32221] FLJ10824 (Accession XP_051956.8) is another GAM193 target gene, herein designated TARGET GENE. FLJ10824 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10824, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ10824 BINDING SITE, designated SEQ ID:13628, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32222] Another function of GAM193 is therefore inhibition of FLJ10824 (Accession XP_051956.8) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10824.

[32223] FLJ20265 (Accession NP_060203.2) is another GAM193 target gene, herein designated TARGET GENE. FLJ20265 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20265, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20265 BINDING SITE, designated SEQ ID:15924, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32224] Another function of GAM193 is therefore inhibition of FLJ20265 (Accession NP_060203.2) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20265.

[32225] FLJ21302 (Accession NP_075052.1) is another GAM193 target gene, herein designated TARGET GENE. FLJ21302 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21302, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21302 BINDING SITE, designated SEQ ID:17809, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32226] Another function of GAM193 is therefore inhibition of FLJ21302 (Accession NP_075052.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21302.

[32227] GAS41 (Accession NP_006521.1) is another GAM193 target gene, herein designated TARGET GENE. GAS41 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAS41, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAS41

BINDING SITE, designated SEQ ID:14327, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32228] Another function of GAM193 is therefore inhibition of GAS41 (Accession NP_006521.1), a gene which may also represent a transcription factor. and therefore may be associated with Glioma. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of Glioma, and of other diseases and clinical conditions associated with GAS41.

[32229] The function of GAS41 has been established by previous studies. Gene amplification, which is generally considered to occur late in tumor development, is a common feature of high- grade glioma. Fischer et al. (1997) reported cloning and sequencing a cDNA, termed glioma- amplified sequence- 41 (GAS41) by them, that was identified in a glioblastoma cell line by microdissection- mediated cDNA capture. An increased copy number of GAS41 was found in glioblastoma multiforme and astrocytoma III, and at a high frequency in astrocytoma grades I and II. Sequence comparison indicated high similarity between the GAS41 protein, the yeast and human AF9 (OMIM Ref. No. 159558), and human ENL (OMIM Ref. No. 159556). Fischer

et al. (1997) noted that both AF9 and ENL belong to a new class of transcription factors, indicating that GAS41 may also represent a transcription factor. With GAS41 being the first gene found with increased copy number in low-grade glioma, this study provided the first evidence that gene amplification can occur in early tumor development. The GAS41 gene had been isolated from a homogeneously staining region (HSR) at 12q13- q15 by microdissection-mediated cDNA capture (Gracia et al., 1996).

[32230]

[32231] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32232] Fischer, U.; Heckel, D.; Michel, A.; Janka, M.; Hulsebos, T.; Meese, E. : Cloning of a novel transcription factor- like gene amplified in human glioma including astrocytoma grade I. Hum. Molec. Genet. 6: 1817- 1822, 1997. ; and

[32233] Gracia, E.; Fischer, U.; Elkahloun, A.; Trent, J. M.; Meese, E.; Meltzer, P. S. : Isolation of genes amplified in human cancers by microdissection mediated cDNA capture. Hum. Molec. Gen.

[32234] Further studies establishing the function and utilities of GAS41 are found in John Hopkins OMIM database record

ID 602116, and in cited publications listed in Table 5, which are hereby incorporated by reference.Glutamate receptor, ionotropic, n-methyl d-aspartate 2b (GRIN2B, Accession NP_000825.1) is another GAM193 target gene, herein designated TARGET GENE. GRIN2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRIN2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRIN2B BINDING SITE, designated SEQ ID:16251, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32235] Another function of GAM193 is therefore inhibition of Glutamate receptor, ionotropic, n-methyl d-aspartate 2b (GRIN2B, Accession NP_000825.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIN2B.

[32236] General transcription factor iih, polypeptide 2, 44kda (GTF2H2, Accession NP_001506.1) is another GAM193 target gene, herein designated TARGET GENE. GTF2H2 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by GTF2H2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2H2 BINDING SITE, designated SEQ ID:8307, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32237] Another function of GAM193 is therefore inhibition of General transcription factor iih, polypeptide 2, 44kda (GTF2H2, Accession NP_001506.1), a gene which is subunit of RNA polymerase II transcription initiation factor IIH and involves in transcription and DNA repair. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2H2.

[32238] The function of GTF2H2 has been established by previous studies. Transcription factor IIH (TFIIH; OMIM Ref. No. 189972) is associated with the RNA polymerase II transcription complex, which is involved in transcription and transcription- mediated DNA repair. Humbert et al. (1994) described the cloning of the genes encoding the human 44- kD subunit and the 34- kD subunit (OMIM Ref. No. 601750) of TFIIH. The 44- kD subunit gene (also symbol-

ized GTF2H2) appears to be the human counterpart of yeast SSL1, a gene involved in UV resistance. The childhood- onset spinal muscular atrophies are a clinical heterogeneous group of autosomal recessive disorders characterized by selective degeneration of the anterior horn cells with subsequent weakness and atrophy of limb muscles; see SMA1 (OMIM Ref. No. 253300). The disease locus maps to 5q13, a region characterized by genetic instability and DNA duplication. Carter et al. (1997) noted that, among the duplicated genes in this region, the telomeric copy of the SMN (survival motor neuron) gene (SMN1; 600354) is thought to be the major disease- determining gene, since it is missing in the majority of SMA patients and since small, intragenic mutations in the gene have been associated with the disorder. Approximately half of the severely affected SMA1 patients are also missing both homologs of a neighboring gene, the neuronal apoptosis inhibitory protein (NAIP; 600355). The loss of NAIP may affect disease severity. Clearly, the molecular event underlying the childhood- onset SMAs are complex, possibly involving multiple genes. Carter et al. (1997) reported a third multicopy gene in the SMA region, encoding the p44 subunit of basal transcription factor II (BTF2). One copy of

this transcription- repair gene (symbolized BTF2p44 by them) was deleted in at least 15% of all SMA cases. A single copy of the gene was mapped to the SMA region on 5q by van der Steege et al. (1995). Carter et al. (1997) reported the presence of multiple copies of the gene in the SMA region located in close proximity to NAIP and SMN1. Furthermore, they reported a 1- bp polymorphism that distinguished 2 gene copies and they documented the SMA- associated deletion of 1 version of the gene. The 2 polymorphic forms of the p44 gene differ by 2 nonconservative changes (ile- to- met in exon 7 and leu- to- val in exon 10), appear to be ubiquitously expressed, and are present in fetal and adult tissues and in SMA and control lymphoblasts. Carter et al. (1997) stated that physical mapping in the SMA region is complicated and imprecise, presumably due to the great instability and variability arising from the duplication, deletion, and gene conversion of highly homologous DNA in this region.

[32239]

[32240] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32241] Humbert, S.; van Vuuren, H.; Lutz, Y.; Hoeijmakers, J. H.;

Egly, J. M.; Moncollin, V. : p44 and p34 subunits of the BTF2/TFIIH transcription factor have homologies with SSL1, a yeast protein involved in DNA repair. EMBO J. 13: 2393- 2398, 1994. ; and

[32242] Carter, T. A.; Bonnemann, C. G.; Wang, C. H.; Obici, S.; Parano, E.; De Fatima Bonaldo, M.; Ross, B. M.; Penchaszadeh, G. K.; Mackenzie, A.; Bento Soares, M.; Kunkel, L. M.; Gilliam, T.

[32243] Further studies establishing the function and utilities of GTF2H2 are found in John Hopkins OMIM database record ID 601748, and in cited publications listed in Table 5, which are hereby incorporated by reference.Glycogenin 2 (GYG2, Accession NP_003909.1) is another GAM193 target gene, herein designated TARGET GENE. GYG2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYG2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GYG2 BINDING SITE, designated SEQ ID:9556, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32244] Another function of GAM193 is therefore inhibition of

Glycogenin 2 (GYG2, Accession NP_003909.1), a gene which primes de novo glycogen synthesis and can determine glycogen accumulation. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GYG2.

[32245] The function of GYG2 has been established by previous studies. Glycogenin is a self- glucosylating protein covalently linked to glycogen that acts as a primer for the action of glycogen synthase. See GYG, the muscle glycogenin (OMIM Ref. No. 603942). By searching an EST database for sequences related to GYG, Mu et al. (1997) isolated cDNAs encoding a related protein, which they designated glycogenin- 2 (GN2). They suggested that muscle glycogenin be referred to as glycogenin- 1. Sequence analysis revealed that the cDNAs encode several different GN2 isoforms, 3 of which are found in liver. The liver isoforms, which have different N termini, share 42 to 45% protein sequence identity with glycogenin- 1. Mu et al. (1997) demonstrated that recombinant GN2 exhibited all of the biochemical properties of glycogenin; it self-glucosylated, acted as a substrate for glycogen synthase, and was released from glycogen by alpha- amylase treatment. Northern blot analysis revealed that the 3.6- kb

GN2 mRNA was expressed most strongly in liver. Mu and Roach (1998) determined that human liver extracts contain both glycogenin- 1 and GN2. In vitro and coimmunoprecipitation studies demonstrated that the 2 glycogenins interact with each other. Unlike glycogenin- 1, overexpression of GN2 in mammalian cells resulted in a significant increase in glycogen accumulation in the cell, indicating that the level of GN2 can determine glycogen accumulation.

[32246]

[32247] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32248] Mu, J.; Roach, P. J. : Characterization of human glycogenin- 2, a self- glucosylating initiator of liver glycogen metabolism. J. Biol. Chem. 273: 34850- 34856, 1998. ; and

[32249] Mu, J.; Skurat, A. V.; Roach, P. J. : Glycogenin- 2, a novel self- glucosylating protein involved in liver glycogen biosynthesis. J. Biol. Chem. 272: 27589- 27597, 1997.

[32250] Further studies establishing the function and utilities of GYG2 are found in John Hopkins OMIM database record ID 300198, and in cited publications listed in Table 5, which

are hereby incorporated by reference.HSPC230 (Accession NP_057571.1) is another GAM193 target gene, herein designated TARGET GENE. HSPC230 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSPC230, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPC230 BINDING SITE, designated SEQ ID:9132, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32251] Another function of GAM193 is therefore inhibition of HSPC230 (Accession NP_057571.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC230.

[32252] IRTA1 (Accession NP_112572.1) is another GAM193 target gene, herein designated TARGET GENE. IRTA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IRTA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRTA1 BIND-

ING SITE, designated SEQ ID:7687, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32253] Another function of GAM193 is therefore inhibition of IRTA1 (Accession NP_112572.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRTA1.

[32254] Integrin, alpha v (vitronectin receptor, alpha polypeptide, antigen cd51) (ITGAV, Accession NP_002201.1) is another GAM193 target gene, herein designated TARGET GENE. ITGAV BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITGAV, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITGAV BINDING SITE, designated SEQ ID:12126, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32255] Another function of GAM193 is therefore inhibition of Integrin, alpha v (vitronectin receptor, alpha polypeptide, antigen cd51) (ITGAV, Accession NP_002201.1), a gene which is a member of the integrin family of cell- surface proteins. Accordingly, utilities of GAM193 include diagno-

sis, prevention and treatment of diseases and clinical conditions associated with ITGAV.

[32256] The function of ITGAV and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.KIAA0555 (Accession NP_055605.1) is another GAM193 target gene, herein designated TARGET GENE. KIAA0555 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0555, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0555 BINDING SITE, designated SEQ ID:6266, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32257] Another function of GAM193 is therefore inhibition of KIAA0555 (Accession NP_055605.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0555.

[32258] KIAA1046 (Accession NP_055743.1) is another GAM193 target gene, herein designated TARGET GENE. KIAA1046 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1046, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1046 BINDING SITE, designated SEQ ID:17833, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32259] Another function of GAM193 is therefore inhibition of KIAA1046 (Accession NP_055743.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1046.

[32260] KIAA1265 (Accession XP_047707.1) is another GAM193 target gene, herein designated TARGET GENE. KIAA1265 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1265, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1265 BINDING SITE, designated SEQ ID:8735, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32261] Another function of GAM193 is therefore inhibition of

KIAA1265 (Accession XP_047707.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1265.

[32262] KIAA1935 (Accession XP_087672.1) is another GAM193 target gene, herein designated TARGET GENE. KIAA1935 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1935, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1935 BINDING SITE, designated SEQ ID:5530, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32263] Another function of GAM193 is therefore inhibition of KIAA1935 (Accession XP_087672.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1935.

[32264] KIDINS220 (Accession XP_291015.1) is another GAM193 target gene, herein designated TARGET GENE. KIDINS220 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIDINS220, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIDINS220 BINDING SITE, designated SEQ ID:5248, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32265] Another function of GAM193 is therefore inhibition of KIDINS220 (Accession XP_291015.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIDINS220.

[32266] V-kit hardy-zuckerman 4 feline sarcoma viral oncogene homolog (KIT, Accession NP_000213.1) is another GAM193 target gene, herein designated TARGET GENE. KIT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIT BINDING SITE, designated SEQ ID:17832, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32267] Another function of GAM193 is therefore inhibition of V-

kit hardy-zuckerman 4 feline sarcoma viral oncogene homolog (KIT, Accession NP_000213.1), a gene which is the receptor for stem cell factor (mast cell growth factor) and has a tyrosine- protein kinase activity. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIT.

[32268] The function of KIT has been established by previous studies. Geissler et al. (1988) showed that in the mouse the kit gene is disrupted in 2 spontaneous mutant W alleles. It was previously known that mutations at the W locus in the mouse (producing changes, including white- coat color, sterility, and anemia, attributable to failure of stem cell populations to migrate and/or proliferate effectively during development) map in the same region as kit. Thus, the KIT protooncogene, which encodes a putative tyrosine kinase receptor, was a candidate for the W locus. The protooncogene KIT encodes a transmembrane tyrosine kinase. A strong structural homology of KIT to the CSF1 receptor (OMIM Ref. No. 164770) and the platelet- derived growth factor receptor (OMIM Ref. No. 173490) suggests a model for the action of the KIT gene product during differentiation. The phenotypes of W mutants suggest that 3

cell populations in which KIT function is critical are the pluripotent hematopoietic stem cell, the migrating melanoblast during early embryonic development, and the primordial germ cell during this same period of development. Identification of the ligand for KIT will help in the understanding of its function. A genetic clue to its nature may be found through characterization of the Sl ('steel') locus of the mouse. The phenotypes of mutants at this locus closely resemble mutants at the W locus; however, unlike W, the defect in Sl is not intrinsic to the progenitor stem cells of the affected tissues, but rather lies in the environment in which melanoblast, germ cell, and hematopoietic progenitors differentiate and proliferate. Chabot et al. (1988) also related kit to a W mutation in the mouse. These findings will prompt search for comparable changes in disorders such as Fanconi anemia (OMIM Ref. No. 227650). In the dominant W(42) spotting phenotype in the mouse, Tan et al. (1990) demonstrated an asp790- to- asparagine mutation in the KIT protein product. Aspartic acid- 790 is a conserved residue in all protein kinases. Nocka et al. (1990) identified mutations in other alleles at the W locus: W(37), E- to- K at position 582; W(v), T- to- M at position 660; and W(41), V- to- M at po-

sition 831. The W mutation is the result of a 78- amino acid deletion that includes the transmembrane of the KIT protein. Nocka et al. (1990) detected a 125- kD KIT protein in homozygous W/W mast cells which lacked kinase activity and did not express KIT on the cell surface. Thus, in mice, the c- kit receptor tyrosine kinase is the gene product of the W locus, whereas Sl encodes the ligand for this growth factor receptor. Microphthalmia (mi/mi) in mice also shows deficiency in melanocytes and mast cells. In addition, whereas W and Sl mutants can be anemic and sterile, 'mi' mice are osteopetrotic due to a monocyte/ macrophage defect. Dubreuil et al. (1991) found that the fms gene (OMIM Ref. No. 164770) complements the mitogenic defect in mast cells of mutant W mice but not of mi/ mi mice. Brannan et al. (1991) detected a HaeIII polymorphism in the KIT gene. This polymorphism was linked to other 4q markers. Poduslo et al. (1991) described a strategy for identifying polymorphic genetic markers in the 3- prime untranslated regions of coding loci. The method combined PCR and single- strand conformation polymorphism (SSCP) analysis

[32269] Animal model experiments lend further support to the function of KIT. Signaling from the KIT receptor tyrosine

kinase is essential for primordial germ cell growth both in vivo and in vitro. Many downstream effectors of the KIT signaling pathway have been identified in other cell types, but how these molecules control primordial germ cell survival and proliferation are unknown. Determination of the KIT effectors acting in primoridial germ cells has been hampered by the lack of effective methods to manipulate easily gene expression in these cells. De Miguel et al. (2002) overcame this problem by testing the efficacy of retroviral- mediated gene transfer for manipulating gene expression in mammalian germ cells. They found that primordial germ cells can successfully be infected with a variety of types of retroviruses. They used this method to demonstrate an important role of the AKT1 (OMIM Ref. No. 164730) in regulating primordial germ cell growth

[32270] It is appreciated that the abovementioned animal model for KIT is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[32271] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32272] Poduslo, S. E.; Dean, M.; Kolch, U.; O'Brien, S. J. : Detecting

high- resolution polymorphisms in human coding loci by combining PCR and single- strand conformation polymorphism (SSCP) analysis. Am. J. Hum. Genet. 49: 106- 111, 1991. ; and

[32273] De Miguel, M. P.; Cheng, L.; Holland, E. C.; Federspiel, M. J.; Donovan, P. J. : Dissection of the c- Kit signaling pathway in mouse primordial germ cells by retroviral- mediated gene tran.

[32274] Further studies establishing the function and utilities of KIT are found in John Hopkins OMIM database record ID 164920, and in cited publications listed in Table 5, which are hereby incorporated by reference.Lysosomal-associated membrane protein 2 (LAMP2, Accession NP_054701.1) is another GAM193 target gene, herein designated TARGET GENE. LAMP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LAMP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMP2 BINDING SITE, designated SEQ ID:1978, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32275] Another function of GAM193 is therefore inhibition of Lysosomal-associated membrane protein 2 (LAMP2, Accession NP_054701.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP2.

[32276] LOC115548 (Accession XP_291142.1) is another GAM193 target gene, herein designated TARGET GENE. LOC115548 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC115548, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115548 BINDING SITE, designated SEQ ID:13272, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32277] Another function of GAM193 is therefore inhibition of LOC115548 (Accession XP_291142.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115548.

[32278] LOC142955 (Accession XP_084389.1) is another GAM193 target gene, herein designated TARGET GENE. LOC142955 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC142955, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC142955 BINDING SITE, designated SEQ ID:5300, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32279] Another function of GAM193 is therefore inhibition of LOC142955 (Accession XP_084389.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142955.

[32280] LOC146517 (Accession XP_085491.1) is another GAM193 target gene, herein designated TARGET GENE. LOC146517 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146517, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146517 BINDING SITE, designated SEQ ID:19666, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32281] Another function of GAM193 is therefore inhibition of

LOC146517 (Accession XP_085491.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146517.

[32282] LOC149684 (Accession XP_097710.1) is another GAM193 target gene, herein designated TARGET GENE. LOC149684 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149684, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149684 BINDING SITE, designated SEQ ID:17873, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32283] Another function of GAM193 is therefore inhibition of LOC149684 (Accession XP_097710.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149684.

[32284] LOC152200 (Accession XP_098174.1) is another GAM193 target gene, herein designated TARGET GENE. LOC152200 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152200, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152200 BINDING SITE, designated SEQ ID:17088, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32285] Another function of GAM193 is therefore inhibition of LOC152200 (Accession XP_098174.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152200.

[32286] LOC219392 (Accession XP_165921.1) is another GAM193 target gene, herein designated TARGET GENE. LOC219392 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC219392, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219392 BINDING SITE, designated SEQ ID:19644, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32287] Another function of GAM193 is therefore inhibition of LOC219392 (Accession XP_165921.1) . Accordingly, utili-

ties of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219392.

[32288] LOC254100 (Accession XP_172851.1) is another GAM193 target gene, herein designated TARGET GENE. LOC254100 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC254100, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254100 BINDING SITE, designated SEQ ID:8379, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32289] Another function of GAM193 is therefore inhibition of LOC254100 (Accession XP_172851.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254100.

[32290] LOC284020 (Accession XP_208151.1) is another GAM193 target gene, herein designated TARGET GENE. LOC284020 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284020, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284020 BINDING SITE, designated SEQ ID:12022, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32291] Another function of GAM193 is therefore inhibition of LOC284020 (Accession XP_208151.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284020.

[32292] LOC338597 (Accession XP_290482.1) is another GAM193 target gene, herein designated TARGET GENE. LOC338597 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338597, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338597 BINDING SITE, designated SEQ ID:13628, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32293] Another function of GAM193 is therefore inhibition of LOC338597 (Accession XP_290482.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC338597.

[32294] LOC338739 (Accession XP_294690.1) is another GAM193 target gene, herein designated TARGET GENE. LOC338739 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338739, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338739 BINDING SITE, designated SEQ ID:17845, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32295] Another function of GAM193 is therefore inhibition of LOC338739 (Accession XP_294690.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338739.

[32296] LOC338961 (Accession XP_294753.1) is another GAM193 target gene, herein designated TARGET GENE. LOC338961 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338961, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC338961 BINDING SITE, designated SEQ ID:12926, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32297] Another function of GAM193 is therefore inhibition of LOC338961 (Accession XP_294753.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338961.

[32298] LOC339003 (Accession XP_290660.1) is another GAM193 target gene, herein designated TARGET GENE. LOC339003 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339003, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339003 BINDING SITE, designated SEQ ID:10159, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32299] Another function of GAM193 is therefore inhibition of LOC339003 (Accession XP_290660.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC339003.

[32300] LOC339952 (Accession XP_295110.1) is another GAM193 target gene, herein designated TARGET GENE. LOC339952 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339952, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339952 BINDING SITE, designated SEQ ID:2352, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32301] Another function of GAM193 is therefore inhibition of LOC339952 (Accession XP_295110.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339952.

[32302] LOC347774 (Accession XP_290475.1) is another GAM193 target gene, herein designated TARGET GENE. LOC347774 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC347774, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC347774 BINDING SITE, designated SEQ ID:13628, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32303] Another function of GAM193 is therefore inhibition of LOC347774 (Accession XP_290475.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347774.

[32304] LOC349277 (Accession XP_303016.1) is another GAM193 target gene, herein designated TARGET GENE. LOC349277 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349277, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349277 BINDING SITE, designated SEQ ID:3953, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32305] Another function of GAM193 is therefore inhibition of LOC349277 (Accession XP_303016.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349277.

[32306] LOC349299 (Accession XP_303021.1) is another GAM193 target gene, herein designated TARGET GENE. LOC349299 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349299, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349299 BINDING SITE, designated SEQ ID:3953, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32307] Another function of GAM193 is therefore inhibition of LOC349299 (Accession XP_303021.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349299.

[32308] LOC54103 (Accession XP_168508.4) is another GAM193 target gene, herein designated TARGET GENE. LOC54103 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC54103, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC54103 BINDING SITE, designated SEQ ID:12980, to the

nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32309] Another function of GAM193 is therefore inhibition of LOC54103 (Accession XP_168508.4) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC54103.

[32310] LOC91149 (Accession XP_036480.1) is another GAM193 target gene, herein designated TARGET GENE. LOC91149 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91149 BINDING SITE, designated SEQ ID:6578, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32311] Another function of GAM193 is therefore inhibition of LOC91149 (Accession XP_036480.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91149.

[32312] LOC92497 (Accession XP_045436.1) is another GAM193

target gene, herein designated TARGET GENE. LOC92497 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC92497, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92497 BINDING SITE, designated SEQ ID:16786, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32313] Another function of GAM193 is therefore inhibition of LOC92497 (Accession XP_045436.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92497.

[32314] Lim domain containing preferred translocation partner in lipoma (LPP, Accession NP_005569.1) is another GAM193 target gene, herein designated TARGET GENE. LPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LPP BINDING SITE, designated SEQ ID:14339, to the nucleotide se-

quence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32315] Another function of GAM193 is therefore inhibition of Lim domain containing preferred translocation partner in lipoma (LPP, Accession NP_005569.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPP.

[32316] Methyl cpg binding protein 2 (rett syndrome) (MECP2, Accession NP_004983.1) is another GAM193 target gene, herein designated TARGET GENE. MECP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MECP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MECP2 BINDING SITE, designated SEQ ID:10015, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32317] Another function of GAM193 is therefore inhibition of Methyl cpg binding protein 2 (rett syndrome) (MECP2, Accession NP_004983.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with MECP2.

[32318] MGC14353 (Accession NP_116120.1) is another GAM193 target gene, herein designated TARGET GENE. MGC14353 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14353, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14353 BINDING SITE, designated SEQ ID:10146, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32319] Another function of GAM193 is therefore inhibition of MGC14353 (Accession NP_116120.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14353.

[32320] MGC2776 (Accession NP_079541.1) is another GAM193 target gene, herein designated TARGET GENE. MGC2776 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2776, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC2776 BINDING SITE, designated SEQ ID:2621, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32321] Another function of GAM193 is therefore inhibition of MGC2776 (Accession NP_079541.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2776.

[32322] Makorin, ring finger protein, 3 (MKRN3, Accession NP_005655.1) is another GAM193 target gene, herein designated TARGET GENE. MKRN3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MKRN3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MKRN3 BINDING SITE, designated SEQ ID:3557, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32323] Another function of GAM193 is therefore inhibition of Makorin, ring finger protein, 3 (MKRN3, Accession NP_005655.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKRN3.

[32324] MU (Accession NP_071368.1) is another GAM193 target gene, herein designated TARGET GENE. MU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MU BINDING SITE, designated SEQ ID:2785, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32325] Another function of GAM193 is therefore inhibition of MU (Accession NP_071368.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MU.

[32326] Neuroligin 4, y linked (NLGN4Y, Accession NP_055708.1) is another GAM193 target gene, herein designated TARGET GENE. NLGN4Y BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NLGN4Y, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NLGN4Y BINDING SITE, designated SEQ ID:6577, to the nucleotide sequence of GAM193 RNA,

herein designated GAM RNA, also designated SEQ ID:268.

[32327] Another function of GAM193 is therefore inhibition of Neuroligin 4, y linked (NLGN4Y, Accession NP_055708.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NLGN4Y.

[32328] Neuropeptide y (NPY, Accession NP_000896.1) is another GAM193 target gene, herein designated TARGET GENE. NPY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPY BINDING SITE, designated SEQ ID:549, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32329] Another function of GAM193 is therefore inhibition of Neuropeptide y (NPY, Accession NP_000896.1), a gene which is implicated in the control of feeding and in the secretion of gonadotrophin- release hormone. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPY.

[32330] The function of NPY has been established by previous studies. Hansel et al. (2001) identified a role for NPY in promoting proliferation of postnatal neuronal precursor cells. NPY is synthesized in the postnatal olfactory epithelium by sustentacular cells, previously proposed to function only in structural support. Mice with a targeted deletion of NPY contained half as many dividing olfactory neuronal precursor cells as did controls. Furthermore, NPY-deficient mice developed significantly fewer olfactory neurons by adulthood. NPY acts on multipotent neuronal precursor or basal cells to activate rapidly and transiently the extracellular signal- regulated kinase (ERK) 1/2 (OMIM Ref. No. 601795) subgroup of mitogen- activated protein kinases. The NPY Y1 receptor subtype (OMIM Ref. No. 162641) appears to mediate this effect. The ability of NPY to induce neuronal precursor proliferation is mediated by protein kinase C (PKC; 176960), indicating an upstream PKC- dependent activation of ERK1/2. These results indicate that NPY may regulate neuronal precursor proliferation in the adult mammal.

[32331] Animal model experiments lend further support to the function of NPY. Neuropeptide Y is a neuromodulator implicated in the control of energy balance and is overpro-

duced in the hypothalamus of ob/ob mice. To determine the role of NPY in the response to leptin (OMIM Ref. No. 164160) deficiency, Erickson et al. (1996) generated ob/ob mice deficient in NPY. In the absence of NPY, ob/ob mice were less obese because of reduced food intake and increased energy expenditure, and were less severely affected by diabetes, sterility, and somatotropic defects. These results were interpreted as indicating that NPY is a central effector of leptin deficiency.

[32332] It is appreciated that the abovementioned animal model for NPY is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[32333] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32334] Erickson, J. C.; Hollopeter, G.; Palmiter, R. D. : Attenuation of the obesity syndrome of ob/ob mice by the loss of neuropeptide Y. Science 274: 1704- 1706, 1996. ; and

[32335] Hansel, D. E.; Eipper, B. A.; Ronnett, G. V. : Neuropeptide Y functions as a neuroproliferative factor. Nature 410: 940- 943, 2001.

[32336] Further studies establishing the function and utilities of

NPY are found in John Hopkins OMIM database record ID 162640, and in cited publications listed in Table 5, which are hereby incorporated by reference.P114-RHO-GEF (Accession NP_056133.1) is another GAM193 target gene, herein designated TARGET GENE. P114-RHO-GEF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P114-RHO-GEF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P114-RHO-GEF BINDING SITE, designated SEQ ID:6818, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32337] Another function of GAM193 is therefore inhibition of P114-RHO-GEF (Accession NP_056133.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P114-RHO-GEF.

[32338] Pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3, Accession NP_005382.1) is another GAM193 target gene, herein designated TARGET GENE. PDK3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDK3, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDK3 BINDING SITE, designated SEQ ID:13449, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32339] Another function of GAM193 is therefore inhibition of Pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3, Accession NP_005382.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDK3.

[32340] Protein kinase (camp-dependent, catalytic) inhibitor alpha (PKIA, Accession NP_006814.1) is another GAM193 target gene, herein designated TARGET GENE. PKIA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PKIA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PKIA BINDING SITE, designated SEQ ID:11912, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32341] Another function of GAM193 is therefore inhibition of

Protein kinase (camp-dependent, catalytic) inhibitor alpha (PKIA, Accession NP_006814.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKIA.

[32342] Pou domain, class 2, associating factor 1 (POU2AF1, Accession NP_006226.1) is another GAM193 target gene, herein designated TARGET GENE. POU2AF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POU2AF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POU2AF1 BINDING SITE, designated SEQ ID:3129, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32343] Another function of GAM193 is therefore inhibition of Pou domain, class 2, associating factor 1 (POU2AF1, Accession NP_006226.1), a gene which is a transcriptional coactivator that specifically associates with either oct1 or oct2 and therefore may be associated with A form of b- cell leukemia. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of A form of b- cell leukemia, and of other diseases and clinical conditions

associated with POU2AF1.

[32344] The function of POU2AF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.RCBTB1 (Accession NP_060661.2) is another GAM193 target gene, herein designated TARGET GENE. RCBTB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RCBTB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RCBTB1 BINDING SITE, designated SEQ ID:13748, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32345] Another function of GAM193 is therefore inhibition of RCBTB1 (Accession NP_060661.2) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RCBTB1.

[32346] Restin (reed-steinberg cell-expressed intermediate filament-associated protein) (RSN, Accession NP_002947.1) is another GAM193 target gene, herein designated TARGET GENE. RSN BINDING SITE is a target binding site found

in the 3` untranslated region of mRNA encoded by RSN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RSN BINDING SITE, designated SEQ ID:9415, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32347] Another function of GAM193 is therefore inhibition of Restin (reed-steinberg cell-expressed intermediate filament-associated protein) (RSN, Accession NP_002947.1), a gene which seems to be a intermediate filament associated protein that links endocytic vesicles to microtubules. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RSN.

[32348] The function of RSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Sel-1 suppressor of lin-12-like (c. elegans) (SEL1L, Accession NP_005056.3) is another GAM193 target gene, herein designated TARGET GENE. SEL1L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEL1L, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEL1L BINDING SITE, designated SEQ ID:1707, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32349] Another function of GAM193 is therefore inhibition of Sel-1 suppressor of lin-12-like (c. elegans) (SEL1L, Accession NP_005056.3), a gene which may play a role in notch signaling (by similarity). Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEL1L.

[32350] The function of SEL1L has been established by previous studies. Biunno et al. (1997) isolated a novel cDNA, designated SEL1L by them, that shows sequence similarities to sel- 1, a gene identified as an extragenic suppressor of the lin- 12 hypomorphic mutant from C. elegans (3,4:Grant and Greenwald, 1996, 1997). SEL1L exhibited a tissue- specific pattern of expression: high levels of a single 7.5- kb transcript were detected only in the pancreas of healthy individuals, whereas low to undetectable levels were observed in other adult tissues and in some fetal tissues. Because of the tissue- specific expression of the

gene, Biunno et al. (1997) studied the gene in human pancreatic carcinomas. They found that 17% of adenocarcinomas of the pancreas did not express SEL1L to a detectable level; however, no gross genomic alterations were apparent within a few hundred kb of the relevant region. By somatic cell hybrid analysis and fluorescence in situ hybridization, Biunno et al. (1997) mapped the SEL1L gene to chromosome 14q31. Donoviel and Bernstein (1999) localized the gene to 14q24.3- q31 by FISH and radiation hybrid analysis.

[32351]

[32352] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32353] Biunno, I.; Appierto, V.; Cattaneo, M.; Leone, B. E.; Balzano, G.; Socci, C.; Saccone, S.; Letizia, A.; Valle, G. D.; Sgaramella, V. : Isolation of a pancreas- specific gene located on human chromosome 14q31: expression analysis in human pancreatic ductal carcinomas. Genomics 46: 284- 286, 1997. ; and

[32354] Donoviel, D. B.; Bernstein, A. : SEL- 1L maps to human chromosome 14, near the insulin- dependent diabetes mellitus locus 11. Genomics 56: 232- 233, 1999.

[32355] Further studies establishing the function and utilities of SEL1L are found in John Hopkins OMIM database record ID 602329, and in cited publications listed in Table 5, which are hereby incorporated by refer-ence.Serum/glucocorticoid regulated kinase-like (SGKL, Accession NP_037389.4) is another GAM193 target gene, herein designated TARGET GENE. SGKL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SGKL, corre-sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-trates the complementarity of the nucleotide sequences of SGKL BINDING SITE, designated SEQ ID:19551, to the nu-cleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32356] Another function of GAM193 is therefore inhibition of Serum/glucocorticoid regulated kinase-like (SGKL, Acces-sion NP_037389.4) . Accordingly, utilities of GAM193 in-clude diagnosis, prevention and treatment of diseases and clinical conditions associated with SGKL.

[32357] Serum/glucocorticoid regulated kinase-like (SGKL, Acces-sion NP_733827.2) is another GAM193 target gene, herein designated TARGET GENE. SGKL BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SGKL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SGKL BINDING SITE, designated SEQ ID:19551, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32358] Another function of GAM193 is therefore inhibition of Serum/glucocorticoid regulated kinase-like (SGKL, Accession NP_733827.2) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SGKL.

[32359] SIMP (Accession XP_114346.2) is another GAM193 target gene, herein designated TARGET GENE. SIMP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIMP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIMP BINDING SITE, designated SEQ ID:20030, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32360] Another function of GAM193 is therefore inhibition of SIMP (Accession XP_114346.2) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIMP.

[32361] Solute carrier family 12 (sodium/potassium/chloride transporters), member 2 (SLC12A2, Accession NP_001037.1) is another GAM193 target gene, herein designated TARGET GENE. SLC12A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC12A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC12A2 BINDING SITE, designated SEQ ID:2850, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32362] Another function of GAM193 is therefore inhibition of Solute carrier family 12 (sodium/potassium/chloride transporters), member 2 (SLC12A2, Accession NP_001037.1), a gene which transports chloride ions across secretory epithelia. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC12A2.

[32363] The function of SLC12A2 has been established by previous studies. By moving chloride into epithelial cells, the Na- K- Cl cotransporter aids transcellular movement of chloride across both secretory and absorptive epithelia. Using cDNA probes from the elasmobranch secretory Na-K- Cl cotransporter reported by Xu et al. (1994), Payne et al. (1995) identified the human homolog, which they referred to as NKCC1. By screening cDNA libraries of a human colonic carcinoma cell line, they identified a sequence of 4,115 bases that encoded a deduced protein of 1,212 amino acids with 12 transmembrane segments. By fluorescence in situ hybridization, they localized the cotransporter gene to 5q23.3. Human embryonic kidney cells stably transfected with the full- length cDNA expressed a protein of approximately 170 kD which was recognized by anti- cotransporter antibodies. Following treatment with N- glycosidase F, the molecular mass of the expressed protein was similar to that predicted for the core protein from the cDNA sequence. Evans et al. (2000) tested directly the possibility that the salivary fluid secretory mechanism requires Na+/K+/2Cl- cotransporter-mediated Cl- uptake. They studied the in vivo and in vitro functioning of acinar cells from the parotid glands of mice

with targeted disruption of the Nkcc1 gene, which encodes the salivary cotransporter. In wildtype mice Nkcc1 was localized to the basolateral membranes of parotid acinar cells, whereas expression was not detected in duct cells. The lack of functional Nkcc1 resulted in a dramatic reduction (greater than 60%) in the volume of saliva secreted in response to a muscarinic agonist, the primary in situ salivation signal. Expression of the chloride/bicarbonate exchanger AE2 (SLC4A2; 109280) was enhanced, suggesting that this transporter compensates for the loss of functional Nkcc1. The ability of the parotid gland to conserve NaCl was abolished in Nkcc1- deficient mice. Evans et al. (2000) suggested that some cases of 'idiopathic' dry mouth disease may have a basis in a defect of Nkcc1.

[32364]

[32365] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32366] Payne, J. A.; Xu, J.- C.; Haas, M.; Lytle, C. Y.; Ward, D.; Forbush, B., III : Primary structure, functional expression, and chromosomal localization of the bumetanide- sensitive Na- K- Cl cotransporter in human colon. J. Biol.

Chem. 270: 17977- 17985, 1995. ; and

[32367] Evans, R. L.; Park, K.; Turner, R. J.; Watson, G. E.; Nguyen, H.- V.; Dennett, M. R.; Hand, A. R.; Flagella, M.; Shull, G. E.; Melvin, J. E. : Severe impairment of salivation in Na+/K+/2Cl.

[32368] Further studies establishing the function and utilities of SLC12A2 are found in John Hopkins OMIM database record ID 600840, and in cited publications listed in Table 5, which are hereby incorporated by reference.Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) is another GAM193 target gene, herein designated TARGET GENE. SLC16A6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC16A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A6 BINDING SITE, designated SEQ ID:2622, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32369] Another function of GAM193 is therefore inhibition of Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) . Accord-

ingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A6.

[32370] Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (SLC6A3, Accession NP_001035.1) is another GAM193 target gene, herein designated TARGET GENE. SLC6A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC6A3 BINDING SITE, designated SEQ ID:9121, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32371] Another function of GAM193 is therefore inhibition of Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (SLC6A3, Accession NP_001035.1), a gene which terminates the action of dopamine by its high affinity sodium- dependent reuptake into presynaptic terminals. Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A3.

[32372] The function of SLC6A3 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.SMARCAD1 (Accession NP_064544.1) is another GAM193 target gene, herein designated TARGET GENE. SMARCAD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SMARCAD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMARCAD1 BINDING SITE, designated SEQ ID:8809, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32373] Another function of GAM193 is therefore inhibition of SMARCAD1 (Accession NP_064544.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMARCAD1.

[32374] ST18 (Accession NP_055497.1) is another GAM193 target gene, herein designated TARGET GENE. ST18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ST18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ST18 BINDING SITE, designated SEQ ID:4579, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32375] Another function of GAM193 is therefore inhibition of ST18 (Accession NP_055497.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ST18.

[32376] Staufen, rna binding protein, homolog 2 (drosophila) (STAU2, Accession NP_055208.1) is another GAM193 target gene, herein designated TARGET GENE. STAU2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STAU2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAU2 BINDING SITE, designated SEQ ID:19453, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32377] Another function of GAM193 is therefore inhibition of Staufen, rna binding protein, homolog 2 (drosophila) (STAU2, Accession NP_055208.1) . Accordingly, utilities of

GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAU2.

[32378] Stanniocalcin 2 (STC2, Accession NP_003705.1) is another GAM193 target gene, herein designated TARGET GENE. STC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STC2 BINDING SITE, designated SEQ ID:696, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32379] Another function of GAM193 is therefore inhibition of Stanniocalcin 2 (STC2, Accession NP_003705.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STC2.

[32380] Tubulointerstitial nephritis antigen (TINAG, Accession NP_055279.1) is another GAM193 target gene, herein designated TARGET GENE. TINAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TINAG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TINAG BINDING SITE, designated SEQ ID:12710, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32381] Another function of GAM193 is therefore inhibition of Tubulointerstitial nephritis antigen (TINAG, Accession NP_055279.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TINAG.

[32382] Unc-51-like kinase 2 (c. elegans) (ULK2, Accession NP_055498.2) is another GAM193 target gene, herein designated TARGET GENE. ULK2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ULK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ULK2 BINDING SITE, designated SEQ ID:17181, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32383] Another function of GAM193 is therefore inhibition of Unc-51-like kinase 2 (c. elegans) (ULK2, Accession

NP_055498.2) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ULK2.

[32384] ZAK (Accession NP_598407.1) is another GAM193 target gene, herein designated TARGET GENE. ZAK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZAK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAK BINDING SITE, designated SEQ ID:7242, to the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, also designated SEQ ID:268.

[32385] Another function of GAM193 is therefore inhibition of ZAK (Accession NP_598407.1) . Accordingly, utilities of GAM193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAK.

[32386]

[32387] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 194 (GAM194), which modulates expression of respective target genes thereof, the function and utility of which target

genes is known in the art.

[32388] GAM194 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM194 was detected is described hereinabove with reference to Figs. 8-15.

[32389] GAM194 gene, herein designated GAM GENE, and GAM194 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[32390] GAM194 gene encodes a GAM194 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM194 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM194 precursor RNA is designated SEQ ID:40, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:40 is located at position 49043012 relative to chromosome 13.

[32391] GAM194 precursor RNA folds onto itself, forming GAM194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32392] GAM194 precursor RNA folds onto itself, forming GAM194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[32393] Nucleotide sequence of GAM194 precursor RNA, designated SEQ-ID: 40, and a schematic representation of a predicted secondary folding of GAM194 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[32394] An enzyme complex designated DICER COMPLEX, `dices` the GAM194 folded precursor RNA into GAM194 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM194 RNA is designated SEQ ID:350, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[32395] GAM194 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM194 target RNA, herein designated GAM TARGET RNA. GAM194 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[32396] GAM194 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM194 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM194 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated

that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM194 RNA may have a different number of target binding sites in untranslated regions of a GAM194 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[32397] The complementary binding of GAM194 RNA, herein designated GAM RNA, to target binding sites on GAM194 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM194 target RNA into GAM194 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32398] It is appreciated that GAM194 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM194 target genes. The mRNA of each one of this plurality of GAM194 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM194 RNA, herein designated GAM RNA, and which when bound by

GAM194 RNA causes inhibition of translation of respective one or more GAM194 target proteins.

[32399] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM194 gene, herein designated GAM GENE, on one or more GAM194 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32400] It is appreciated that specific functions and accordingly utilities of GAM194 correlate with, and may be deduced from, the identity of the target genes which GAM194 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32401]

[32402]

[32403] FLJ10716 (Accession NM_018191.2) is a GAM194 target gene, herein designated TARGET GENE. FLJ10716 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10716, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10716 BINDING SITE, designated SEQ ID:11429, to the nucleotide sequence of GAM194 RNA, herein designated GAM RNA, also designated SEQ ID:350.

[32404] A function of GAM194 is therefore inhibition of FLJ10716 (Accession NM_018191.2) . Accordingly, utilities of GAM194 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10716.

[32405]

[32406] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 195 (GAM195), which modulates expression of respective target genes thereof, the function and utility of which target

genes is known in the art.

[32407] GAM195 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM195 was detected is described hereinabove with reference to Figs. 8-15.

[32408] GAM195 gene, herein designated GAM GENE, and GAM195 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[32409] GAM195 gene encodes a GAM195 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM195 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM195 precursor RNA is designated SEQ ID:122, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:122 is located at position 39124959 relative to chromosome 4.

[32410] GAM195 precursor RNA folds onto itself, forming GAM195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32411] GAM195 precursor RNA folds onto itself, forming GAM195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[32412] Nucleotide sequence of GAM195 precursor RNA, designated SEQ-ID: 122, and a schematic representation of a predicted secondary folding of GAM195 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[32413] An enzyme complex designated DICER COMPLEX, `dices` the GAM195 folded precursor RNA into GAM195 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: B) nucleotide sequence of GAM195 RNA is designated SEQ ID:334, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[32414] GAM195 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM195 target RNA, herein designated GAM TARGET RNA. GAM195 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[32415] GAM195 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM195 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM195 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated

that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM195 RNA may have a different number of target binding sites in untranslated regions of a GAM195 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[32416] The complementary binding of GAM195 RNA, herein designated GAM RNA, to target binding sites on GAM195 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM195 target RNA into GAM195 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32417] It is appreciated that GAM195 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM195 target genes. The mRNA of each one of this plurality of GAM195 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM195 RNA, herein designated GAM RNA, and which when bound by

GAM195 RNA causes inhibition of translation of respective one or more GAM195 target proteins.

[32418] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM195 gene, herein designated GAM GENE, on one or more GAM195 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32419] It is appreciated that specific functions and accordingly utilities of GAM195 correlate with, and may be deduced from, the identity of the target genes which GAM195 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32420]

[32421]

[32422] Atpase inhibitory factor 1 (ATPIF1, Accession NP_835497.1) is a GAM195 target gene, herein designated TARGET GENE. ATPIF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ATPIF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATPIF1 BINDING SITE, designated SEQ ID:13146, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32423] A function of GAM195 is therefore inhibition of Atpase inhibitory factor 1 (ATPIF1, Accession NP_835497.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATPIF1.

[32424] Atpase inhibitory factor 1 (ATPIF1, Accession NP_057395.1) is another GAM195 target gene, herein designated TARGET GENE. ATPIF1 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by ATPIF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATPIF1 BINDING SITE, designated SEQ ID:13146, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32425] Another function of GAM195 is therefore inhibition of Atpase inhibitory factor 1 (ATPIF1, Accession NP_057395.1). Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATPIF1.

[32426] Atpase inhibitory factor 1 (ATPIF1, Accession NP_835498.1) is another GAM195 target gene, herein designated TARGET GENE. ATPIF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ATPIF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATPIF1 BINDING SITE, designated SEQ ID:13146, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32427] Another function of GAM195 is therefore inhibition of Atpase inhibitory factor 1 (ATPIF1, Accession NP_835498.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATPIF1.

[32428] Cat eye syndrome chromosome region, candidate 7 (CECR7, Accession XP_086803.1) is another GAM195 target gene, herein designated TARGET GENE. CECR7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CECR7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR7 BINDING SITE, designated SEQ ID:4000, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32429] Another function of GAM195 is therefore inhibition of Cat eye syndrome chromosome region, candidate 7 (CECR7, Accession XP_086803.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR7.

[32430] Desmocollin 1 (DSC1, Accession NP_004939.1) is another GAM195 target gene, herein designated TARGET GENE.

DSC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC1 BINDING SITE, designated SEQ ID:19861, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32431] Another function of GAM195 is therefore inhibition of Desmocollin 1 (DSC1, Accession NP_004939.1), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC1.

[32432] The function of DSC1 has been established by previous studies. The desmosome is a complex adhesive structure that plays a fundamental role in maintaining the strength and integrity of epithelial tissues. Central to this role are transmembrane glycoproteins that mediate cell- cell adhesion at the extracellular surface and interact with the cytoskeleton (via components of the desmosomal plaque), thus linking the intermediate filament networks of adja-

cent cells. Desmosomal glycoproteins comprise 2 distinct groups, the desmogleins and the desmocollins, both of which are members of the cadherin superfamily of Ca(2+)- dependent cell adhesion molecules. In the human, 2 types of desmocollins had been identified, symbolized DSC1 and DSC2 (OMIM Ref. No. 125645), and each occurs in 2 alternatively spliced forms (variants a and b) that have different cytoplasmic domains reflecting different interactions with components of the desmosomal plaque (Troyanovsky et al., 1993). King et al. (1993) isolated cDNA clones encoding a human desmocollin that is expressed in the more differentiated layers of human epidermis. This isoform has 53% amino acid identity with the previously isolated type 3 desmocollin, which is expressed in the basal layers of the epidermis. However, the N and C termini of the mature proteins are more highly conserved. Using a panel of somatic cell hybrids, King et al. (1993) assigned the DSC1 gene to chromosome 18, where the DSC2 gene and the 3 desmoglein genes (DSG1, 125670; DSG2, 125671; DSG3, 169615) had previously been mapped.

[32433]

[32434] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[32435] King, I. A.; Arnemann, J.; Spurr, N. K.; Buxton, R. S. : Cloning of the cDNA (DSC1) coding for human type 1 desmocollin and its assignment to chromosome 18. Genomics 18: 185- 194, 1993. ; and

[32436] Troyanovsky, S. M.; Eshkind, L. G.; Troyanovsky, R. B.; Leube, R. E.; Franke, W. W. : Contributions of cytoplasmic domains of desmosomal cadherins to desmosome assembly and intermediate.

[32437] Further studies establishing the function and utilities of DSC1 are found in John Hopkins OMIM database record ID 125643, and in cited publications listed in Table 5, which are hereby incorporated by reference.Desmocollin 1 (DSC1, Accession NP_077739.1) is another GAM195 target gene, herein designated TARGET GENE. DSC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC1 BINDING SITE, designated SEQ ID:19861, to the nucleotide sequence of GAM195 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:334.

[32438] Another function of GAM195 is therefore inhibition of Desmocollin 1 (DSC1, Accession NP_077739.1), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC1.

[32439] The function of DSC1 has been established by previous studies. The desmosome is a complex adhesive structure that plays a fundamental role in maintaining the strength and integrity of epithelial tissues. Central to this role are transmembrane glycoproteins that mediate cell- cell adhesion at the extracellular surface and interact with the cytoskeleton (via components of the desmosomal plaque), thus linking the intermediate filament networks of adjacent cells. Desmosomal glycoproteins comprise 2 distinct groups, the desmogleins and the desmocollins, both of which are members of the cadherin superfamily of Ca(2+)- dependent cell adhesion molecules. In the human, 2 types of desmocollins had been identified, symbolized DSC1 and DSC2 (OMIM Ref. No. 125645), and each occurs in 2 alternatively spliced forms (variants a and b) that have different cytoplasmic domains reflecting dif-

ferent interactions with components of the desmosomal plaque (Troyanovsky et al., 1993). King et al. (1993) isolated cDNA clones encoding a human desmocollin that is expressed in the more differentiated layers of human epidermis. This isoform has 53% amino acid identity with the previously isolated type 3 desmocollin, which is expressed in the basal layers of the epidermis. However, the N and C termini of the mature proteins are more highly conserved. Using a panel of somatic cell hybrids, King et al. (1993) assigned the DSC1 gene to chromosome 18, where the DSC2 gene and the 3 desmoglein genes (DSG1, 125670; DSG2, 125671; DSG3, 169615) had previously been mapped.

[32440]

[32441] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32442] King, I. A.; Arnemann, J.; Spurr, N. K.; Buxton, R. S. : Cloning of the cDNA (DSC1) coding for human type 1 desmocollin and its assignment to chromosome 18. Genomics 18: 185- 194, 1993. ; and

[32443] Troyanovsky, S. M.; Eshkind, L. G.; Troyanovsky, R. B.; Leube, R. E.; Franke, W. W. : Contributions of cytoplasmic

domains of desmosomal cadherins to desmosome assembly and intermediate.

[32444] Further studies establishing the function and utilities of DSC1 are found in John Hopkins OMIM database record ID 125643, and in cited publications listed in Table 5, which are hereby incorporated by reference.Fibroblast growth factor 2 (basic) (FGF2, Accession NP_001997.3) is another GAM195 target gene, herein designated TARGET GENE. FGF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FGF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF2 BINDING SITE, designated SEQ ID:18914, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32445] Another function of GAM195 is therefore inhibition of Fibroblast growth factor 2 (basic) (FGF2, Accession NP_001997.3), a gene which the Basic fibroblast growth factor 2; is mitogenic, angiogenic, and neurotrophic factor. Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF2.

[32446] The function of FGF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM36.1.FLJ12787 (Accession NP_115551.1) is another GAM195 target gene, herein designated TARGET GENE. FLJ12787 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12787, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12787 BINDING SITE, designated SEQ ID:1139, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32447] Another function of GAM195 is therefore inhibition of FLJ12787 (Accession NP_115551.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12787.

[32448] FLJ20086 (Accession NP_060131.1) is another GAM195 target gene, herein designated TARGET GENE. FLJ20086 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20086, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20086 BINDING SITE, designated SEQ ID:11844, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32449] Another function of GAM195 is therefore inhibition of FLJ20086 (Accession NP_060131.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20086.

[32450] FLJ20727 (Accession NP_060414.2) is another GAM195 target gene, herein designated TARGET GENE. FLJ20727 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20727, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20727 BINDING SITE, designated SEQ ID:18778, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32451] Another function of GAM195 is therefore inhibition of FLJ20727 (Accession NP_060414.2) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20727.

[32452] FLJ21269 (Accession NP_079383.1) is another GAM195 target gene, herein designated TARGET GENE. FLJ21269 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21269, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21269 BINDING SITE, designated SEQ ID:2872, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32453] Another function of GAM195 is therefore inhibition of FLJ21269 (Accession NP_079383.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21269.

[32454] FLJ23749 (Accession NP_689484.1) is another GAM195 target gene, herein designated TARGET GENE. FLJ23749 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23749, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ23749 BINDING SITE, designated SEQ ID:1179, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32455] Another function of GAM195 is therefore inhibition of FLJ23749 (Accession NP_689484.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23749.

[32456] Gap junction protein, beta 2, 26kda (connexin 26) (GJB2, Accession NP_003995.1) is another GAM195 target gene, herein designated TARGET GENE. GJB2 BINDING SITE1 and GJB2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GJB2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GJB2 BINDING SITE1 and GJB2 BINDING SITE2, designated SEQ ID:18295 and SEQ ID:11557 respectively, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32457] Another function of GAM195 is therefore inhibition of Gap junction protein, beta 2, 26kda (connexin 26) (GJB2, Ac-

cession NP_003995.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GJB2.

[32458] Glypican 3 (GPC3, Accession NP_004475.1) is another GAM195 target gene, herein designated TARGET GENE. GPC3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPC3 BINDING SITE, designated SEQ ID:10408, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32459] Another function of GAM195 is therefore inhibition of Glypican 3 (GPC3, Accession NP_004475.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPC3.

[32460] Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_061128.1) is another GAM195 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA

encoded by KCNJ16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:3607, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32461] Another function of GAM195 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_061128.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[32462] Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733937.1) is another GAM195 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by KCNJ16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:3607, to the nucleotide sequence of

GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32463] Another function of GAM195 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733937.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[32464] Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733938.1) is another GAM195 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by KCNJ16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:3607, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32465] Another function of GAM195 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733938.1) . Accordingly,

utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[32466] KIAA0173 (Accession NP_055455.1) is another GAM195 target gene, herein designated TARGET GENE. KIAA0173 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0173, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0173 BINDING SITE, designated SEQ ID:8331, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32467] Another function of GAM195 is therefore inhibition of KIAA0173 (Accession NP_055455.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0173.

[32468] KIAA1954 (Accession XP_085375.4) is another GAM195 target gene, herein designated TARGET GENE. KIAA1954 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1954, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1954 BINDING SITE, designated SEQ ID:16208, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32469] Another function of GAM195 is therefore inhibition of KIAA1954 (Accession XP_085375.4) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1954.

[32470] KIAA1972 (Accession XP_166279.1) is another GAM195 target gene, herein designated TARGET GENE. KIAA1972 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1972 BINDING SITE, designated SEQ ID:3715, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32471] Another function of GAM195 is therefore inhibition of KIAA1972 (Accession XP_166279.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA1972.

[32472] LOC143891 (Accession XP_084661.3) is another GAM195 target gene, herein designated TARGET GENE. LOC143891 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC143891, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143891 BINDING SITE, designated SEQ ID:17605, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32473] Another function of GAM195 is therefore inhibition of LOC143891 (Accession XP_084661.3) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143891.

[32474] LOC145453 (Accession XP_085120.1) is another GAM195 target gene, herein designated TARGET GENE. LOC145453 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145453, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC145453 BINDING SITE, designated SEQ ID:1564, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32475] Another function of GAM195 is therefore inhibition of LOC145453 (Accession XP_085120.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145453.

[32476] LOC146443 (Accession XP_085461.6) is another GAM195 target gene, herein designated TARGET GENE. LOC146443 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146443, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146443 BINDING SITE, designated SEQ ID:4001, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32477] Another function of GAM195 is therefore inhibition of LOC146443 (Accession XP_085461.6) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC146443.

[32478] LOC151057 (Accession XP_097998.1) is another GAM195 target gene, herein designated TARGET GENE. LOC151057 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151057, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151057 BINDING SITE, designated SEQ ID:13828, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32479] Another function of GAM195 is therefore inhibition of LOC151057 (Accession XP_097998.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151057.

[32480] LOC284231 (Accession XP_208184.1) is another GAM195 target gene, herein designated TARGET GENE. LOC284231 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284231, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC284231 BINDING SITE, designated SEQ ID:4846, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32481] Another function of GAM195 is therefore inhibition of LOC284231 (Accession XP_208184.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284231.

[32482] LOC284396 (Accession XP_211452.1) is another GAM195 target gene, herein designated TARGET GENE. LOC284396 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284396, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284396 BINDING SITE, designated SEQ ID:13621, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32483] Another function of GAM195 is therefore inhibition of LOC284396 (Accession XP_211452.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284396.

[32484] LOC284927 (Accession XP_211689.1) is another GAM195 target gene, herein designated TARGET GENE. LOC284927 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284927, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284927 BINDING SITE, designated SEQ ID:1922, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32485] Another function of GAM195 is therefore inhibition of LOC284927 (Accession XP_211689.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284927.

[32486] LOC285953 (Accession XP_209820.1) is another GAM195 target gene, herein designated TARGET GENE. LOC285953 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285953, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285953 BINDING SITE, designated SEQ ID:2646, to

the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32487] Another function of GAM195 is therefore inhibition of LOC285953 (Accession XP_209820.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285953.

[32488] LOC286470 (Accession XP_212325.1) is another GAM195 target gene, herein designated TARGET GENE. LOC286470 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286470, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286470 BINDING SITE, designated SEQ ID:1532, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32489] Another function of GAM195 is therefore inhibition of LOC286470 (Accession XP_212325.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286470.

[32490] LOC339778 (Accession XP_295061.1) is another GAM195

target gene, herein designated TARGET GENE. LOC339778 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339778, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339778 BINDING SITE, designated SEQ ID:17583, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32491] Another function of GAM195 is therefore inhibition of LOC339778 (Accession XP_295061.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339778.

[32492] Metallothionein-like 5, testis-specific (tesmin) (MTL5, Accession NP_004914.1) is another GAM195 target gene, herein designated TARGET GENE. MTL5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTL5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTL5 BINDING SITE, designated SEQ ID:16748, to the nucleotide sequence of

GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32493] Another function of GAM195 is therefore inhibition of Metallothionein-like 5, testis-specific (tesmin) (MTL5, Accession NP_004914.1), a gene which functions in metal homeostasis and protects against heavy- metal toxicity. Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTL5.

[32494] The function of MTL5 has been established by previous studies. By randomized RT- PCR on mRNA from mouse tissues, Sugihara et al. (1999) isolated a testis- specific transcript, which they called TF1. By screening a human testis cDNA library with TF1 as a probe, they cloned a novel cDNA, which they called testis- specific metallothionein- like protein, or tesmin. Tesmin encodes a predicted cysteine- rich, 295- amino acid protein that is 76.3% homologous to mouse tesmin. Sequence analysis revealed the presence of 2 metallothionein (MT)- like motifs. MT expression has been observed to be higher in testes than in liver tissue (Salehi- Ashtiani et al., 1993) and to be actively expressed in a developmentally regulated fashion in mouse male germ cells (De et al., 1991).

Tesmin shows no homology to other testis- specific genes. In situ hybridization of adult mouse testicular sections showed that expression of tesmin is restricted to spermatocytes. RT- PCR analysis on testicular transcripts from mice showed that expression of tesmin occurs as early as day 8 and coincides with the entry of germ cells in meiosis.

[32495]

[32496] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32497] De, S. K.; Enders, G. C.; Andrews, G. K. : High levels of metallothionein messenger RNAs in male germ cells of the adult mouse. Molec. Endocr. 5: 628- 636, 1991. ; and

[32498] Salehi- Ashtiani, K.; Widrow, R. J.; Markert, C. L.; Goldberg, E. : Testis- specific expression of a metallothionein I- driven transgene correlates with undermethylation of the locus in te.

[32499] Further studies establishing the function and utilities of MTL5 are found in John Hopkins OMIM database record ID 604374, and in cited publications listed in Table 5, which are hereby incorporated by reference.Neuronal cell adhesion molecule (NRCAM, Accession NP_005001.1) is an-

other GAM195 target gene, herein designated TARGET GENE. NRCAM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NR-CAM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRCAM BINDING SITE, designated SEQ ID:1144, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32500] Another function of GAM195 is therefore inhibition of Neuronal cell adhesion molecule (NRCAM, Accession NP_005001.1), a gene which functions as a cell surface protein and belongs to the immunoglobulin superfamily. Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRCAM.

[32501] The function of NRCAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM148.1.NUCKS (Accession NP_073568.1) is another GAM195 target gene, herein designated TARGET GENE. NUCKS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NUCKS, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUCKS BINDING SITE, designated SEQ ID:19959, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32502] Another function of GAM195 is therefore inhibition of NUCKS (Accession NP_073568.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUCKS.

[32503] Oligophrenin 1 (OPHN1, Accession NP_002538.1) is another GAM195 target gene, herein designated TARGET GENE. OPHN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OPHN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OPHN1 BINDING SITE, designated SEQ ID:1488, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32504] Another function of GAM195 is therefore inhibition of Oligophrenin 1 (OPHN1, Accession NP_002538.1) . Accordingly, utilities of GAM195 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with OPHN1.

[32505] P450RAI-2 (Accession NP_063938.1) is another GAM195 target gene, herein designated TARGET GENE. P450RAI-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P450RAI-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P450RAI-2 BINDING SITE, designated SEQ ID:14707, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32506] Another function of GAM195 is therefore inhibition of P450RAI-2 (Accession NP_063938.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P450RAI-2.

[32507] PDIP1 (Accession XP_170803.1) is another GAM195 target gene, herein designated TARGET GENE. PDIP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PDIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of PDIP1 BINDING SITE, designated SEQ ID:8489, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32508] Another function of GAM195 is therefore inhibition of PDIP1 (Accession XP_170803.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDIP1.

[32509] PDIP1 (Accession NP_849194.1) is another GAM195 target gene, herein designated TARGET GENE. PDIP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PDIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDIP1 BINDING SITE, designated SEQ ID:8489, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32510] Another function of GAM195 is therefore inhibition of PDIP1 (Accession NP_849194.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDIP1.

[32511] Plasminogen-like (PLGL, Accession NP_002656.1) is an-

other GAM195 target gene, herein designated TARGET GENE. PLGL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLGL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PLGL BINDING SITE, designated SEQ ID:2694, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32512] Another function of GAM195 is therefore inhibition of Plasminogen-like (PLGL, Accession NP_002656.1), a gene which is necessary for extracellular matrix destruction. Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLGL.

[32513] The function of PLGL has been established by previous studies. Frank et al. (1989) used a plasminogen probe encoding kringles 1- 3 to detect homologous loci on human chromosomes 6 and 2 by somatic cell hybrid analysis. Regional localization by in situ hybridization placed the loci at 6q26- q27 and 2p11- q11. Further analysis by varying washing stringencies of hybridization filters showed greater homology with the chromosome 6 locus than with

the chromosome 2 locus. The results were interpreted as confirming localization of the plasminogen gene (OMIM Ref. No. 173350) to chromosome 6 and indicating that a homologous sequence of unknown identity is located on chromosome 2. The sequence on chromosome 2 may represent a pseudogene or it may be an unidentified kringle-containing protein. Magnaghi et al. (1995), in their Figure 3, presented a restriction map showing the orientation of the PLG and PLGL genes to each other and to the LPA gene (OMIM Ref. No. 152200) and the LPA- like gene.

[32514]

[32515] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32516] Frank, S. L.; Klisak, I.; Sparkes, R. S.; Lusis, A. J. : A gene homologous to plasminogen located on human chromosome 2q11- p11. Genomics 4: 449- 451, 1989. ; and

[32517] Magnaghi, P.; Agazzi, A.; Semino, O.; Ferrari, M.; Barbui, T.; D'Angelo, A.; Taramelli, R. : A recombination event in the closely linked plasminogen and apolipoprotein(a) gene loci. Cli.

[32518] Further studies establishing the function and utilities of PLGL are found in John Hopkins OMIM database record ID

173340, and in cited publications listed in Table 5, which are hereby incorporated by reference.RNF41 (Accession NP_005776.1) is another GAM195 target gene, herein designated TARGET GENE. RNF41 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF41, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF41 BINDING SITE, designated SEQ ID:14646, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32519] Another function of GAM195 is therefore inhibition of RNF41 (Accession NP_005776.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF41.

[32520] Sh3 and multiple ankyrin repeat domains 2 (SHANK2, Accession NP_036441.1) is another GAM195 target gene, herein designated TARGET GENE. SHANK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SHANK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of SHANK2 BINDING SITE, designated SEQ ID:11675, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32521] Another function of GAM195 is therefore inhibition of Sh3 and multiple ankyrin repeat domains 2 (SHANK2, Accession NP_036441.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHANK2.

[32522] Solute carrier family 38, member 2 (SLC38A2, Accession NP_061849.2) is another GAM195 target gene, herein designated TARGET GENE. SLC38A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC38A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC38A2 BINDING SITE, designated SEQ ID:451, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32523] Another function of GAM195 is therefore inhibition of Solute carrier family 38, member 2 (SLC38A2, Accession NP_061849.2), a gene which is an amino acid transporter.

Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC38A2.

[32524] The function of SLC38A2 has been established by previous studies. . Sugawara et al. (2000) cloned a rat skeletal muscle Ata2 cDNA. The deduced Ata2 protein shares 55% sequence identity with the rat glutamine transporter GlnT (Ata1). When expressed in mammalian cells, Ata2 mediated sodium- dependent transport of MeAIB. The Ata2 transporter was specific for neutral amino acids. It was pH- sensitive and lithium- intolerant. The sodium:amino acid stoichiometry was 1:1. When expressed in Xenopus oocytes, transport of neutral amino acids via Ata2 was associated with inward currents. The substrate- induced current was sodium- dependent and pH- sensitive. By screening human fetal brain cDNAs for the potential to encode large proteins, Nagase et al. (2000) isolated a partial ATA2 cDNA, which they called KIAA1382, that lacks 5-prime coding sequence. The deduced 462- amino acid ATA2 partial protein shares 57% amino acid sequence identity with the human transporter protein g17 across 98% of its length. RT- PCR followed by ELISA detected ATA2 expression in all human tissues examined, with the

highest level in adult brain. Within the brain, ATA2 expression was found in all regions tested, with the highest level in the subthalamic nucleus.

[32525]

[32526] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32527] Nagase, T.; Kikuno, R.; Ishikawa, K.; Hirosawa, M.; Ohara, O. : Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro. DNA Res. 7: 65- 73, 2000. ; and

[32528] Sugawara, M.; Nakanishi, T.; Fei, Y.- J.; Huang, W.; Ganapathy, M. E.; Leibach, F. H.; Ganapathy, V. : Cloning of an amino acid transporter with functional characteristics and tissue exp.

[32529] Further studies establishing the function and utilities of SLC38A2 are found in John Hopkins OMIM database record ID 605180, and in cited publications listed in Table 5, which are hereby incorporated by reference.Tripartite motif-containing 9 (TRIM9, Accession NP_443210.1) is another GAM195 target gene, herein designated TARGET GENE. TRIM9 BINDING SITE is a target binding site found

in the 3` untranslated region of multiple transcripts of mRNA encoded by TRIM9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM9 BINDING SITE, designated SEQ ID:10464, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32530] Another function of GAM195 is therefore inhibition of Tripartite motif-containing 9 (TRIM9, Accession NP_443210.1), a gene which may function as a positive regulator for mannosylphosphate transferase and is required to mediate mannosylphosphate transfer in both the core and outer chain portions of n- linked. oligosaccharides. Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM9.

[32531] The function of TRIM9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Was protein family, member 3 (WASF3, Accession NP_006637.2) is another GAM195 target gene, herein designated TARGET GENE. WASF3 BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by WASF3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WASF3 BINDING SITE, designated SEQ ID:12232, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32532] Another function of GAM195 is therefore inhibition of Was protein family, member 3 (WASF3, Accession NP_006637.2), a gene which stimulates actin polymerization. Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WASF3.

[32533] The function of WASF3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.2.Zinc finger protein 2 (a1-5) (ZNF2, Accession NP_066574.1) is another GAM195 target gene, herein designated TARGET GENE. ZNF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF2 BINDING SITE, designated SEQ ID:8545, to the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, also designated SEQ ID:334.

[32534] Another function of GAM195 is therefore inhibition of Zinc finger protein 2 (a1-5) (ZNF2, Accession NP_066574.1) . Accordingly, utilities of GAM195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF2.

[32535]

[32536] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 196 (GAM196), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32537] GAM196 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM196 was detected is described hereinabove with reference to Figs. 8-15.

[32538] GAM196 gene, herein designated GAM GENE, and GAM196 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[32539] GAM196 gene encodes a GAM196 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM196 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM196 precursor RNA is designated SEQ ID:67, and is provided hereinbelow with reference to the sequence listing part.

[32540] GAM196 precursor RNA folds onto itself, forming GAM196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32541] GAM196 precursor RNA folds onto itself, forming GAM196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first

half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[32542] Nucleotide sequence of GAM196 precursor RNA, designated SEQ-ID: 67, and a schematic representation of a predicted secondary folding of GAM196 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[32543] An enzyme complex designated DICER COMPLEX, `dices` the GAM196 folded precursor RNA into GAM196 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM196 RNA is designated SEQ ID:209, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[32544] GAM196 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM196 target RNA, herein designated GAM TARGET RNA. GAM196 tar-

get RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[32545] GAM196 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM196 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM196 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM196 RNA may have a different number of target binding sites in untranslated regions of a GAM196 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[32546] The complementary binding of GAM196 RNA, herein designated GAM RNA, to target binding sites on GAM196 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM196 target RNA into GAM196 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32547] It is appreciated that GAM196 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM196 target genes. The mRNA of each one of this plurality of GAM196 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM196 RNA, herein designated GAM RNA, and which when bound by GAM196 RNA causes inhibition of translation of respective one or more GAM196 target proteins.

[32548] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM196 gene, herein designated GAM GENE, on one or more GAM196 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the back-

ground section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32549] It is appreciated that specific functions and accordingly utilities of GAM196 correlate with, and may be deduced from, the identity of the target genes which GAM196 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32550]

[32551]

[32552] Adaptor-related protein complex 1, mu 1 subunit (AP1M1, Accession NM_032493.2) is a GAM196 target gene, herein designated TARGET GENE. AP1M1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AP1M1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1M1 BINDING SITE, designated SEQ ID:18556, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32553] A function of GAM196 is therefore inhibition of Adaptor-related protein complex 1, mu 1 subunit (AP1M1, Accession NM_032493.2), a gene which promotes the formation of clathrin- coated pits and vesicles. Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1M1.

[32554] The function of AP1M1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Adaptor-related protein complex 1, sigma 1 subunit (AP1S1, Accession NM_057089.1) is another GAM196 target gene, herein designated TARGET GENE. AP1S1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1S1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1S1 BINDING SITE, designated

SEQ ID:1717, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32555] Another function of GAM196 is therefore inhibition of Adaptor-related protein complex 1, sigma 1 subunit (AP1S1, Accession NM_057089.1), a gene which promotes the formation of clathrin- coated pits and vesicles. Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1S1.

[32556] The function of AP1S1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Chloride channel 6 (CLCN6, Accession NM_021735.1) is another GAM196 target gene, herein designated TARGET GENE. CLCN6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLCN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLCN6 BINDING SITE, designated SEQ ID:17159, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32557] Another function of GAM196 is therefore inhibition of Chloride channel 6 (CLCN6, Accession NM_021735.1), a gene which is a voltage- gated chloride channel. Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN6.

[32558] The function of CLCN6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.FLJ11722 (Accession NM_024970.1) is another GAM196 target gene, herein designated TARGET GENE. FLJ11722 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11722, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11722 BINDING SITE, designated SEQ ID:1140, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32559] Another function of GAM196 is therefore inhibition of FLJ11722 (Accession NM_024970.1) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ11722.

[32560] FLJ14107 (Accession NM_025026.1) is another GAM196 target gene, herein designated TARGET GENE. FLJ14107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14107 BINDING SITE, designated SEQ ID:17744, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32561] Another function of GAM196 is therefore inhibition of FLJ14107 (Accession NM_025026.1) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14107.

[32562] FLJ14280 (Accession NM_024886.1) is another GAM196 target gene, herein designated TARGET GENE. FLJ14280 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14280, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ14280 BINDING SITE, designated SEQ ID:2799, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32563] Another function of GAM196 is therefore inhibition of FLJ14280 (Accession NM_024886.1) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14280.

[32564] FLJ23447 (Accession NM_024825.1) is another GAM196 target gene, herein designated TARGET GENE. FLJ23447 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ23447, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23447 BINDING SITE, designated SEQ ID:7447, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32565] Another function of GAM196 is therefore inhibition of FLJ23447 (Accession NM_024825.1) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23447.

[32566] KIAA1691 (Accession XM_166523.1) is another GAM196 target gene, herein designated TARGET GENE. KIAA1691 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1691, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1691 BINDING SITE, designated SEQ ID:14970, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32567] Another function of GAM196 is therefore inhibition of KIAA1691 (Accession XM_166523.1) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1691.

[32568] KIAA1940 (Accession XM_086981.2) is another GAM196 target gene, herein designated TARGET GENE. KIAA1940 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1940, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1940 BINDING SITE, designated SEQ ID:12635, to the

nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32569] Another function of GAM196 is therefore inhibition of KIAA1940 (Accession XM_086981.2) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1940.

[32570] LOC138128 (Accession) is another GAM196 target gene, herein designated TARGET GENE. LOC138128 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC138128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC138128 BINDING SITE, designated SEQ ID:16109, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32571] Another function of GAM196 is therefore inhibition of LOC138128 (Accession) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138128.

[32572] LOC149657 (Accession XM_097702.2) is another GAM196

target gene, herein designated TARGET GENE. LOC149657 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149657, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149657 BINDING SITE, designated SEQ ID:10864, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32573] Another function of GAM196 is therefore inhibition of LOC149657 (Accession XM_097702.2) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149657.

[32574] LOC150837 (Accession XM_087019.1) is another GAM196 target gene, herein designated TARGET GENE. LOC150837 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150837, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150837 BINDING SITE, designated SEQ ID:9457, to the nucleotide sequence of GAM196 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:209.

[32575] Another function of GAM196 is therefore inhibition of LOC150837 (Accession XM_087019.1) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150837.

[32576] LOC151556 (Accession) is another GAM196 target gene, herein designated TARGET GENE. LOC151556 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151556, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151556 BINDING SITE, designated SEQ ID:2480, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32577] Another function of GAM196 is therefore inhibition of LOC151556 (Accession) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151556.

[32578] LOC254016 (Accession) is another GAM196 target gene, herein designated TARGET GENE. LOC254016 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC254016, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254016 BINDING SITE, designated SEQ ID:17846, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32579] Another function of GAM196 is therefore inhibition of LOC254016 (Accession) . Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254016.

[32580] Nebulin-related anchoring protein (Nrap, Accession NM_006175.2) is another GAM196 target gene, herein designated TARGET GENE. Nrap BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Nrap, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Nrap BINDING SITE, designated SEQ ID:5880, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32581] Another function of GAM196 is therefore inhibition of Nebulin-related anchoring protein (Nrap, Accession NM_006175.2), a gene which performs an anchoring function to link the terminal actin filaments of myofibrils to protein complexes located beneath the sarcolemma. Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Nrap.

[32582] The function of Nrap and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Shb (src homology 2 domain containing) adaptor protein b (SHB, Accession NM_003028.1) is another GAM196 target gene, herein designated TARGET GENE. SHB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SHB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SHB BINDING SITE, designated SEQ ID:5017, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32583] Another function of GAM196 is therefore inhibition of Shb

(src homology 2 domain containing) adaptor protein b (SHB, Accession NM_003028.1), a gene which is an adaptor protein, mediates the interaction of other proteins. Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHB.

[32584] The function of SHB has been established by previous studies. Many proteins involved in the regulation of cellular proliferation contain sequence motifs named SH2 and SH3 (Pawson and Gish, 1992). These domains mediate interaction with other proteins; the SH2 domain interacts with tyrosine phosphorylation sites, while SH3 domains interact with proline- rich sequences. Many signal transduction pathways involve the induction of the formation of complexes of proteins such as growth factor receptors, adaptor proteins, and target enzymes through SH2 and SH3 interactions. Adaptor proteins are molecules with multiple protein interaction motifs that do not appear to have catalytic activity of their own but mediate the interaction of other proteins. The SHB gene encodes 2 such adaptor proteins (from 2 different start methionines) of 67 and 56 kD (Welsh et al., 1994). By PCR analysis of a somatic cell hybrid mapping panel, Yulug et al. (1994)

mapped the SHB gene to chromosome 9. By fluorescence in situ hybridization, they regionalized the gene to 9p12-p11.

[32585]

[32586] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32587] Welsh, M.; Mares, J.; Karlsson, T.; Lavergne, C.; Breant, B.; Claesson- Welsh, L. : Shb is a ubiquitously expressed Src homology 2 protein. Oncogene 9: 19- 27, 1994. ; and

[32588] Yulug, I. G.; Hillermann, R.; Fisher, E. M. C. : The SHB adaptor protein maps to human chromosome 9. Genomics 24: 615- 617, 1994.

[32589] Further studies establishing the function and utilities of SHB are found in John Hopkins OMIM database record ID 600314, and in cited publications listed in Table 5, which are hereby incorporated by reference.TSLP (Accession NM_033035.2) is another GAM196 target gene, herein designated TARGET GENE. TSLP BINDING SITE is a target binding site found in the 5` untranslated region of multi-ple transcripts of mRNA encoded by TSLP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of TSLP BINDING SITE, designated SEQ ID:8451, to the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, also designated SEQ ID:209.

[32590] Another function of GAM196 is therefore inhibition of TSLP (Accession NM_033035.2), a gene which may contribute directly to the activation of Langerhans cells and inhibit apoptosis. Accordingly, utilities of GAM196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSLP.

[32591] The function of TSLP has been established by previous studies. By EST and genomic database screening for sequences similar to IL7, followed by screening a lung fibroblast sarcoma cDNA library, Reche et al. (2001) obtained a cDNA encoding TSLP. The deduced 159- amino acid protein, which is only 43% identical to mouse Tslp, contains a 28- residue signal sequence, 6 cysteines, and 2 N- glycosylation sites. SDS- PAGE analysis showed expression of a 23- kD protein, larger than the predicted 15 kD, suggesting that TSLP is glycosylated. PCR analysis of a panel of cDNA libraries and cultured cell lines indicated that expression of a 1.3- kb TSLP transcript may be restricted to a few lung libraries. Reche et al. (2001) also

identified TSLP receptor, which is composed of TSLPR (CRLF2; 300357) and IL7R (OMIM Ref. No. 146661) subunits. Dendritic cells (DCs) and monocytes coexpress IL7R and TSLPR. Quentmeier et al. (2001) also cloned and characterized TSLP. They noted the presence of 7 basic C- terminal amino acids (KKRRKRK) in the protein and that 6 of the 7 cysteines in the mouse protein (those involved in disulfide bond formation) are conserved in human, whereas the sites for N- glycosylation are distinct. Northern blot analysis revealed wide expression of an approximately 1.1- kb transcript, with highest levels in heart, liver, testis, and prostate. Reche et al. (2001) showed that incubation of DCs or monocytes with TSLP enhanced the expression of CCL17 (OMIM Ref. No. 601520), CCL18 (OMIM Ref. No. 603757), CCL22 (OMIM Ref. No. 602957), and CCL19 (OMIM Ref. No. 602227). IL7, on the other hand, induced expression of CCL17, CCL22, and CCL19, but also CXCL8 (OMIM Ref. No. 146930), CXCL7 (OMIM Ref. No. 121010), CXCL5 (OMIM Ref. No. 600324), CXCL1 (OMIM Ref. No. 155730), CXCL2 (OMIM Ref. No. 139110), and CXCL3 (OMIM Ref. No. 139111). Functional analysis indicated that TSLP enhances the DC maturation process, as evidenced by upregulation of DC markers and costimu-

latory molecules and stronger T- cell proliferation. By screening myeloid cell lines, Quentmeier et al. (2001) established that an acute myeloid leukemia line, MUTZ- 3, responds by proliferating in response to TSLP. TSLP also inhibited apoptosis in these cells. Proliferation in response to TSLP could not be attributed to the production of other growth factors tested and could be inhibited by relatively high concentrations of anti- IL7R. TSLP, like IL7, stimulated phosphorylation of STAT5 (OMIM Ref. No. 601511), but unlike IL7, it did not activate JAK3 (OMIM Ref. No. 600173). TSLP did not phosphorylate mitogen- activated protein kinases (e.g., ERK1; 601795). By flow cytometric analysis, Soumelis et al. (2002) showed that TSLP- activated DCs (TSLP- DCs) express higher levels of HLA- DR and DCLAMP (OMIM Ref. No. 605883) than do nonactivated or IL7- activated DCs, and that TSLP- DCs induce marked proliferation and expansion of allogeneic naive CD4 (OMIM Ref. No. 186940)- positive T cells. Quantitative mRNA screening and ELISA analysis showed that TSLP- DCs do not produce detectable proinflammatory cytokines, but do produce high levels of TARC (CCL17) and MDC (CCL22) chemokines, which preferentially attract CCR4 (OMIM Ref. No. 604836)- expressing Th2 lympho-

cytes. TSLP- DCs induced CD4 cells to produce high amounts of IL13 (OMIM Ref. No. 147683), IL5 (OMIM Ref. No. 147850), and the proinflammatory cytokine tumor necrosis factor (TNF; 191160), but only low amounts of IL10 (OMIM Ref. No. 124092) and gamma- interferon (IFNG; 147570). RT- PCR analysis did not detect TSLP in most hemopoietic cells, the exception being mast cells. Keratinocytes, epithelial cells, smooth muscle cells, and lung fibroblasts also expressed high levels of TSLP. Within tonsils, highest levels were in crypt epithelial cells. Soumelis et al. (2002) suggested that TSLP may contribute to constitutive inflammation in this tissue and sporadic inflammation in squamous epithelium. Immunohistochemical analysis of allergic inflammatory tissue showed high expression of TSLP in keratinocytes of acute and chronic atopic dermatitis lesions, but no expression in normal skin. Strong TSLP expression in atopic dermatitis was associated with the disappearance of langerin (OMIM Ref. No. 604862)- positive Langerhans cells within the epidermis and the concurrent appearance of many DCLAMP- activated DCs within the dermis, many of which expressed langerin. Soumelis et al. (2002) proposed that TSLP expression by keratinocytes in atopic dermatitis le-

sions may contribute directly to the activation of Langerhans cells, which may migrate into the dermis and then the draining lymph nodes where they can prime allergen-specific Th2 responses.

[32592]

[32593] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32594] Reche, P. A.; Soumelis, V.; Gorman, D. M.; Clifford, T.; Liu, M.; Travis, M.; Zurawski, S. M.; Johnston, J.; Liu, Y.- J.; Spits, H.; de Waal Malefyt, R.; Kastelein, R. A.; Bazan, J. F. : Human thymic stromal lymphopoietin preferentially stimulates myeloid cells. J. Immun. 167: 336- 343, 2001. ; and

[32595] Soumelis, V.; Reche, P. A.; Kanzler, H.; Yuan, W.; Edward, G.; Homey, B.; Gilliet, M.; Ho, S.; Antonenko, S.; Lauerma, A.; Smith, K.; Gorman, D.; Zurawski, S.; Abrams, J.; Menon, S.; Mc.

[32596] Further studies establishing the function and utilities of TSLP are found in John Hopkins OMIM database record ID 607003, and in cited publications listed in Table 5, which are hereby incorporated by reference.

[32597] Fig. 8 further provides a conceptual description of a novel

bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 281 (GAM281), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[32598] GAM281 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM281 was detected is described hereinabove with reference to Figs. 8-15.

[32599] GAM281 gene, herein designated GAM GENE, and GAM281 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[32600] GAM281 gene encodes a GAM281 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM281 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM281 precursor RNA is designated SEQ ID:164, and is provided hereinbelow with reference to the sequence listing part.

[32601] GAM281 precursor RNA folds onto itself, forming GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin

structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[32602] GAM281 precursor RNA folds onto itself, forming GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[32603] Nucleotide sequence of GAM281 precursor RNA, designated SEQ-ID: 164, and a schematic representation of a predicted secondary folding of GAM281 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[32604] An enzyme complex designated DICER COMPLEX, `dices` the GAM281 folded precursor RNA into GAM281 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: B) nucleotide sequence of GAM281 RNA is designated SEQ ID:278, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[32605] GAM281 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM281 target RNA, herein designated GAM TARGET RNA. GAM281 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[32606] GAM281 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM281 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM281 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target

binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM281 RNA may have a different number of target binding sites in untranslated regions of a GAM281 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[32607] The complementary binding of GAM281 RNA, herein designated GAM RNA, to target binding sites on GAM281 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM281 target RNA into GAM281 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[32608] It is appreciated that GAM281 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM281 target genes. The mRNA of each one of this plurality of GAM281 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM281 RNA, herein designated GAM RNA, and which when bound by GAM281 RNA causes inhibition of translation of respective one or more GAM281 target proteins.

[32609] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM281 gene, herein designated GAM GENE, on one or more GAM281 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[32610] It is appreciated that specific functions and accordingly utilities of GAM281 correlate with, and may be deduced

from, the identity of the target genes which GAM281 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[32611]

[32612]

[32613] (Accession NP_444285.1) is a GAM281 target gene, herein designated TARGET GENE. BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BINDING SITE, designated SEQ ID:13946, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32614] A function of GAM281 is therefore inhibition of (Accession NP_444285.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with .

[32615] 15E1.2 (Accession XP_290596.1) is another GAM281 target gene, herein designated TARGET GENE. 15E1.2 BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by 15E1.2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of 15E1.2 BINDING SITE, designated SEQ ID:12868, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32616] Another function of GAM281 is therefore inhibition of 15E1.2 (Accession XP_290596.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 15E1.2.

[32617] Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2) is another GAM281 target gene, herein designated TARGET GENE. A1BG BINDING SITE1 and A1BG BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by A1BG, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A1BG BINDING SITE1 and A1BG BINDING SITE2, designated SEQ ID:18868 and SEQ ID:2534 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32618] Another function of GAM281 is therefore inhibition of Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2), a gene which a plasma protein of unknown function. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A1BG.

[32619] The function of A1BG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Aminoadipate-semialdehyde synthase (AASS, Accession NP_005754.2) is another GAM281 target gene, herein designated TARGET GENE. AASS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AASS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AASS BINDING SITE, designated SEQ ID:6339, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32620] Another function of GAM281 is therefore inhibition of Aminoadipate-semialdehyde synthase (AASS, Accession NP_005754.2) . Accordingly, utilities of GAM281 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with AASS.

[32621] ABCA13 (Accession NP_689914.2) is another GAM281 target gene, herein designated TARGET GENE. ABCA13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCA13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCA13 BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32622] Another function of GAM281 is therefore inhibition of ABCA13 (Accession NP_689914.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCA13.

[32623] Atp-binding cassette, sub-family c (cftr/mrp), member 11 (ABCC11, Accession NP_149163.2) is another GAM281 target gene, herein designated TARGET GENE. ABCC11 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ABCC11, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCC11 BINDING SITE, designated SEQ ID:7022, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32624] Another function of GAM281 is therefore inhibition of Atp-binding cassette, sub-family c (cftr/mrp), member 11 (ABCC11, Accession NP_149163.2), a gene which acts as a multispecific organic anion pump which can transport nucleotide analogs (by similarity). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC11.

[32625] The function of ABCC11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Actin binding lim protein 2 (ABLIM2, Accession NP_115808.1) is another GAM281 target gene, herein designated TARGET GENE. ABLIM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABLIM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABLIM2 BINDING SITE, desig-

nated SEQ ID:3488, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32626] Another function of GAM281 is therefore inhibition of Actin binding lim protein 2 (ABLIM2, Accession NP_115808.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABLIM2.

[32627] Acyl-coenzyme a dehydrogenase, short/branched chain (ACADSB, Accession NP_001600.1) is another GAM281 target gene, herein designated TARGET GENE. ACADSB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACADSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACADSB BINDING SITE, designated SEQ ID:16689, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32628] Another function of GAM281 is therefore inhibition of Acyl-coenzyme a dehydrogenase, short/branched chain (ACADSB, Accession NP_001600.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with ACADSB.

[32629] A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3, Accession NP_055058.1) is another GAM281 target gene, herein designated TARGET GENE. ADAMTS3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ADAMTS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAMTS3 BINDING SITE, designated SEQ ID:16811, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32630] Another function of GAM281 is therefore inhibition of A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3, Accession NP_055058.1), a gene which cleaves the propeptides of type ii collagen prior to fibril assembly. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAMTS3.

[32631] The function of ADAMTS3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM216.1.A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4 (ADAMTS4, Accession NP_005090.1) is another GAM281 target gene, herein designated TARGET GENE. ADAMTS4 BINDING SITE1 and ADAMTS4 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ADAMTS4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAMTS4 BINDING SITE1 and ADAMTS4 BINDING SITE2, designated SEQ ID:13757 and SEQ ID:1651 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32632] Another function of GAM281 is therefore inhibition of A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4 (ADAMTS4, Accession NP_005090.1), a gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAMTS4.

[32633] The function of ADAMTS4 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Adenosine deaminase, rna-specific, b1 (red1 homolog rat) (ADARB1, Accession NP_056648.1) is another GAM281 target gene, herein designated TARGET GENE. ADARB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADARB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADARB1 BINDING SITE, designated SEQ ID:12610, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32634] Another function of GAM281 is therefore inhibition of Adenosine deaminase, rna-specific, b1 (red1 homolog rat) (ADARB1, Accession NP_056648.1), a gene which RNA editing involves the deamination of adenosines at specific sites. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADARB1.

[32635] The function of ADARB1 has been established by previous studies. RNA editing involves the deamination of

adenosines at specific sites, the result of which can be a change in the amino acid sequence of the protein so that it differs from that predicted by the sequence of the DNA. Editing of the glutamate receptor B (GluRB; 138247) pre-mRNA has been shown to alter a codon (referred to as the Q/R site) for a channel determinant that controls the calcium permeability of the AMPA glutamate receptors. Melcher et al. (1996) tested the candidate dsRNA adenosine deaminase DRADA (OMIM Ref. No. 601059) and showed that when coexpressed with a GluR- B minigene in HEK 293 cells, DRADA produced low- level editing at the GluR- B Q/R site. The authors then screened a rat brain cDNA library with the predicted catalytic domain of rat DRADA to identify other potential editing enzymes. A cDNA encoding a predicted 711- amino acid protein was isolated that gave about 90% of the expected activity in their editing assay. Melcher et al. (1996) designated this novel mammalian RNA editing protein RNA- editing enzyme- 1 (RED1). Rat RED1 and DRADA share about 31% overall identity primarily due to their conservation in the C- terminal catalytic domain. Northern blots showed highest expression of RED1 in rat brain. Melcher et al. (1996) further observed that while RED1 was more effi-

cient at deaminating some sites, DRADA had stronger activity at others. They speculated that a combination of these and perhaps other editing enzymes may be involved in determining the overall editing process for a given transcript. Higuchi et al. (2000) studied ADAR2- mediated RNA editing by generating mice that were homozygous for a targeted functional null allele. Editing in Adar2 - /- mice was substantially reduced at most of 25 positions in diverse transcripts; the mutant mice became prone to seizures and died young. The impaired phenotype appeared to result entirely from a single underedited position, since it reverted to normal when both alleles for the underedited transcript were substituted with alleles encoding the edited version exonically. The critical position specifies an ion channel determinant, the Q/R site, in AMPA receptor GluRB premessenger RNA. Higuchi et al. (2000) concluded that this transcript is physiologically the most important substrate of ADAR2.

[32636]

[32637] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32638] Melcher, T.; Maas, S.; Herb, A.; Sprengel, R.; Seeburg, P.

H.; Higuchi, M. : A mammalian RNA editing enzyme. Nature 379: 460- 463, 1996. ; and

[32639] Higuchi, M.; Maas, S.; Single, F. N.; Hartner, J.; Rozov, A.; Burnashev, N.; Feldmeyer, D.; Sprengel, R.; Seeburg, P. H. : Point mutation in an AMPA receptor gene rescues lethality in mi.

[32640] Further studies establishing the function and utilities of ADARB1 are found in John Hopkins OMIM database record ID 601218, and in cited publications listed in Table 5, which are hereby incorporated by reference.Adenylate cyclase 1 (brain) (ADCY1, Accession NP_066939.1) is another GAM281 target gene, herein designated TARGET GENE. ADCY1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADCY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY1 BINDING SITE, designated SEQ ID:6261, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32641] Another function of GAM281 is therefore inhibition of Adenylate cyclase 1 (brain) (ADCY1, Accession

NP_066939.1), a gene which a calmodulin- sensitive adenylyl cyclase. it may play a role in memory acquisition and learning. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY1.

[32642] The function of ADCY1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.Adenylate cyclase 6 (ADCY6, Accession NP_056085.1) is another GAM281 target gene, herein designated TARGET GENE. ADCY6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ADCY6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY6 BINDING SITE, designated SEQ ID:16688, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32643] Another function of GAM281 is therefore inhibition of Adenylate cyclase 6 (ADCY6, Accession NP_056085.1), a gene which this a membrane- bound, ca(2+)- inhibitable adenylyl cyclase (by similarity). Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY6.

[32644] The function of ADCY6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.2.Adenosine a2a receptor (ADORA2A, Accession NP_000666.2) is another GAM281 target gene, herein designated TARGET GENE. ADORA2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADORA2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADORA2A BINDING SITE, designated SEQ ID:19456, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32645] Another function of GAM281 is therefore inhibition of Adenosine a2a receptor (ADORA2A, Accession NP_000666.2), a gene which regulates phagocytosis, apoptosis and platelet aggregation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADORA2A.

[32646] The function of ADORA2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Agmatine ureohydrolase (agmatinase) (AGMAT, Accession NP_079034.2) is another GAM281 target gene, herein designated TARGET GENE. AGMAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AGMAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGMAT BINDING SITE, designated SEQ ID:9193, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32647] Another function of GAM281 is therefore inhibition of Agmatine ureohydrolase (agmatinase) (AGMAT, Accession NP_079034.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGMAT.

[32648] Angiotensin ii receptor-associated protein (AGTRAP, Accession NP_065083.2) is another GAM281 target gene, herein designated TARGET GENE. AGTRAP BINDING SITE is a target binding site found in the 3` untranslated region

of mRNA encoded by AGTRAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGTRAP BINDING SITE, designated SEQ ID:3359, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32649] Another function of GAM281 is therefore inhibition of Angiotensin ii receptor-associated protein (AGTRAP, Accession NP_065083.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGTRAP.

[32650] Aryl hydrocarbon receptor (AHR, Accession NP_001612.1) is another GAM281 target gene, herein designated TARGET GENE. AHR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AHR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AHR BINDING SITE, designated SEQ ID:8217, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32651] Another function of GAM281 is therefore inhibition of Aryl

hydrocarbon receptor (AHR, Accession NP_001612.1), a gene which plays a role in modulating carcinogenesis through the induction of xenobiotic- metabolizing enzymes and therefore may be associated with Stomach tumors. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Stomach tumors, and of other diseases and clinical conditions associated with AHR.

[32652] The function of AHR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Absent in melanoma 1 (AIM1, Accession XP_166300.1) is another GAM281 target gene, herein designated TARGET GENE. AIM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AIM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AIM1 BINDING SITE, designated SEQ ID:16864, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32653] Another function of GAM281 is therefore inhibition of Absent in melanoma 1 (AIM1, Accession XP_166300.1), a

gene which is altered in association with tumor suppression in a model of human melanoma and therefore may be associated with Malignant melanoma. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Malignant melanoma, and of other diseases and clinical conditions associated with AIM1.

[32654] The function of AIM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Aldehyde dehydrogenase 1 family, member b1 (ALDH1B1, Accession NP_000683.3) is another GAM281 target gene, herein designated TARGET GENE. ALDH1B1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALDH1B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALDH1B1 BINDING SITE, designated SEQ ID:2153, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32655] Another function of GAM281 is therefore inhibition of Aldehyde dehydrogenase 1 family, member b1 (ALDH1B1, Accession NP_000683.3) . Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH1B1.

[32656] Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1) is another GAM281 target gene, herein designated TARGET GENE. ALOX15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALOX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALOX15 BINDING SITE, designated SEQ ID:19939, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32657] Another function of GAM281 is therefore inhibition of Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1), a gene which converts arachidonic acid to 15s- hydroperoxyeicosatetraenoic acid. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALOX15.

[32658] The function of ALOX15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM189.1.AMID (Accession NP_116186.1) is another GAM281 target gene, herein designated TARGET GENE. AMID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AMID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMID BINDING SITE, designated SEQ ID:5895, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32659] Another function of GAM281 is therefore inhibition of AMID (Accession NP_116186.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMID.

[32660] Ankyrin repeat domain 6 (ANKRD6, Accession NP_055757.1) is another GAM281 target gene, herein designated TARGET GENE. ANKRD6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ANKRD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANKRD6 BINDING SITE, designated SEQ ID:1746, to the nucleotide se-

quence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32661] Another function of GAM281 is therefore inhibition of Ankyrin repeat domain 6 (ANKRD6, Accession NP_055757.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKRD6.

[32662] Alanyl (membrane) aminopeptidase (aminopeptidase n, aminopeptidase m, microsomal aminopeptidase, cd13, p150) (ANPEP, Accession NP_001141.1) is another GAM281 target gene, herein designated TARGET GENE. ANPEP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ANPEP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANPEP BINDING SITE, designated SEQ ID:6737, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32663] Another function of GAM281 is therefore inhibition of Alanyl (membrane) aminopeptidase (aminopeptidase n, aminopeptidase m, microsomal aminopeptidase, cd13, p150) (ANPEP, Accession NP_001141.1), a gene which is a

cell- surface transmembrane glycosylated metalloprotease that processes signaling peptides. and therefore may be associated with Leukemia, lymphoma. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Leukemia, lymphoma, and of other diseases and clinical conditions associated with ANPEP.

[32664] The function of ANPEP has been established by previous studies. A surface antigen glycoprotein of molecular weight about 150,000 is recognized by monoclonal antibodies MY7 and MCS2. Look et al. (1986) isolated the complete ANPEP gene, which they called GP150, from a human placental genomic library. By study of somatic cell hybrid DNA and by in situ hybridization, the GP150 gene was assigned to 15q25- q26. This chromosomal location coincides with that of the oncogene FES (OMIM Ref. No. 190030), which is also expressed in myeloid cells. They are separate loci, however, because FES probes do not hybridize to cloned sequences spanning the GP150 gene and the 2 genes have different restriction maps. Like FES, GP150 is distal to the breakpoint in t(15;17)(q22;q21.1) of acute promyelocytic leukemia. By analysis of mouse- human somatic cell hybrids, Watt and Willard (1990) assigned the ANPEP gene, which they called PEPN, to 15q11-

qter. With a genomic DNA probe, they detected a frequent DraIII polymorphism useful as a marker for human chromosome 15. Look et al. (1989) determined the complete primary structure of GP150, known as CD13. The large extracellular carboxyterminal domain contained a pentapeptide consensus sequence characteristic of members of the zinc- binding metalloproteinase superfamily. Sequence comparisons with known enzymes of this class showed that CD13 and aminopeptidase N are identical. The latter enzyme was thought to be involved in the metabolism of regulatory peptides by diverse cell types, including small intestinal and renal tubular epithelial cells, macrophages, granulocytes, and synaptic membranes from the CNS.

[32665]

[32666] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32667] Look, A. T.; Ashmun, R. A.; Shapiro, L. H.; Peiper, S. C. : Human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminopeptidase N. J. Clin. Invest. 83: 1299- 1307, 1989. ; and

[32668] Look, A. T.; Peiper, S. C.; Rebentisch, M. B.; Ashmun, R. A.;

Roussel, M. F.; Lemons, R. S.; Le Beau, M. M.; Rubin, C. M.; Sherr, C. J. : Molecular cloning, expression, and chromosomal.

[32669] Further studies establishing the function and utilities of ANPEP are found in John Hopkins OMIM database record ID 151530, and in cited publications listed in Table 5, which are hereby incorporated by reference.AP1S3 (Accession XP_291023.1) is another GAM281 target gene, herein designated TARGET GENE. AP1S3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1S3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1S3 BINDING SITE, designated SEQ ID:10109, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32670] Another function of GAM281 is therefore inhibition of AP1S3 (Accession XP_291023.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1S3.

[32671] Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) is another GAM281 tar-

get gene, herein designated TARGET GENE. AP3S2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AP3S2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP3S2 BINDING SITE, designated SEQ ID:19874, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32672] Another function of GAM281 is therefore inhibition of Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3S2.

[32673] Apoptotic protease activating factor (APAF1, Accession NP_001151.1) is another GAM281 target gene, herein designated TARGET GENE. APAF1 BINDING SITE1 and APAF1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APAF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE1 and APAF1

BINDING SITE2, designated SEQ ID:16578 and SEQ ID:19360 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32674] Another function of GAM281 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_001151.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[32675] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apoptotic protease activating factor (APAF1, Accession NP_037361.1) is another GAM281 target gene, herein designated TARGET GENE. APAF1 BINDING SITE1 and APAF1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APAF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of APAF1 BINDING SITE1 and APAF1 BINDING SITE2, designated SEQ ID:16578 and SEQ ID:19360 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32676] Another function of GAM281 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_037361.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[32677] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.APG-1 (Accession NP_055093.2) is another GAM281 target gene, herein designated TARGET GENE. APG-1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by APG-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of APG-1 BINDING SITE, designated SEQ ID:17324, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32678] Another function of GAM281 is therefore inhibition of APG-1 (Accession NP_055093.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APG-1.

[32679] APM1 (Accession NP_004788.1) is another GAM281 target gene, herein designated TARGET GENE. APM1 BINDING SITE1 through APM1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by APM1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APM1 BINDING SITE1 through APM1 BINDING SITE3, designated SEQ ID:20035, SEQ ID:5598 and SEQ ID:11707 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32680] Another function of GAM281 is therefore inhibition of APM1 (Accession NP_004788.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1.

[32681] Apolipoprotein b mrna editing enzyme, catalytic polypeptide-like 3f (APOBEC3F, Accession NP_660341.2) is another GAM281 target gene, herein designated TARGET GENE. APOBEC3F BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APOBEC3F, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOBEC3F BINDING SITE, designated SEQ ID:5622, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32682] Another function of GAM281 is therefore inhibition of Apolipoprotein b mrna editing enzyme, catalytic polypeptide-like 3f (APOBEC3F, Accession NP_660341.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOBEC3F.

[32683] Apolipoprotein l, 2 (APOL2, Accession NP_663612.1) is another GAM281 target gene, herein designated TARGET GENE. APOL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL2 BINDING SITE, designated SEQ ID:8064, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32684] Another function of GAM281 is therefore inhibition of Apolipoprotein l, 2 (APOL2, Accession NP_663612.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL2.

[32685] Apolipoprotein l, 2 (APOL2, Accession NP_112092.1) is another GAM281 target gene, herein designated TARGET GENE. APOL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL2 BINDING SITE, designated SEQ ID:8064, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32686] Another function of GAM281 is therefore inhibition of Apolipoprotein l, 2 (APOL2, Accession NP_112092.1) . Ac-

cordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL2.

[32687] Amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2, Accession NP_006371.2) is another GAM281 target gene, herein designated TARGET GENE. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APPBP2 BINDING SITE, designated SEQ ID:4095, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32688] Another function of GAM281 is therefore inhibition of Amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2, Accession NP_006371.2), a gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore may be associated with Alzheimer's disease. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer's disease, and of other diseases and clinical conditions associated with APPBP2.

[32689] The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.APPL (Accession NP_036228.1) is another GAM281 target gene, herein designated TARGET GENE. APPL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APPL BINDING SITE, designated SEQ ID:12068, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32690] Another function of GAM281 is therefore inhibition of APPL (Accession NP_036228.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APPL.

[32691] Aquaporin 2 (collecting duct) (AQP2, Accession NP_000477.1) is another GAM281 target gene, herein designated TARGET GENE. AQP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AQP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP2 BINDING SITE, designated SEQ ID:18318, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32692] Another function of GAM281 is therefore inhibition of Aquaporin 2 (collecting duct) (AQP2, Accession NP_000477.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP2.

[32693] Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1) is another GAM281 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:3169, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32694] Another function of GAM281 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession

NP_445738.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[32695] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1) is another GAM281 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:3169, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32696] Another function of GAM281 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1), a gene which participates in distinct physi-

ologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[32697] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Archain 1 (ARCN1, Accession NP_001646.2) is another GAM281 target gene, herein designated TARGET GENE. ARCN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARCN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARCN1 BINDING SITE, designated SEQ ID:13747, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32698] Another function of GAM281 is therefore inhibition of Archain 1 (ARCN1, Accession NP_001646.2), a gene which plays a fundamental role in eukaryotic cell biology. Accordingly, utilities of GAM281 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with ARCN1.

[32699] The function of ARCN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Adp-ribosylation factor related protein 1 (ARFRP1, Accession NP_003215.1) is another GAM281 target gene, herein designated TARGET GENE. ARFRP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARFRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARFRP1 BINDING SITE, designated SEQ ID:6901, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32700] Another function of GAM281 is therefore inhibition of Adp-ribosylation factor related protein 1 (ARFRP1, Accession NP_003215.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARFRP1.

[32701] Ras homolog gene family, member f (in filopodia) (ARHF, Accession NP_061907.1) is another GAM281 target gene,

herein designated TARGET GENE. ARHF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHF BINDING SITE, designated SEQ ID:7962, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32702] Another function of GAM281 is therefore inhibition of Ras homolog gene family, member f (in filopodia) (ARHF, Accession NP_061907.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHF.

[32703] Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) is another GAM281 target gene, herein designated TARGET GENE. ARHGAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP1 BINDING SITE, designated SEQ ID:4096, to the nucleotide se-

quence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32704] Another function of GAM281 is therefore inhibition of Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP1.

[32705] ARHGAP11A (Accession NP_055598.1) is another GAM281 target gene, herein designated TARGET GENE. ARHGAP11A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGAP11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP11A BINDING SITE, designated SEQ ID:17742, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32706] Another function of GAM281 is therefore inhibition of ARHGAP11A (Accession NP_055598.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP11A.

[32707] Rho guanine nucleotide exchange factor (gef) 4 (ARHGEF4, Accession NP_127462.1) is another GAM281 target gene, herein designated TARGET GENE. ARHGEF4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ARHGEF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGEF4 BINDING SITE, designated SEQ ID:14328, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32708] Another function of GAM281 is therefore inhibition of Rho guanine nucleotide exchange factor (gef) 4 (ARHGEF4, Accession NP_127462.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF4.

[32709] Rho guanine nucleotide exchange factor (gef) 4 (ARHGEF4, Accession NP_056135.2) is another GAM281 target gene, herein designated TARGET GENE. ARHGEF4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ARHGEF4, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGEF4 BINDING SITE, designated SEQ ID:14328, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32710] Another function of GAM281 is therefore inhibition of Rho guanine nucleotide exchange factor (gef) 4 (ARHGEF4, Accession NP_056135.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF4.

[32711] ARPP-19 (Accession NP_006619.1) is another GAM281 target gene, herein designated TARGET GENE. ARPP-19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARPP-19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARPP-19 BINDING SITE, designated SEQ ID:944, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32712] Another function of GAM281 is therefore inhibition of ARPP-19 (Accession NP_006619.1) . Accordingly, utilities

of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARPP-19.

[32713] Arylsulfatase b (ARSB, Accession NP_000037.1) is another GAM281 target gene, herein designated TARGET GENE. ARSB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ARSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARSB BINDING SITE, designated SEQ ID:13855, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32714] Another function of GAM281 is therefore inhibition of Arylsulfatase b (ARSB, Accession NP_000037.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARSB.

[32715] Ankyrin repeat and socs box-containing 16 (ASB16, Accession NP_543139.4) is another GAM281 target gene, herein designated TARGET GENE. ASB16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASB16, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB16 BINDING SITE, designated SEQ ID:14722, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32716] Another function of GAM281 is therefore inhibition of Ankyrin repeat and socs box-containing 16 (ASB16, Accession NP_543139.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB16.

[32717] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) is another GAM281 target gene, herein designated TARGET GENE. ASB6 BINDING SITE1 and ASB6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ASB6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE1 and ASB6 BINDING SITE2, designated SEQ ID:10305 and SEQ ID:2196 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32718] Another function of GAM281 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[32719] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) is another GAM281 target gene, herein designated TARGET GENE. ASB6 BINDING SITE1 and ASB6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ASB6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE1 and ASB6 BINDING SITE2, designated SEQ ID:10305 and SEQ ID:2196 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32720] Another function of GAM281 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[32721] ASE-1 (Accession NP_036231.1) is another GAM281 target

gene, herein designated TARGET GENE. ASE-1 BINDING SITE1 and ASE-1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ASE-1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASE-1 BINDING SITE1 and ASE-1 BINDING SITE2, designated SEQ ID:3101 and SEQ ID:1741 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32722] Another function of GAM281 is therefore inhibition of ASE-1 (Accession NP_036231.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASE-1.

[32723] ATF7IP2 (Accession NP_079273.1) is another GAM281 target gene, herein designated TARGET GENE. ATF7IP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATF7IP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATF7IP2 BINDING SITE, designated SEQ ID:9602, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[32724] Another function of GAM281 is therefore inhibition of ATF7IP2 (Accession NP_079273.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATF7IP2.

[32725] Ataxia telangiectasia mutated (includes complementation groups a, c and d) (ATM, Accession NP_000042.2) is another GAM281 target gene, herein designated TARGET GENE. ATM BINDING SITE1 and ATM BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ATM, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATM BINDING SITE1 and ATM BINDING SITE2, designated SEQ ID:12000 and SEQ ID:1837 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32726] Another function of GAM281 is therefore inhibition of Ataxia telangiectasia mutated (includes complementation groups a, c and d) (ATM, Accession NP_000042.2) . Accordingly, utilities of GAM281 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with ATM.

[32727] Atpase, na+/k+ transporting, beta 2 polypeptide (ATP1B2, Accession NP_001669.1) is another GAM281 target gene, herein designated TARGET GENE. ATP1B2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP1B2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP1B2 BINDING SITE, designated SEQ ID:16916, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32728] Another function of GAM281 is therefore inhibition of Atpase, na+/k+ transporting, beta 2 polypeptide (ATP1B2, Accession NP_001669.1), a gene which catalyzes the hydrolysis of ATP coupled with the exchange of Na +/K+ ions across the plasma membrane. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B2.

[32729] The function of ATP1B2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM130.1.Atpase, (na+)/k+ transporting, beta 4 polypeptide (ATP1B4, Accession NP_036201.1) is another GAM281 target gene, herein designated TARGET GENE. ATP1B4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP1B4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP1B4 BINDING SITE, designated SEQ ID:13042, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32730] Another function of GAM281 is therefore inhibition of Atpase, (na+)/k+ transporting, beta 4 polypeptide (ATP1B4, Accession NP_036201.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B4.

[32731] Atpase, h+ transporting, lysosomal 38kda, v0 subunit d isoform 2 (ATP6V0D2, Accession NP_689778.1) is another GAM281 target gene, herein designated TARGET GENE. ATP6V0D2 BINDING SITE1 and ATP6V0D2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ATP6V0D2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP6V0D2 BINDING SITE1 and ATP6V0D2 BINDING SITE2, designated SEQ ID:17102 and SEQ ID:15039 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32732] Another function of GAM281 is therefore inhibition of Atpase, h+ transporting, lysosomal 38kda, v0 subunit d isoform 2 (ATP6V0D2, Accession NP_689778.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V0D2.

[32733] ATP6V1A (Accession NP_001681.2) is another GAM281 target gene, herein designated TARGET GENE. ATP6V1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP6V1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP6V1A BINDING SITE, designated SEQ ID:18868, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32734] Another function of GAM281 is therefore inhibition of

ATP6V1A (Accession NP_001681.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V1A.

[32735] Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) is another GAM281 target gene, herein designated TARGET GENE. ATP7A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:4112, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32736] Another function of GAM281 is therefore inhibition of Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A.

[32737] Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) is another GAM281 target gene, herein

designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:11802, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32738] Another function of GAM281 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[32739] Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) is another GAM281 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:11802, to the nucleotide

sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32740] Another function of GAM281 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[32741] Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 4 (B4GALT4, Accession NP_003769.1) is another GAM281 target gene, herein designated TARGET GENE. B4GALT4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B4GALT4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B4GALT4 BINDING SITE, designated SEQ ID:11028, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32742] Another function of GAM281 is therefore inhibition of Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 4 (B4GALT4, Accession NP_003769.1) . Accordingly, utilities of GAM281 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with B4GALT4.

[32743] Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5, Accession NP_004767.1) is another GAM281 target gene, herein designated TARGET GENE. B4GALT5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B4GALT5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B4GALT5 BINDING SITE, designated SEQ ID:16140, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32744] Another function of GAM281 is therefore inhibition of Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5, Accession NP_004767.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT5.

[32745] Xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase i) (B4GALT7, Accession NP_009186.1) is another GAM281 target gene, herein

designated TARGET GENE. B4GALT7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B4GALT7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B4GALT7 BINDING SITE, designated SEQ ID:18475, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32746] Another function of GAM281 is therefore inhibition of Xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase i) (B4GALT7, Accession NP_009186.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT7.

[32747] BA108L7.2 (Accession NP_112233.2) is another GAM281 target gene, herein designated TARGET GENE. BA108L7.2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BA108L7.2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BA108L7.2 BINDING SITE, designated SEQ ID:10888, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32748] Another function of GAM281 is therefore inhibition of BA108L7.2 (Accession NP_112233.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BA108L7.2.

[32749] Beta-site app-cleaving enzyme (BACE, Accession NP_620429.1) is another GAM281 target gene, herein designated TARGET GENE. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE BINDING SITE, designated SEQ ID:16660, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32750] Another function of GAM281 is therefore inhibition of Beta-site app-cleaving enzyme (BACE, Accession NP_620429.1), a gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore may be associated with Alzheimer disease. Ac-

cordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer disease, and of other diseases and clinical conditions associated with BACE.

[32751] The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.Beta-site app-cleaving enzyme (BACE, Accession NP_036236.1) is another GAM281 target gene, herein designated TARGET GENE. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE BINDING SITE, designated SEQ ID:16660, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32752] Another function of GAM281 is therefore inhibition of Beta-site app-cleaving enzyme (BACE, Accession NP_036236.1), a gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore may be associated with Alzheimer disease. Accordingly, utilities of GAM281 include diagnosis, preven-

tion and treatment of Alzheimer disease, and of other diseases and clinical conditions associated with BACE.

[32753] The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.Beta-site app-cleaving enzyme (BACE, Accession NP_620427.1) is another GAM281 target gene, herein designated TARGET GENE. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE BINDING SITE, designated SEQ ID:16660, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32754] Another function of GAM281 is therefore inhibition of Beta-site app-cleaving enzyme (BACE, Accession NP_620427.1), a gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore may be associated with Alzheimer disease. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer disease, and of other dis-

eases and clinical conditions associated with BACE.

[32755] The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.Beta-site app-cleaving enzyme (BACE, Accession NP_620428.1) is another GAM281 target gene, herein designated TARGET GENE. BACE BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE BINDING SITE, designated SEQ ID:16660, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32756] Another function of GAM281 is therefore inhibition of Beta-site app-cleaving enzyme (BACE, Accession NP_620428.1), a gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore may be associated with Alzheimer disease. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alzheimer disease, and of other diseases and clinical conditions associated with BACE.

[32757] The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.Btb and cnc homology 1, basic leucine zipper transcription factor 2 (BACH2, Accession NP_068585.1) is another GAM281 target gene, herein designated TARGET GENE. BACH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BACH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACH2 BINDING SITE, designated SEQ ID:2573, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32758] Another function of GAM281 is therefore inhibition of Btb and cnc homology 1, basic leucine zipper transcription factor 2 (BACH2, Accession NP_068585.1), a gene which acts as repressor or activator, binds to maf recognition elements and therefore may be associated with Non-hodgkin lymphoma. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Non-hodgkin lymphoma, and of other diseases and clinical conditions associated with BACH2.

[32759] The function of BACH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.Bcl2-associated athanogene 5 (BAG5, Accession NP_004864.1) is another GAM281 target gene, herein designated TARGET GENE. BAG5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BAG5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAG5 BINDING SITE, designated SEQ ID:5695, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32760] Another function of GAM281 is therefore inhibition of Bcl2-associated athanogene 5 (BAG5, Accession NP_004864.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAG5.

[32761] Bromodomain adjacent to zinc finger domain, 2a (BAZ2A, Accession NP_038477.1) is another GAM281 target gene, herein designated TARGET GENE. BAZ2A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BAZ2A, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAZ2A BINDING SITE, designated SEQ ID:8852, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32762] Another function of GAM281 is therefore inhibition of Bromodomain adjacent to zinc finger domain, 2a (BAZ2A, Accession NP_038477.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAZ2A.

[32763] Butyrylcholinesterase (BCHE, Accession NP_000046.1) is another GAM281 target gene, herein designated TARGET GENE. BCHE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BCHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCHE BINDING SITE, designated SEQ ID:7089, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32764] Another function of GAM281 is therefore inhibition of Butyrylcholinesterase (BCHE, Accession NP_000046.1) . Ac-

cordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCHE.

[32765] B-cell cll/lymphoma 10 (BCL10, Accession NP_003912.1) is another GAM281 target gene, herein designated TARGET GENE. BCL10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCL10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCL10 BINDING SITE, designated SEQ ID:19576, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32766] Another function of GAM281 is therefore inhibition of B-cell cll/lymphoma 10 (BCL10, Accession NP_003912.1), a gene which is a positive regulator of lymphocyte proliferation, NF- kappaB activator. and therefore may be associated with Malt lymphoma, follicular lymphoma. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Malt lymphoma, follicular lymphoma, and of other diseases and clinical conditions associated with BCL10.

[32767] The function of BCL10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Bradykinin receptor b1 (BDKRB1, Accession NP_000701.2) is another GAM281 target gene, herein designated TARGET GENE. BDKRB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BDKRB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BDKRB1 BINDING SITE, designated SEQ ID:8663, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32768] Another function of GAM281 is therefore inhibition of Bradykinin receptor b1 (BDKRB1, Accession NP_000701.2), a gene which mediates intracellular calcium flux. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDKRB1.

[32769] The function of BDKRB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM136.1.Bradykinin receptor b2 (BDKRB2, Accession NP_000614.1) is another GAM281 target gene, herein designated TARGET GENE. BDKRB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BDKRB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BDKRB2 BINDING SITE, designated SEQ ID:15590, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32770] Another function of GAM281 is therefore inhibition of Bradykinin receptor b2 (BDKRB2, Accession NP_000614.1), a gene which involves in inflammation, vasodilation, smooth muscle contraction, relaxation, and response to pain and therefore may be associated with Cardiovascular diseases. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Cardiovascular diseases, and of other diseases and clinical conditions associated with BDKRB2.

[32771] The function of BDKRB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM94.1.B double prime 1, subunit of rna polymerase iii transcription initiation factor iiib (BDP1, Accession NP_060899.1) is another GAM281 target gene, herein designated TARGET GENE. BDP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BDP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BDP1 BINDING SITE, designated SEQ ID:19556, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32772] Another function of GAM281 is therefore inhibition of B double prime 1, subunit of rna polymerase iii transcription initiation factor iiib (BDP1, Accession NP_060899.1), a gene which activates RNA polymerase III transcription. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDP1.

[32773] The function of BDP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM146.1.BENE (Accession NP_005425.1) is another

GAM281 target gene, herein designated TARGET GENE. BENE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BENE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BENE BINDING SITE, designated SEQ ID:6009, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32774] Another function of GAM281 is therefore inhibition of BENE (Accession NP_005425.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BENE.

[32775] BHD (Accession NP_659434.2) is another GAM281 target gene, herein designated TARGET GENE. BHD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BHD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BHD BINDING SITE, designated SEQ ID:9036, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32776] Another function of GAM281 is therefore inhibition of BHD (Accession NP_659434.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BHD.

[32777] BIA2 (Accession NP_056246.1) is another GAM281 target gene, herein designated TARGET GENE. BIA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BIA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BIA2 BINDING SITE, designated SEQ ID:6389, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32778] Another function of GAM281 is therefore inhibition of BIA2 (Accession NP_056246.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIA2.

[32779] Bh3 interacting domain death agonist (BID, Accession NP_001187.1) is another GAM281 target gene, herein designated TARGET GENE. BID BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BID, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BID BINDING SITE, designated SEQ ID:10620, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32780] Another function of GAM281 is therefore inhibition of Bh3 interacting domain death agonist (BID, Accession NP_001187.1), a gene which induces ice- like proteases and apoptosis and therefore may be associated with Cat eye syndrome. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Cat eye syndrome, and of other diseases and clinical conditions associated with BID.

[32781] The function of BID has been established by previous studies. Wang et al. (1996) identified a gene they termed BID (BH3 Interacting domain Death agonist) that encodes a novel death agonist that heterodimerizes with either agonists (BAX) or antagonists (BCL2). BID possesses only the BH3 domain, lacks a C- terminal signal- anchor segment, and is found in both cytosolic and membrane locations. BID's only homology with the BCL2 family is the conserved BH3 domain. BID counters the protective effect of BCL2.

Expression of BID induces ICE- like proteases which are thought to be downstream of BCL2, activated in apoptosis, and required for aspects of cell death. Wang et al. (1996) stated that the discovery of this BH3- only molecule supports the identification of BH3 as a death domain and favors a model in which BID represents a death ligand for the membrane- bound receptor BAX. Luo et al. (1998) reported the purification of a cytosolic protein that induces cytochrome c release from mitochondria in response to caspase- 8 (CASP8; 601763), the apical caspase activated by cell surface death receptors such as FAS (OMIM Ref. No. 134637) and TNF (OMIM Ref. No. 191160). Peptide mass fingerprinting identified this protein as BID. CASP8 cleaves BID, and the COOH- terminal part translocates to mitochondria where it triggers cytochrome c release. Immunodepletion of BID from cell extracts eliminated the cytochrome c releasing activity. The cytochrome c releasing activity of BID was antagonized by BCL2 (OMIM Ref. No. 151430). A mutation at the BH3 domain diminished its cytochrome c releasing activity. BID, therefore, relays an apoptotic signal from the cell surface to mitochondria. Li et al. (1998) reported that BID is a specific proximal substrate of CASP8 in the Fas apoptotic signal-

ing pathway. While full- length BID is localized in cytosol, truncated BID translocates to mitochondria and thus transduces apoptotic signals from cytoplasmic membrane to mitochondria. Truncated BID induces first the clustering of mitochondria around the nuclei and release of cytochrome c independent of caspase activity, and then the loss of mitochondrial membrane potential, cell shrinkage, and nuclear condensation in a caspase- dependent fashion. The results of Li et al. (1998) indicated that BID is a mediator of mitochondrial damage induced by CASP8.

[32782] Animal model experiments lend further support to the function of BID. Yin et al. (1999) generated mice deficient in Bid by homologous recombination. Bid - /- mice were born at the expected frequency and had no developmental abnormalities. When Bid - /- mice were injected with an antibody against Fas, nearly all survived, whereas wildtype mice died from hepatocellular apoptosis and hemorrhagic necrosis. About half of the Bid - /- mice had no apparent liver injury and showed no evidence of activation of the effector caspases 3 (OMIM Ref. No. 600636) and 7 (OMIM Ref. No. 601761), although the initiator caspase- 8 had been activated. Other Bid- deficient mice survived with only moderate damage: all 3 caspases (3, 7, and 8) were

activated, but their cell nuclei were intact, and no mitochondrial cytochrome c was released. Yin et al. (1999) also investigated the effects of Bid deficiency in cultured cells treated with anti- Fas antibody or with TNF- alpha. In these Bid - /- cells, mitochondrial dysfunction was delayed, cytochrome c was not released, effector caspase activity was reduced, and the cleavage of apoptosis substrates was altered. This loss- of- function model indicates that Bid is a critical substrate in vivo for signaling by death- receptor agonists that mediates a mitochondrial amplification loop that is essential for the apoptosis of selected cells.

[32783] It is appreciated that the abovementioned animal model for BID is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[32784] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32785] Li, H.; Zhu, H.; Xu, C.; Yuan, J. : Cleavage of BID by caspase 8 mediates the mitochondrial damage in the Fas pathway of apoptosis. Cell 94: 491- 501, 1998. ; and

[32786] Yin, X.- M.; Wang, K.; Gross, A.; Zhao, Y.; Zinkel, S.;

Klocke, B.; Roth, K. A.; Korsmeyer, S. J. : Bid- deficient mice are resistant to Fas- induced hepatocellular apoptosis. Nature 400:.

[32787] Further studies establishing the function and utilities of BID are found in John Hopkins OMIM database record ID 601997, and in cited publications listed in Table 5, which are hereby incorporated by reference.BMF (Accession NP_277038.1) is another GAM281 target gene, herein designated TARGET GENE. BMF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BMF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BMF BINDING SITE, designated SEQ ID:759, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32788] Another function of GAM281 is therefore inhibition of BMF (Accession NP_277038.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMF.

[32789] Bone morphogenetic protein 6 (BMP6, Accession NP_001709.1) is another GAM281 target gene, herein designated TARGET GENE. BMP6 BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by BMP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BMP6 BINDING SITE, designated SEQ ID:6882, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32790] Another function of GAM281 is therefore inhibition of Bone morphogenetic protein 6 (BMP6, Accession NP_001709.1), a gene which induces cartilage and bone formation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMP6.

[32791] The function of BMP6 has been established by previous studies. See BMP5 (OMIM Ref. No. 112265). Hahn et al. (1992) mapped both BMP5 and BMP6 to human chromosome 6 by study of human/rodent somatic cell hybrid lines with cDNA probes. Olavesen et al. (1997) reported fine mapping of 39 ESTs on 6p25- p23. Most of the ESTs (31 of 39) were positioned in the 6p24- p23 interval; of these, 8 were located within a single PAC clone. BMP6 was 1 of the 8 loci on the PAC, between TFAP2 (OMIM Ref. No. 107580) at the centromeric side and DSP (OMIM Ref. No.

125647) on the telomeric side. Rickard et al. (1998) presented evidence that the skeletal effects of estrogen on bone and cartilage may be mediated by increased production of BMP6 by osteoblasts. They investigated the effect of estrogen on BMP production in 2 estrogen- responsive, human immortalized cell lines that display the mature osteoblast phenotype.

[32792]

[32793] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[32794] Hahn, G. V.; Cohen, R. B.; Wozney, J. M.; Levitz, C. L.; Shore, E. M.; Zasloff, M. A.; Kaplan, F. S. : A bone morphogenetic protein subfamily: chromosomal localization of human genes for BMP5, BMP6, and BMP7. Genomics 14: 759- 762, 1992. ; and

[32795] Rickard, D. J.; Hofbauer, L. C.; Bonde, S. K.; Gori, F.; Spelsberg, T. C.; Riggs, B. L. : Bone morphogenetic protein- 6 production in human osteoblastic cell lines: selective regulation b.

[32796] Further studies establishing the function and utilities of BMP6 are found in John Hopkins OMIM database record ID 112266, and in cited publications listed in Table 5, which

are hereby incorporated by reference.BNIP-S (Accession NP_612122.1) is another GAM281 target gene, herein designated TARGET GENE. BNIP-S BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BNIP-S, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BNIP-S BINDING SITE, designated SEQ ID:5845, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32797] Another function of GAM281 is therefore inhibition of BNIP-S (Accession NP_612122.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BNIP-S.

[32798] BRIP1 (Accession NP_114432.1) is another GAM281 target gene, herein designated TARGET GENE. BRIP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BRIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BRIP1 BINDING SITE, designated SEQ ID:13904, to the nucleotide se-

quence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32799] Another function of GAM281 is therefore inhibition of BRIP1 (Accession NP_114432.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRIP1.

[32800] Bromodomain and phd finger containing, 3 (BRPF3, Accession XP_166450.1) is another GAM281 target gene, herein designated TARGET GENE. BRPF3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BRPF3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BRPF3 BINDING SITE, designated SEQ ID:7755, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32801] Another function of GAM281 is therefore inhibition of Bromodomain and phd finger containing, 3 (BRPF3, Accession XP_166450.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRPF3.

[32802] Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession

NP_008979.2) is another GAM281 target gene, herein designated TARGET GENE. BTN3A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTN3A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTN3A1 BINDING SITE, designated SEQ ID:2067, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32803] Another function of GAM281 is therefore inhibition of Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession NP_008979.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN3A1.

[32804] BXDC1 (Accession XP_166303.1) is another GAM281 target gene, herein designated TARGET GENE. BXDC1 BINDING SITE1 and BXDC1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by BXDC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BXDC1 BINDING SITE1 and BXDC1

BINDING SITE2, designated SEQ ID:4549 and SEQ ID:12129 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32805] Another function of GAM281 is therefore inhibition of BXDC1 (Accession XP_166303.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BXDC1.

[32806] BY55 (Accession NP_008984.1) is another GAM281 target gene, herein designated TARGET GENE. BY55 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BY55, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BY55 BINDING SITE, designated SEQ ID:7101, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32807] Another function of GAM281 is therefore inhibition of BY55 (Accession NP_008984.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BY55.

[32808] Chromosome 11 open reading frame 13 (C11orf13, Accession NP_003466.1) is another GAM281 target gene,

herein designated TARGET GENE. C11orf13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C11orf13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C11orf13 BINDING SITE, designated SEQ ID:3521, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32809] Another function of GAM281 is therefore inhibition of Chromosome 11 open reading frame 13 (C11orf13, Accession NP_003466.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf13.

[32810] Chromosome 11 open reading frame 17 (C11orf17, Accession NP_065693.2) is another GAM281 target gene, herein designated TARGET GENE. C11orf17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C11orf17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C11orf17 BINDING SITE, designated SEQ ID:11525, to the nucleotide

sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32811] Another function of GAM281 is therefore inhibition of Chromosome 11 open reading frame 17 (C11orf17, Accession NP_065693.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf17.

[32812] Chromosome 13 open reading frame 1 (C13orf1, Accession NP_065189.1) is another GAM281 target gene, herein designated TARGET GENE. C13orf1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C13orf1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C13orf1 BINDING SITE, designated SEQ ID:5746, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32813] Another function of GAM281 is therefore inhibition of Chromosome 13 open reading frame 1 (C13orf1, Accession NP_065189.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C13orf1.

[32814] Chromosome 14 open reading frame 1 (C14orf1, Accession NP_009107.1) is another GAM281 target gene, herein designated TARGET GENE. C14orf1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf1 BINDING SITE, designated SEQ ID:12744, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32815] Another function of GAM281 is therefore inhibition of Chromosome 14 open reading frame 1 (C14orf1, Accession NP_009107.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf1.

[32816] C14orf113 (Accession NP_060100.1) is another GAM281 target gene, herein designated TARGET GENE. C14orf113 BINDING SITE1 and C14orf113 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C14orf113, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of C14orf113 BINDING SITE1 and C14orf113 BINDING SITE2, designated SEQ ID:18863 and SEQ ID:5052 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32817] Another function of GAM281 is therefore inhibition of C14orf113 (Accession NP_060100.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf113.

[32818] C14orf115 (Accession NP_060698.1) is another GAM281 target gene, herein designated TARGET GENE. C14orf115 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C14orf115, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf115 BINDING SITE, designated SEQ ID:1480, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32819] Another function of GAM281 is therefore inhibition of C14orf115 (Accession NP_060698.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with C14orf115.

[32820] C14orf143 (Accession NP_660274.1) is another GAM281 target gene, herein designated TARGET GENE. C14orf143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf143 BINDING SITE, designated SEQ ID:17955, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32821] Another function of GAM281 is therefore inhibition of C14orf143 (Accession NP_660274.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf143.

[32822] C14orf92 (Accession NP_055643.1) is another GAM281 target gene, herein designated TARGET GENE. C14orf92 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf92, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of C14orf92 BINDING SITE, designated SEQ ID:14861, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32823] Another function of GAM281 is therefore inhibition of C14orf92 (Accession NP_055643.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf92.

[32824] Chromosome 16 open reading frame 7 (C16orf7, Accession NP_004904.1) is another GAM281 target gene, herein designated TARGET GENE. C16orf7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C16orf7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C16orf7 BINDING SITE, designated SEQ ID:16110, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32825] Another function of GAM281 is therefore inhibition of Chromosome 16 open reading frame 7 (C16orf7, Accession NP_004904.1) . Accordingly, utilities of GAM281 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with C16orf7.

[32826] Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) is another GAM281 target gene, herein designated TARGET GENE. C1orf24 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C1orf24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:19538, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32827] Another function of GAM281 is therefore inhibition of Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24.

[32828] C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) is another GAM281 target gene, herein designated TARGET GENE. C1QTNF6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1QTNF6, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1QTNF6 BINDING SITE, designated SEQ ID:14882, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32829] Another function of GAM281 is therefore inhibition of C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QTNF6.

[32830] Chromosome 20 open reading frame 147 (C20orf147, Accession NP_689880.1) is another GAM281 target gene, herein designated TARGET GENE. C20orf147 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf147, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf147 BINDING SITE, designated SEQ ID:16257, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32831] Another function of GAM281 is therefore inhibition of

Chromosome 20 open reading frame 147 (C20orf147, Accession NP_689880.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf147.

[32832] Chromosome 21 open reading frame 67 (C21orf67, Accession NP_478068.1) is another GAM281 target gene, herein designated TARGET GENE. C21orf67 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C21orf67, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C21orf67 BINDING SITE, designated SEQ ID:6569, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32833] Another function of GAM281 is therefore inhibition of Chromosome 21 open reading frame 67 (C21orf67, Accession NP_478068.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf67.

[32834] Chromosome 22 open reading frame 19 (C22orf19, Accession NP_003669.2) is another GAM281 target gene, herein designated TARGET GENE. C22orf19 BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by C22orf19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C22orf19 BINDING SITE, designated SEQ ID:18897, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32835] Another function of GAM281 is therefore inhibition of Chromosome 22 open reading frame 19 (C22orf19, Accession NP_003669.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C22orf19.

[32836] C3IP1 (Accession NP_067646.1) is another GAM281 target gene, herein designated TARGET GENE. C3IP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C3IP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C3IP1 BINDING SITE, designated SEQ ID:2482, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32837] Another function of GAM281 is therefore inhibition of C3IP1 (Accession NP_067646.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C3IP1.

[32838] C4orf9 (Accession XP_035572.1) is another GAM281 target gene, herein designated TARGET GENE. C4orf9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C4orf9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C4orf9 BINDING SITE, designated SEQ ID:15574, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32839] Another function of GAM281 is therefore inhibition of C4orf9 (Accession XP_035572.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C4orf9.

[32840] Chromosome 6 open reading frame 33 (C6orf33, Accession NP_588608.1) is another GAM281 target gene, herein designated TARGET GENE. C6orf33 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf33, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf33 BINDING SITE, designated SEQ ID:6896, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32841] Another function of GAM281 is therefore inhibition of Chromosome 6 open reading frame 33 (C6orf33, Accession NP_588608.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf33.

[32842] C6orf5 (Accession NP_056339.2) is another GAM281 target gene, herein designated TARGET GENE. C6orf5 BINDING SITE1 and C6orf5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C6orf5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf5 BINDING SITE1 and C6orf5 BINDING SITE2, designated SEQ ID:12805 and SEQ ID:10099 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32843] Another function of GAM281 is therefore inhibition of C6orf5 (Accession NP_056339.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf5.

[32844] C6orf57 (Accession NP_660310.1) is another GAM281 target gene, herein designated TARGET GENE. C6orf57 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf57, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf57 BINDING SITE, designated SEQ ID:2114, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32845] Another function of GAM281 is therefore inhibition of C6orf57 (Accession NP_660310.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf57.

[32846] Complement component 7 (C7, Accession NP_000578.1) is another GAM281 target gene, herein designated TARGET GENE. C7 BINDING SITE1 and C7 BINDING SITE2 are target binding sites found in untranslated regions of

mRNA encoded by C7, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C7 BINDING SITE1 and C7 BINDING SITE2, designated SEQ ID:17778 and SEQ ID:9684 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32847] Another function of GAM281 is therefore inhibition of Complement component 7 (C7, Accession NP_000578.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C7.

[32848] Chromosome 9 open reading frame 5 (C9orf5, Accession NP_114401.1) is another GAM281 target gene, herein designated TARGET GENE. C9orf5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C9orf5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C9orf5 BINDING SITE, designated SEQ ID:14258, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32849] Another function of GAM281 is therefore inhibition of Chromosome 9 open reading frame 5 (C9orf5, Accession NP_114401.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf5.

[32850] Chromosome 9 open reading frame 9 (C9orf9, Accession NP_061829.2) is another GAM281 target gene, herein designated TARGET GENE. C9orf9 BINDING SITE1 and C9orf9 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C9orf9, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C9orf9 BINDING SITE1 and C9orf9 BINDING SITE2, designated SEQ ID:5477 and SEQ ID:11520 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32851] Another function of GAM281 is therefore inhibition of Chromosome 9 open reading frame 9 (C9orf9, Accession NP_061829.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf9.

[32852] CAB2 (Accession NP_219487.2) is another GAM281 target

gene, herein designated TARGET GENE. CAB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAB2 BINDING SITE, designated SEQ ID:9181, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32853] Another function of GAM281 is therefore inhibition of CAB2 (Accession NP_219487.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAB2.

[32854] Calcium binding protein 4 (CABP4, Accession NP_660201.1) is another GAM281 target gene, herein designated TARGET GENE. CABP4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CABP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CABP4 BINDING SITE, designated SEQ ID:7624, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32855] Another function of GAM281 is therefore inhibition of Calcium binding protein 4 (CABP4, Accession NP_660201.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CABP4.

[32856] Calcium modulating ligand (CAMLG, Accession NP_001736.1) is another GAM281 target gene, herein designated TARGET GENE. CAMLG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAMLG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMLG BINDING SITE, designated SEQ ID:18944, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32857] Another function of GAM281 is therefore inhibition of Calcium modulating ligand (CAMLG, Accession NP_001736.1), a gene which is likely involved in the mobilization of calcium as a result of the tcr/cd3 complex interaction. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMLG.

[32858] The function of CAMLG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.CAPRI (Accession NP_008920.3) is another GAM281 target gene, herein designated TARGET GENE. CAPRI BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAPRI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAPRI BINDING SITE, designated SEQ ID:4271, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32859] Another function of GAM281 is therefore inhibition of CAPRI (Accession NP_008920.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPRI.

[32860] Caspase recruitment domain family, member 6 (CARD6, Accession NP_115976.2) is another GAM281 target gene, herein designated TARGET GENE. CARD6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CARD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CARD6 BINDING SITE, designated SEQ ID:9036, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32861] Another function of GAM281 is therefore inhibition of Caspase recruitment domain family, member 6 (CARD6, Accession NP_115976.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD6.

[32862] Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116766.1) is another GAM281 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE, designated SEQ ID:16398, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32863] Another function of GAM281 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116766.1), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[32864] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116765.1) is another GAM281 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE, designated SEQ ID:16398, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[32865] Another function of GAM281 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116765.1), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[32866] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_001215.1) is another GAM281 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE, designated SEQ ID:16398, to the nucleotide sequence of

GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32867] Another function of GAM281 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_001215.1), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[32868] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116764.1) is another GAM281 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE,

designated SEQ ID:16398, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32869] Another function of GAM281 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116764.1), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[32870] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203520.1) is another GAM281 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated

SEQ ID:15049, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32871] Another function of GAM281 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203520.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[32872] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203521.1) is another GAM281 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32873] Another function of GAM281 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203521.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[32874] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_001219.2) is another GAM281 target gene, herein designated TARGET GENE.

CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32875] Another function of GAM281 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_001219.2), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[32876] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203519.1) is another GAM281 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32877] Another function of GAM281 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203519.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[32878] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_787060.1) is another GAM281 target gene, herein designated TARGET GENE. CBFA2T2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CBFA2T2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CBFA2T2 BINDING SITE, designated SEQ ID:8242, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32879] Another function of GAM281 is therefore inhibition of Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_787060.1), a gene which is a putative transcription factor. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T2.

[32880] The function of CBFA2T2 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Chemokine (c-c motif) ligand 16 (CCL16, Accession NP_004581.1) is another GAM281 target gene, herein designated TARGET GENE. CCL16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL16 BINDING SITE, designated SEQ ID:9543, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32881] Another function of GAM281 is therefore inhibition of Chemokine (c-c motif) ligand 16 (CCL16, Accession NP_004581.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL16.

[32882] Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) is another GAM281 target gene, herein designated TARGET GENE. CCL22 BINDING SITE1 and CCL22 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CCL22, corre-

sponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL22 BINDING SITE1 and CCL22 BINDING SITE2, designated SEQ ID:15049 and SEQ ID:1679 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32883] Another function of GAM281 is therefore inhibition of Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL22.

[32884] Cyclin f (CCNF, Accession NP_001752.1) is another GAM281 target gene, herein designated TARGET GENE. CCNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCNF BINDING SITE, designated SEQ ID:17624, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32885] Another function of GAM281 is therefore inhibition of Cy-

clin f (CCNF, Accession NP_001752.1), a gene which likely to be involved in the control of the cell cycle during s phase and g2. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNF.

[32886] The function of CCNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Ccr4 carbon catabolite repression 4-like (s. cerevisiae) (CCRN4L, Accession NP_036250.2) is another GAM281 target gene, herein designated TARGET GENE. CCRN4L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCRN4L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCRN4L BINDING SITE, designated SEQ ID:4698, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32887] Another function of GAM281 is therefore inhibition of Ccr4 carbon catabolite repression 4-like (s. cerevisiae) (CCRN4L, Accession NP_036250.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with CCRN4L.

[32888] Cd209 antigen (CD209, Accession NP_066978.1) is another GAM281 target gene, herein designated TARGET GENE. CD209 BINDING SITE1 and CD209 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CD209, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD209 BINDING SITE1 and CD209 BINDING SITE2, designated SEQ ID:4298 and SEQ ID:17051 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32889] Another function of GAM281 is therefore inhibition of Cd209 antigen (CD209, Accession NP_066978.1), a gene which may play an important role in the CD4- independent association of HIV with cells. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD209.

[32890] The function of CD209 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM96.1.Cd24 antigen (small cell lung carcinoma cluster 4 antigen) (CD24, Accession NP_037362.1) is another GAM281 target gene, herein designated TARGET GENE. CD24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD24 BINDING SITE, designated SEQ ID:19572, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32891] Another function of GAM281 is therefore inhibition of Cd24 antigen (small cell lung carcinoma cluster 4 antigen) (CD24, Accession NP_037362.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD24.

[32892] Cdc14 cell division cycle 14 homolog b (s. cerevisiae) (CDC14B, Accession NP_201589.1) is another GAM281 target gene, herein designated TARGET GENE. CDC14B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDC14B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC14B BINDING SITE, designated SEQ ID:17127, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32893] Another function of GAM281 is therefore inhibition of Cdc14 cell division cycle 14 homolog b (s. cerevisiae) (CDC14B, Accession NP_201589.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC14B.

[32894] Cell division cycle 2-like 2 (CDC2L2, Accession NP_296370.1) is another GAM281 target gene, herein designated TARGET GENE. CDC2L2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CDC2L2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC2L2 BINDING SITE, designated SEQ ID:15084, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32895] Another function of GAM281 is therefore inhibition of Cell

division cycle 2-like 2 (CDC2L2, Accession NP_296370.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC2L2.

[32896] Cdc6 cell division cycle 6 homolog (s. cerevisiae) (CDC6, Accession NP_001245.1) is another GAM281 target gene, herein designated TARGET GENE. CDC6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDC6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC6 BINDING SITE, designated SEQ ID:9211, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32897] Another function of GAM281 is therefore inhibition of Cdc6 cell division cycle 6 homolog (s. cerevisiae) (CDC6, Accession NP_001245.1), a gene which is a component of the origin recognition complex (orc) that binds origins of replication. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC6.

[32898] The function of CDC6 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.CDCP1 (Accession NP_073753.3) is another GAM281 target gene, herein designated TARGET GENE. CDCP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDCP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDCP1 BINDING SITE, designated SEQ ID:12091, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32899] Another function of GAM281 is therefore inhibition of CDCP1 (Accession NP_073753.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDCP1.

[32900] Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) is another GAM281 target gene, herein designated TARGET GENE. CDH1 BINDING SITE1 and CDH1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CDH1, corresponding to target binding sites such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH1 BINDING SITE1 and CDH1 BINDING SITE2, designated SEQ ID:12580 and SEQ ID:5514 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32901] Another function of GAM281 is therefore inhibition of Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH1.

[32902] Cadherin 17, li cadherin (liver-intestine) (CDH17, Accession NP_004054.2) is another GAM281 target gene, herein designated TARGET GENE. CDH17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDH17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH17 BINDING SITE, designated SEQ ID:13851, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32903] Another function of GAM281 is therefore inhibition of

Cadherin 17, li cadherin (liver-intestine) (CDH17, Accession NP_004054.2), a gene which may have a role in the morphological organization of liver and intestine and involved in intestinal peptide transport. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH17.

[32904] The function of CDH17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.CDK11 (Accession XP_166324.1) is another GAM281 target gene, herein designated TARGET GENE. CDK11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDK11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDK11 BINDING SITE, designated SEQ ID:8162, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32905] Another function of GAM281 is therefore inhibition of CDK11 (Accession XP_166324.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDK11.

[32906] CDKAL1 (Accession NP_060244.1) is another GAM281 target gene, herein designated TARGET GENE. CDKAL1 BINDING SITE1 and CDKAL1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CDKAL1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDKAL1 BINDING SITE1 and CDKAL1 BINDING SITE2, designated SEQ ID:1255 and SEQ ID:3603 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32907] Another function of GAM281 is therefore inhibition of CDKAL1 (Accession NP_060244.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKAL1.

[32908] CDT6 (Accession NP_066969.1) is another GAM281 target gene, herein designated TARGET GENE. CDT6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDT6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDT6 BINDING SITE, designated SEQ ID:18500, to the nucleotide se-

quence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32909] Another function of GAM281 is therefore inhibition of CDT6 (Accession NP_066969.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDT6.

[32910] Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) is another GAM281 target gene, herein designated TARGET GENE. CEACAM8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CEACAM8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CEACAM8 BINDING SITE, designated SEQ ID:17969, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32911] Another function of GAM281 is therefore inhibition of Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEACAM8.

[32912] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) is another GAM281 target gene, herein designated TARGET GENE. CECR1 BINDING SITE1 and CECR1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CECR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE1 and CECR1 BINDING SITE2, designated SEQ ID:9037 and SEQ ID:4574 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32913] Another function of GAM281 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[32914] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) is another GAM281 target gene, herein designated TARGET GENE. CECR1 BINDING SITE1 and CECR1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts

of mRNA encoded by CECR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE1 and CECR1 BINDING SITE2, designated SEQ ID:4574 and SEQ ID:9037 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32915] Another function of GAM281 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[32916] Centromere protein h (CENPH, Accession NP_075060.1) is another GAM281 target gene, herein designated TARGET GENE. CENPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CENPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENPH BINDING SITE, designated SEQ ID:19549, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ

ID:278.

[32917] Another function of GAM281 is therefore inhibition of Centromere protein h (CENPH, Accession NP_075060.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENPH.

[32918] Centromere protein j (CENPJ, Accession NP_060921.2) is another GAM281 target gene, herein designated TARGET GENE. CENPJ BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CENPJ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENPJ BINDING SITE, designated SEQ ID:13565, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32919] Another function of GAM281 is therefore inhibition of Centromere protein j (CENPJ, Accession NP_060921.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENPJ.

[32920] CGI-150 (Accession NP_057164.1) is another GAM281 target gene, herein designated TARGET GENE. CGI-150

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CGI-150, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-150 BINDING SITE, designated SEQ ID:2191, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32921] Another function of GAM281 is therefore inhibition of CGI-150 (Accession NP_057164.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-150.

[32922] CGI-43 (Accession NP_056437.1) is another GAM281 target gene, herein designated TARGET GENE. CGI-43 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CGI-43, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-43 BINDING SITE, designated SEQ ID:14860, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32923] Another function of GAM281 is therefore inhibition of CGI-43 (Accession NP_056437.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-43.

[32924] Chromodomain helicase dna binding protein 5 (CHD5, Accession NP_056372.1) is another GAM281 target gene, herein designated TARGET GENE. CHD5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHD5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHD5 BINDING SITE, designated SEQ ID:2568, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32925] Another function of GAM281 is therefore inhibition of Chromodomain helicase dna binding protein 5 (CHD5, Accession NP_056372.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHD5.

[32926] Chromatin accessibility complex 1 (CHRAC1, Accession NP_059140.1) is another GAM281 target gene, herein designated TARGET GENE. CHRAC1 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by CHRAC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHRAC1 BINDING SITE, designated SEQ ID:9475, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32927] Another function of GAM281 is therefore inhibition of Chromatin accessibility complex 1 (CHRAC1, Accession NP_059140.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRAC1.

[32928] Carbohydrate (chondroitin) synthase 1 (CHSY1, Accession NP_055733.2) is another GAM281 target gene, herein designated TARGET GENE. CHSY1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHSY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHSY1 BINDING SITE, designated SEQ ID:11924, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ

ID:278.

[32929] Another function of GAM281 is therefore inhibition of Carbohydrate (chondroitin) synthase 1 (CHSY1, Accession NP_055733.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHSY1.

[32930] Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2) is another GAM281 target gene, herein designated TARGET GENE. CIAS1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CIAS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIAS1 BINDING SITE, designated SEQ ID:13461, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32931] Another function of GAM281 is therefore inhibition of Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2), a gene which may mediate protein- protein interactions; contains a leucine rich repeat and therefore may be associated with Familial cold autoinflammatory syndrome, muckle- wells syndrome. Accordingly,

utilities of GAM281 include diagnosis, prevention and treatment of Familial cold autoinflammatory syndrome, muckle- wells syndrome, and of other diseases and clinical conditions associated with CIAS1.

[32932] The function of CIAS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM90.1.CIP29 (Accession NP_115740.3) is another GAM281 target gene, herein designated TARGET GENE. CIP29 BINDING SITE1 and CIP29 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CIP29, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIP29 BINDING SITE1 and CIP29 BINDING SITE2, designated SEQ ID:3509 and SEQ ID:20120 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32933] Another function of GAM281 is therefore inhibition of CIP29 (Accession NP_115740.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIP29.

[32934] Claudin 14 (CLDN14, Accession NP_652763.1) is another

GAM281 target gene, herein designated TARGET GENE. CLDN14 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CLDN14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLDN14 BINDING SITE, designated SEQ ID:3558, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32935] Another function of GAM281 is therefore inhibition of Claudin 14 (CLDN14, Accession NP_652763.1), a gene which provides structural support for the auditory neuroepithelium. and therefore is associated with Deafness. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Deafness., and of other diseases and clinical conditions associated with CLDN14.

[32936] The function of CLDN14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2) is another GAM281

target gene, herein designated TARGET GENE. CLECSF12 BINDING SITE1 and CLECSF12 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CLECSF12, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLECSF12 BINDING SITE1 and CLECSF12 BINDING SITE2, designated SEQ ID:16192 and SEQ ID:15296 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32937] Another function of GAM281 is therefore inhibition of C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2), a gene which is a pattern- recognition receptor . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLECSF12.

[32938] The function of CLECSF12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Chloride intracellular channel 5 (CLIC5, Accession NP_058625.1) is another GAM281 target gene,

herein designated TARGET GENE. CLIC5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CLIC5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLIC5 BINDING SITE, designated SEQ ID:19116, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32939] Another function of GAM281 is therefore inhibition of Chloride intracellular channel 5 (CLIC5, Accession NP_058625.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLIC5.

[32940] Ceroid-lipofuscinosis, neuronal 6, late infantile, variant (CLN6, Accession NP_060352.1) is another GAM281 target gene, herein designated TARGET GENE. CLN6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLN6 BINDING SITE, designated SEQ ID:19830, to the nucleotide se-

quence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32941] Another function of GAM281 is therefore inhibition of Ceroid-lipofuscinosis, neuronal 6, late infantile, variant (CLN6, Accession NP_060352.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLN6.

[32942] Ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) (CLN8, Accession NP_061764.2) is another GAM281 target gene, herein designated TARGET GENE. CLN8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLN8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLN8 BINDING SITE, designated SEQ ID:515, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32943] Another function of GAM281 is therefore inhibition of Ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) (CLN8, Accession NP_061764.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with CLN8.

[32944] Cell matrix adhesion regulator (CMAR, Accession NP_005191.2) is another GAM281 target gene, herein designated TARGET GENE. CMAR BINDING SITE1 and CMAR BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CMAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CMAR BINDING SITE1 and CMAR BINDING SITE2, designated SEQ ID:5053 and SEQ ID:18767 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32945] Another function of GAM281 is therefore inhibition of Cell matrix adhesion regulator (CMAR, Accession NP_005191.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CMAR.

[32946] Calponin 2 (CNN2, Accession NP_004359.1) is another GAM281 target gene, herein designated TARGET GENE. CNN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNN2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNN2 BINDING SITE, designated SEQ ID:9959, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32947] Another function of GAM281 is therefore inhibition of Calponin 2 (CNN2, Accession NP_004359.1), a gene which may be involved in the structural organization and/or anchorage of actin filaments. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNN2.

[32948] The function of CNN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.2',3'-cyclic nucleotide 3' phosphodiesterase (CNP, Accession NP_149124.1) is another GAM281 target gene, herein designated TARGET GENE. CNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNP BINDING SITE, designated SEQ ID:606, to the nucleotide sequence

of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32949] Another function of GAM281 is therefore inhibition of 2',3'-cyclic nucleotide 3' phosphodiesterase (CNP, Accession NP_149124.1), a gene which can link tubulin to membranes and may regulate cytoplasmic microtubule distribution. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNP.

[32950] The function of CNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Collagen, type iv, alpha 4 (COL4A4, Accession NP_000083.1) is another GAM281 target gene, herein designated TARGET GENE. COL4A4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by COL4A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL4A4 BINDING SITE, designated SEQ ID:12506, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32951] Another function of GAM281 is therefore inhibition of Collagen, type iv, alpha 4 (COL4A4, Accession NP_000083.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A4.

[32952] Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) is another GAM281 target gene, herein designated TARGET GENE. COLEC12 BINDING SITE1 and COLEC12 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by COLEC12, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COLEC12 BINDING SITE1 and COLEC12 BINDING SITE2, designated SEQ ID:12507 and SEQ ID:11525 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32953] Another function of GAM281 is therefore inhibition of Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC12.

[32954] COQ4 (Accession NP_057119.1) is another GAM281 target gene, herein designated TARGET GENE. COQ4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by COQ4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COQ4 BINDING SITE, designated SEQ ID:14708, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32955] Another function of GAM281 is therefore inhibition of COQ4 (Accession NP_057119.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COQ4.

[32956] Coronin, actin binding protein, 1c (CORO1C, Accession NP_055140.1) is another GAM281 target gene, herein designated TARGET GENE. CORO1C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CORO1C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CORO1C BINDING SITE, designated SEQ ID:13595, to the nucleotide se-

quence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32957] Another function of GAM281 is therefore inhibition of Coronin, actin binding protein, 1c (CORO1C, Accession NP_055140.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CORO1C.

[32958] Cox15 homolog, cytochrome c oxidase assembly protein (yeast) (COX15, Accession NP_510870.1) is another GAM281 target gene, herein designated TARGET GENE. COX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COX15 BINDING SITE, designated SEQ ID:7552, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32959] Another function of GAM281 is therefore inhibition of Cox15 homolog, cytochrome c oxidase assembly protein (yeast) (COX15, Accession NP_510870.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with COX15.

[32960] Carboxypeptidase a4 (CPA4, Accession NP_057436.1) is another GAM281 target gene, herein designated TARGET GENE. CPA4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPA4 BINDING SITE, designated SEQ ID:8942, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32961] Another function of GAM281 is therefore inhibition of Carboxypeptidase a4 (CPA4, Accession NP_057436.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPA4.

[32962] CPR8 (Accession NP_065790.1) is another GAM281 target gene, herein designated TARGET GENE. CPR8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CPR8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of CPR8 BINDING SITE, designated SEQ ID:13999, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32963] Another function of GAM281 is therefore inhibition of CPR8 (Accession NP_065790.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPR8.

[32964] Carbamoyl-phosphate synthetase 1, mitochondrial (CPS1, Accession NP_001866.2) is another GAM281 target gene, herein designated TARGET GENE. CPS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPS1 BINDING SITE, designated SEQ ID:14493, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32965] Another function of GAM281 is therefore inhibition of Carbamoyl-phosphate synthetase 1, mitochondrial (CPS1, Accession NP_001866.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPS1.

[32966] Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) is another GAM281 target gene, herein designated TARGET GENE. CPSF2 BINDING SITE1 and CPSF2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CPSF2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPSF2 BINDING SITE1 and CPSF2 BINDING SITE2, designated SEQ ID:591 and SEQ ID:1877 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32967] Another function of GAM281 is therefore inhibition of Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPSF2.

[32968] Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000642.2) is another GAM281 target gene, herein designated TARGET GENE. CR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CR1, corresponding to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CR1 BINDING SITE, designated SEQ ID:17292, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32969] Another function of GAM281 is therefore inhibition of Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000642.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CR1.

[32970] Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000564.1) is another GAM281 target gene, herein designated TARGET GENE. CR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CR1 BINDING SITE, designated SEQ ID:17292, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[32971] Another function of GAM281 is therefore inhibition of Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000564.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CR1.

[32972] Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) is another GAM281 target gene, herein designated TARGET GENE. CRLF3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRLF3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRLF3 BINDING SITE, designated SEQ ID:7105, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32973] Another function of GAM281 is therefore inhibition of Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRLF3.

[32974] Cofactor required for sp1 transcriptional activation, sub-

unit 6, 77kda (CRSP6, Accession NP_004259.3) is another GAM281 target gene, herein designated TARGET GENE. CRSP6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRSP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRSP6 BINDING SITE, designated SEQ ID:7661, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32975] Another function of GAM281 is therefore inhibition of Cofactor required for sp1 transcriptional activation, subunit 6, 77kda (CRSP6, Accession NP_004259.3), a gene which is required for Sp1 mediated transcriptional activation with TAF(II)s. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRSP6.

[32976] The function of CRSP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Cartilage associated protein (CRTAP, Accession NP_006362.1) is another GAM281 target gene, herein designated TARGET GENE. CRTAP BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by CRTAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRTAP BINDING SITE, designated SEQ ID:7107, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32977] Another function of GAM281 is therefore inhibition of Cartilage associated protein (CRTAP, Accession NP_006362.1), a gene which is a novel developmentally regulated chick embryo protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRTAP.

[32978] The function of CRTAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Cysteine sulfinic acid decarboxylase (CSAD, Accession NP_057073.2) is another GAM281 target gene, herein designated TARGET GENE. CSAD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CSAD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of CSAD BINDING SITE, designated SEQ ID:7030, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32979] Another function of GAM281 is therefore inhibition of Cysteine sulfinic acid decarboxylase (CSAD, Accession NP_057073.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSAD.

[32980] CSE-C (Accession NP_061851.1) is another GAM281 target gene, herein designated TARGET GENE. CSE-C BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CSE-C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSE-C BINDING SITE, designated SEQ ID:2336, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32981] Another function of GAM281 is therefore inhibition of CSE-C (Accession NP_061851.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE-C.

[32982] Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_803185.1) is another GAM281 target gene, herein designated TARGET GENE. CSE1L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CSE1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSE1L BINDING SITE, designated SEQ ID:6312, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32983] Another function of GAM281 is therefore inhibition of Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_803185.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE1L.

[32984] Casein kinase 1, gamma 2 (CSNK1G2, Accession NP_001310.2) is another GAM281 target gene, herein designated TARGET GENE. CSNK1G2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CSNK1G2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of CSNK1G2 BINDING SITE, designated SEQ ID:14869, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32985] Another function of GAM281 is therefore inhibition of Casein kinase 1, gamma 2 (CSNK1G2, Accession NP_001310.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK1G2.

[32986] Casein kinase 2, alpha prime polypeptide (CSNK2A2, Accession NP_001887.1) is another GAM281 target gene, herein designated TARGET GENE. CSNK2A2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CSNK2A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSNK2A2 BINDING SITE, designated SEQ ID:15382, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32987] Another function of GAM281 is therefore inhibition of Casein kinase 2, alpha prime polypeptide (CSNK2A2, Accession NP_001887.1), a gene which catalyzes the phospho-

rylation of serine or threonine residues in proteins. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK2A2.

[32988] The function of CSNK2A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.CST (Accession NP_004852.1) is another GAM281 target gene, herein designated TARGET GENE. CST BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CST BINDING SITE, designated SEQ ID:9756, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32989] Another function of GAM281 is therefore inhibition of CST (Accession NP_004852.1), a gene which nucleotide- sugar transporter. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CST.

[32990] The function of CST and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM221.1.CTEN (Accession NP_116254.3) is another GAM281 target gene, herein designated TARGET GENE. CTEN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTEN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTEN BINDING SITE, designated SEQ ID:14746, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32991] Another function of GAM281 is therefore inhibition of CTEN (Accession NP_116254.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTEN.

[32992] Cardiotrophin 1 (CTF1, Accession NP_001321.1) is another GAM281 target gene, herein designated TARGET GENE. CTF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of CTF1 BINDING SITE, designated SEQ ID:13287, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32993] Another function of GAM281 is therefore inhibition of Cardiotrophin 1 (CTF1, Accession NP_001321.1), a gene which may play a role in cardiac hypertrophy. and therefore may be associated with Cardiac hypertrophy. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Cardiac hypertrophy, and of other diseases and clinical conditions associated with CTF1.

[32994] The function of CTF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Cathepsin b (CTSB, Accession NP_680090.1) is another GAM281 target gene, herein designated TARGET GENE. CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSB BINDING SITE, designated SEQ ID:12465, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[32995] Another function of GAM281 is therefore inhibition of Cathepsin b (CTSB, Accession NP_680090.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSB.

[32996] Cathepsin b (CTSB, Accession NP_680092.1) is another GAM281 target gene, herein designated TARGET GENE. CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSB BINDING SITE, designated SEQ ID:12465, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32997] Another function of GAM281 is therefore inhibition of Cathepsin b (CTSB, Accession NP_680092.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSB.

[32998] Cathepsin s (CTSS, Accession NP_004070.3) is another

GAM281 target gene, herein designated TARGET GENE. CTSS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSS BINDING SITE, designated SEQ ID:4517, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[32999] Another function of GAM281 is therefore inhibition of Cathepsin s (CTSS, Accession NP_004070.3), a gene which is a lysosomal cysteine (thiol) protease that cleaves elastin. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSS.

[33000] The function of CTSS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Chemokine (c-x-c motif) ligand 16 (CXCL16, Accession NP_071342.1) is another GAM281 target gene, herein designated TARGET GENE. CXCL16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CXCL16, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CXCL16 BINDING SITE, designated SEQ ID:17688, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33001] Another function of GAM281 is therefore inhibition of Chemokine (c-x-c motif) ligand 16 (CXCL16, Accession NP_071342.1), a gene which induces calcium mobilization. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCL16.

[33002] The function of CXCL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Chemokine (c-x-c motif) ligand 6 (granulocyte chemotactic protein 2) (CXCL6, Accession NP_002984.1) is another GAM281 target gene, herein designated TARGET GENE. CXCL6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CXCL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of CXCL6 BINDING SITE, designated SEQ ID:4626, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33003] Another function of GAM281 is therefore inhibition of Chemokine (c-x-c motif) ligand 6 (granulocyte chemotactic protein 2) (CXCL6, Accession NP_002984.1), a gene which is chemotactic for neutrophil granulocytes. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCL6.

[33004] The function of CXCL6 has been established by previous studies. Rovai et al. (1997) cloned the human GCP2 gene, as well as epithelial cell- derived neutrophil- activating peptide- 78 (ENA78, or SCYB5; 600324). Both coding and noncoding portions of the GCP2 gene share very high nucleotide similarity to ENA78, except for the occurrence of a long interspersed sequence 5- prime of the GCP2 gene. The GCP2 gene encodes a propeptide of 114 amino acids. Despite 85% identity of the first 270 nucleotides 5- prime of the transcription start sites, GCP2 and the other CXC chemokine gene ENA78 showed cell- specific differences in regulation. Wuyts et al. (1997) synthesized and purified a human GCP2 protein of 75 amino acids. In vitro, syn-

thetic GCP2 was an equally active chemoattractant for neutrophilic granulocytes as was natural 75- amino acid GCP2. Synthetic GCP2 did not stimulate eosinophil, monocyte, or lymphocyte chemotaxis. The authors showed that GCP2 binds to the chemokine receptors CXCR1 and CXCR2. In vivo studies in rabbit demonstrated that GCP2 is a potent inflammatory mediator.

[33005]

[33006] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[33007] Rovai, L. E.; Herschman, H. R.; Smith, J. B. : Cloning and characterization of the human granulocyte chemotactic protein- 2 gene. J. Immun. 158: 5257- 5266, 1997. ; and

[33008] Wuyts, A.; van Osselaer, N.; Haelens, A.; Samson, I.; Herdewijn, P.; Ben- Baruch, A.; Oppenheim, J. J.; Proost, P.; van Damme, J. : Characterization of synthetic human granulocyte chemot.

[33009] Further studies establishing the function and utilities of CXCL6 are found in John Hopkins OMIM database record ID 138965, and in cited publications listed in Table 5, which are hereby incorporated by reference.Chromosome x open reading frame 12 (CXorf12, Accession

NP_003483.1) is another GAM281 target gene, herein designated TARGET GENE. CXorf12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CXorf12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CXorf12 BINDING SITE, designated SEQ ID:4704, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33010] Another function of GAM281 is therefore inhibition of Chromosome x open reading frame 12 (CXorf12, Accession NP_003483.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXorf12.

[33011] CYCS (Accession NP_061820.1) is another GAM281 target gene, herein designated TARGET GENE. CYCS BINDING SITE1 through CYCS BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by CYCS, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYCS BINDING SITE1 through CYCS BINDING

SITE3, designated SEQ ID:18868, SEQ ID:18991 and SEQ ID:9339 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33012] Another function of GAM281 is therefore inhibition of CYCS (Accession NP_061820.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYCS.

[33013] Cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2, Accession NP_001331.1) is another GAM281 target gene, herein designated TARGET GENE. CYLC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYLC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYLC2 BINDING SITE, designated SEQ ID:15540, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33014] Another function of GAM281 is therefore inhibition of Cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2, Accession NP_001331.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with CYLC2.

[33015] Cytochrome p450, subfamily i (aromatic compound-inducible), polypeptide 2 (CYP1A2, Accession NP_000752.1) is another GAM281 target gene, herein designated TARGET GENE. CYP1A2 BINDING SITE1 through CYP1A2 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by CYP1A2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP1A2 BINDING SITE1 through CYP1A2 BINDING SITE3, designated SEQ ID:18279, SEQ ID:6637 and SEQ ID:13576 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33016] Another function of GAM281 is therefore inhibition of Cytochrome p450, subfamily i (aromatic compound-inducible), polypeptide 2 (CYP1A2, Accession NP_000752.1), a gene which intervenes in an NADPH- dependent electron transport pathway. and therefore may be associated with Porphyria cutanea tarda. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Porphyria cutanea tarda, and of other diseases and clinical conditions associated with CYP1A2.

[33017] The function of CYP1A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1) is another GAM281 target gene, herein designated TARGET GENE. CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CYP2B6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2, designated SEQ ID:10618 and SEQ ID:2194 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33018] Another function of GAM281 is therefore inhibition of Cytochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1), a gene which oxidizes a variety of structurally unrelated compounds, including steroids, fatty acids, and xenobiotics. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with CYP2B6.

[33019] The function of CYP2B6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily ivf, polypeptide 3 (leukotriene b4 omega hydroxylase) (CYP4F3, Accession NP_000887.1) is another GAM281 target gene, herein designated TARGET GENE. CYP4F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP4F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP4F3 BINDING SITE, designated SEQ ID:9158, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33020] Another function of GAM281 is therefore inhibition of Cytochrome p450, subfamily ivf, polypeptide 3 (leukotriene b4 omega hydroxylase) (CYP4F3, Accession NP_000887.1), a gene which converts leukotriene B4 into the less active 20- hydroxy- leukotriene B4. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with CYP4F3.

[33021] The function of CYP4F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.1.CYP51A1 (Accession NP_000777.1) is another GAM281 target gene, herein designated TARGET GENE. CYP51A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP51A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP51A1 BINDING SITE, designated SEQ ID:2152, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33022] Another function of GAM281 is therefore inhibition of CYP51A1 (Accession NP_000777.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP51A1.

[33023] Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1) is another GAM281 target gene, herein designated TARGET GENE. CYP8B1 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by CYP8B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP8B1 BINDING SITE, designated SEQ ID:5978, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33024] Another function of GAM281 is therefore inhibition of Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1), a gene which functions in bile acid biosynthesis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP8B1.

[33025] The function of CYP8B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.D2S448 (Accession XP_056455.2) is another GAM281 target gene, herein designated TARGET GENE. D2S448 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by D2S448, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of D2S448 BINDING SITE, designated SEQ ID:11750, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33026] Another function of GAM281 is therefore inhibition of D2S448 (Accession XP_056455.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with D2S448.

[33027] DBC-1 (Accession NP_066997.3) is another GAM281 target gene, herein designated TARGET GENE. DBC-1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DBC-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DBC-1 BINDING SITE, designated SEQ ID:12841, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33028] Another function of GAM281 is therefore inhibition of DBC-1 (Accession NP_066997.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBC-1.

[33029] Debranching enzyme homolog 1 (s. cerevisiae) (DBR1, Accession NP_057300.1) is another GAM281 target gene, herein designated TARGET GENE. DBR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DBR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DBR1 BINDING SITE, designated SEQ ID:7961, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33030] Another function of GAM281 is therefore inhibition of Debranching enzyme homolog 1 (s. cerevisiae) (DBR1, Accession NP_057300.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBR1.

[33031] Deoxycytidine kinase (DCK, Accession NP_000779.1) is another GAM281 target gene, herein designated TARGET GENE. DCK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DCK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of DCK BINDING SITE, designated SEQ ID:3487, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33032] Another function of GAM281 is therefore inhibition of Deoxycytidine kinase (DCK, Accession NP_000779.1), a gene which mediates the phosphorylation of several deoxyribonucleosides and their analogs. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCK.

[33033] The function of DCK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM148.1.Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835364.1) is another GAM281 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:16590, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33034] Another function of GAM281 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835364.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[33035] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) is another GAM281 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:16590, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33036] Another function of GAM281 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[33037] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) is another GAM281 target

gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:16590, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33038] Another function of GAM281 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[33039] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) is another GAM281 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:16590,

to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33040] Another function of GAM281 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[33041] Dead/h (asp-glu-ala-asp/his) box polypeptide 31 (DDX31, Accession NP_619526.1) is another GAM281 target gene, herein designated TARGET GENE. DDX31 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DDX31, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX31 BINDING SITE, designated SEQ ID:16338, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33042] Another function of GAM281 is therefore inhibition of Dead/h (asp-glu-ala-asp/his) box polypeptide 31 (DDX31, Accession NP_619526.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with DDX31.

[33043] Desmin (DES, Accession NP_001918.2) is another GAM281 target gene, herein designated TARGET GENE. DES BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DES BINDING SITE, designated SEQ ID:14498, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33044] Another function of GAM281 is therefore inhibition of Desmin (DES, Accession NP_001918.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DES.

[33045] Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1) is another GAM281 target gene, herein designated TARGET GENE. DFFB BINDING SITE1 and DFFB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DFFB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DFFB BINDING SITE1 and DFFB BINDING SITE2, designated SEQ ID:2019 and SEQ ID:9091 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33046] Another function of GAM281 is therefore inhibition of Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1), a gene which induces DNA fragmentation and chromatin condensation during apoptosis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DFFB.

[33047] The function of DFFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Dihydrofolate reductase (DHFR, Accession NP_000782.1) is another GAM281 target gene, herein designated TARGET GENE. DHFR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHFR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of DHFR BINDING SITE, designated SEQ ID:8052, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33048] Another function of GAM281 is therefore inhibition of Dihydrofolate reductase (DHFR, Accession NP_000782.1), a gene which converts dihydrofolate into tetrahydrofolate. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DHFR.

[33049] The function of DHFR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM64.1.Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1) is another GAM281 target gene, herein designated TARGET GENE. DIAPH2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DIAPH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DIAPH2 BINDING SITE, designated SEQ ID:14492, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33050] Another function of GAM281 is therefore inhibition of Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1), a gene which may affect in oogenesis and therefore may be associated with Premature ovarian failure . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Premature ovarian failure ., and of other diseases and clinical conditions associated with DIAPH2.

[33051] The function of DIAPH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1) is another GAM281 target gene, herein designated TARGET GENE. DISC1 BINDING SITE1 and DISC1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DISC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DISC1 BINDING SITE1 and DISC1 BINDING SITE2, designated SEQ ID:1298 and SEQ ID:11285 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33052] Another function of GAM281 is therefore inhibition of Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1), a gene which has globular N- terminal domain(s) and a helical C- terminal domain. and therefore may be associated with Schizophrenia . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Schizophrenia ., and of other diseases and clinical conditions associated with DISC1.

[33053] The function of DISC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.DKFZP434B044 (Accession NP_113664.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP434B044 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434B044, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434B044 BINDING SITE, designated SEQ ID:4080, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33054] Another function of GAM281 is therefore inhibition of DK-

FZP434B044 (Accession NP_113664.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434B044.

[33055] DKFZP434B1727 (Accession NP_115519.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP434B1727 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434B1727, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434B1727 BINDING SITE, designated SEQ ID:4014, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33056] Another function of GAM281 is therefore inhibition of DKFZP434B1727 (Accession NP_115519.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434B1727.

[33057] DKFZp434C0923 (Accession NP_060068.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp434C0923 BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by DKFZp434C0923, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434C0923 BINDING SITE, designated SEQ ID:8235, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33058] Another function of GAM281 is therefore inhibition of DKFZp434C0923 (Accession NP_060068.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434C0923.

[33059] DKFZP434C212 (Accession XP_044196.3) is another GAM281 target gene, herein designated TARGET GENE. DKFZP434C212 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434C212, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434C212 BINDING SITE, designated SEQ ID:8661, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[33060] Another function of GAM281 is therefore inhibition of DKFZP434C212 (Accession XP_044196.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C212.

[33061] DKFZP434D146 (Accession NP_056410.2) is another GAM281 target gene, herein designated TARGET GENE. DKFZP434D146 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434D146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434D146 BINDING SITE, designated SEQ ID:2209, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33062] Another function of GAM281 is therefore inhibition of DKFZP434D146 (Accession NP_056410.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434D146.

[33063] DKFZp434E2220 (Accession NP_060082.1) is another

GAM281 target gene, herein designated TARGET GENE. DKFZp434E2220 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp434E2220, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434E2220 BINDING SITE, designated SEQ ID:11326, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33064] Another function of GAM281 is therefore inhibition of DKFZp434E2220 (Accession NP_060082.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E2220.

[33065] DKFZP434F0318 (Accession NP_110444.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP434F0318 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F0318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434F0318 BINDING SITE,

designated SEQ ID:16771, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33066] Another function of GAM281 is therefore inhibition of DKFZP434F0318 (Accession NP_110444.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F0318.

[33067] DKFZp434F1719 (Accession NP_115624.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp434F1719 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434F1719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434F1719 BINDING SITE, designated SEQ ID:3951, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33068] Another function of GAM281 is therefore inhibition of DKFZp434F1719 (Accession NP_115624.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZp434F1719.

[33069] DKFZp434K1210 (Accession NP_060076.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp434K1210 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434K1210, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434K1210 BINDING SITE, designated SEQ ID:4195, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33070] Another function of GAM281 is therefore inhibition of DKFZp434K1210 (Accession NP_060076.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434K1210.

[33071] DKFZp547H025 (Accession NP_064546.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp547H025 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547H025, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547H025 BINDING SITE, designated SEQ ID:14246, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33072] Another function of GAM281 is therefore inhibition of DKFZp547H025 (Accession NP_064546.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547H025.

[33073] DKFZp547I094 (Accession NP_115531.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp547I094 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547I094, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547I094 BINDING SITE, designated SEQ ID:1180, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33074] Another function of GAM281 is therefore inhibition of DKFZp547I094 (Accession NP_115531.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547I094.

[33075] DKFZp547P234 (Accession NP_694590.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp547P234 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547P234, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547P234 BINDING SITE, designated SEQ ID:11057, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33076] Another function of GAM281 is therefore inhibition of DKFZp547P234 (Accession NP_694590.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547P234.

[33077] DKFZP564D166 (Accession NP_108648.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP564D166 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts

of mRNA encoded by DKFZP564D166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564D166 BINDING SITE, designated SEQ ID:17204, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33078] Another function of GAM281 is therefore inhibition of DKFZP564D166 (Accession NP_108648.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D166.

[33079] DKFZP564G092 (Accession NP_056416.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP564G092 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP564G092, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564G092 BINDING SITE, designated SEQ ID:2662, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33080] Another function of GAM281 is therefore inhibition of DKFZP564G092 (Accession NP_056416.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564G092.

[33081] DKFZP564I122 (Accession XP_032397.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP564I122 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564I122, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564I122 BINDING SITE, designated SEQ ID:16590, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33082] Another function of GAM281 is therefore inhibition of DKFZP564I122 (Accession XP_032397.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564I122.

[33083] DKFZP564J0863 (Accession NP_056274.1) is another GAM281 target gene, herein designated TARGET GENE.

DKFZP564J0863 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564J0863, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564J0863 BINDING SITE, designated SEQ ID:1067, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33084] Another function of GAM281 is therefore inhibition of DKFZP564J0863 (Accession NP_056274.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564J0863.

[33085] DKFZP564J157 (Accession NP_060927.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP564J157 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP564J157, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564J157 BINDING SITE, designated SEQ ID:18768, to the nucleotide sequence of

GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33086] Another function of GAM281 is therefore inhibition of DKFZP564J157 (Accession NP_060927.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564J157.

[33087] DKFZP564K0322 (Accession NP_114429.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP564K0322 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564K0322, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564K0322 BINDING SITE, designated SEQ ID:17964, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33088] Another function of GAM281 is therefore inhibition of DKFZP564K0322 (Accession NP_114429.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564K0322.

[33089] DKFZp564K142 (Accession NP_115497.2) is another GAM281 target gene, herein designated TARGET GENE. DKFZp564K142 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp564K142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp564K142 BINDING SITE, designated SEQ ID:2663, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33090] Another function of GAM281 is therefore inhibition of DKFZp564K142 (Accession NP_115497.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp564K142.

[33091] DKFZP564O0423 (Accession XP_166254.2) is another GAM281 target gene, herein designated TARGET GENE. DKFZP564O0423 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O0423, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of DKFZP564O0423 BINDING SITE, designated SEQ ID:10819, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33092] Another function of GAM281 is therefore inhibition of DKFZP564O0423 (Accession XP_166254.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564O0423.

[33093] DKFZP564O0523 (Accession NP_115496.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP564O0523 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O0523, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564O0523 BINDING SITE, designated SEQ ID:3686, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33094] Another function of GAM281 is therefore inhibition of DKFZP564O0523 (Accession NP_115496.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZP564O0523.

[33095] DKFZP566D1346 (Accession NP_110443.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP566D1346 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP566D1346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566D1346 BINDING SITE, designated SEQ ID:10539, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33096] Another function of GAM281 is therefore inhibition of DKFZP566D1346 (Accession NP_110443.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566D1346.

[33097] DKFZP566I1024 (Accession NP_056226.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP566I1024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP566I1024, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566I1024 BINDING SITE, designated SEQ ID:12353, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33098] Another function of GAM281 is therefore inhibition of DKFZP566I1024 (Accession NP_056226.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566I1024.

[33099] DKFZp586C0721 (Accession XP_098416.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp586C0721 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp586C0721, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp586C0721 BINDING SITE, designated SEQ ID:12173, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33100] Another function of GAM281 is therefore inhibition of DK-

FZp586C0721 (Accession XP_098416.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp586C0721.

[33101] DKFZP586D0919 (Accession NP_056248.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZP586D0919 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586D0919, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586D0919 BINDING SITE, designated SEQ ID:11134, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33102] Another function of GAM281 is therefore inhibition of DKFZP586D0919 (Accession NP_056248.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586D0919.

[33103] DKFZp667B1218 (Accession NP_808881.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp667B1218 BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by DKFZp667B1218, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667B1218 BINDING SITE, designated SEQ ID:15574, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33104] Another function of GAM281 is therefore inhibition of DKFZp667B1218 (Accession NP_808881.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp667B1218.

[33105] DKFZp667E0512 (Accession XP_117353.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp667E0512 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp667E0512, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667E0512 BINDING SITE, designated SEQ ID:8492, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[33106] Another function of GAM281 is therefore inhibition of DKFZp667E0512 (Accession XP_117353.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp667E0512.

[33107] DKFZp761B107 (Accession NP_775734.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp761B107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761B107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B107 BINDING SITE, designated SEQ ID:13571, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33108] Another function of GAM281 is therefore inhibition of DKFZp761B107 (Accession NP_775734.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B107.

[33109] DKFZp761B128 (Accession NP_689650.1) is another

GAM281 target gene, herein designated TARGET GENE. DKFZp761B128 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761B128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B128 BINDING SITE, designated SEQ ID:17969, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33110] Another function of GAM281 is therefore inhibition of DKFZp761B128 (Accession NP_689650.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B128.

[33111] DKFZp761H039 (Accession NP_061181.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp761H039 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761H039, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761H039 BINDING SITE,

designated SEQ ID:15190, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33112] Another function of GAM281 is therefore inhibition of DKFZp761H039 (Accession NP_061181.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761H039.

[33113] DKFZp761I2123 (Accession XP_166582.2) is another GAM281 target gene, herein designated TARGET GENE. DKFZp761I2123 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761I2123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761I2123 BINDING SITE, designated SEQ ID:12187, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33114] Another function of GAM281 is therefore inhibition of DKFZp761I2123 (Accession XP_166582.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

DKFZp761I2123.

[33115] DKFZp761J139 (Accession NP_115656.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp761J139 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761J139, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761J139 BINDING SITE, designated SEQ ID:5768, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33116] Another function of GAM281 is therefore inhibition of DKFZp761J139 (Accession NP_115656.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761J139.

[33117] DKFZp761K1423 (Accession NP_060892.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp761K1423 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761K1423, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761K1423 BINDING SITE, designated SEQ ID:7711, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33118] Another function of GAM281 is therefore inhibition of DKFZp761K1423 (Accession NP_060892.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761K1423.

[33119] DKFZp761N1114 (Accession XP_086327.6) is another GAM281 target gene, herein designated TARGET GENE. DKFZp761N1114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761N1114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761N1114 BINDING SITE, designated SEQ ID:13529, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33120] Another function of GAM281 is therefore inhibition of DKFZp761N1114 (Accession XP_086327.6) . Accordingly,

utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761N1114.

[33121] DKFZp761O0113 (Accession NP_060879.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp761O0113 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761O0113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761O0113 BINDING SITE, designated SEQ ID:7699, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33122] Another function of GAM281 is therefore inhibition of DKFZp761O0113 (Accession NP_060879.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761O0113.

[33123] DKFZp761P1121 (Accession NP_690870.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp761P1121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

DKFZp761P1121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761P1121 BINDING SITE, designated SEQ ID:9147, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33124] Another function of GAM281 is therefore inhibition of DKFZp761P1121 (Accession NP_690870.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761P1121.

[33125] DKFZp762C2414 (Accession NP_848637.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp762C2414 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762C2414, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762C2414 BINDING SITE, designated SEQ ID:4056, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33126] Another function of GAM281 is therefore inhibition of DKFZp762C2414 (Accession NP_848637.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762C2414.

[33127] DKFZp762H185 (Accession XP_172976.2) is another GAM281 target gene, herein designated TARGET GENE. DKFZp762H185 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762H185, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762H185 BINDING SITE, designated SEQ ID:13803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33128] Another function of GAM281 is therefore inhibition of DKFZp762H185 (Accession XP_172976.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762H185.

[33129] DKFZp762I137 (Accession NP_689624.1) is another GAM281 target gene, herein designated TARGET GENE.

DKFZp762I137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762I137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762I137 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33130] Another function of GAM281 is therefore inhibition of DKFZp762I137 (Accession NP_689624.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762I137.

[33131] DKFZp762I194 (Accession NP_689597.1) is another GAM281 target gene, herein designated TARGET GENE. DKFZp762I194 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762I194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762I194 BINDING SITE, designated SEQ ID:6884, to the nucleotide sequence of

GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33132] Another function of GAM281 is therefore inhibition of DKFZp762I194 (Accession NP_689597.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762I194.

[33133] DKFZp762L0311 (Accession NP_061189.2) is another GAM281 target gene, herein designated TARGET GENE. DKFZp762L0311 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762L0311, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762L0311 BINDING SITE, designated SEQ ID:9194, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33134] Another function of GAM281 is therefore inhibition of DKFZp762L0311 (Accession NP_061189.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762L0311.

[33135] Discs, large homolog 2, chapsyn-110 (drosophila) (DLG2, Accession NP_001355.1) is another GAM281 target gene, herein designated TARGET GENE. DLG2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DLG2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DLG2 BINDING SITE, designated SEQ ID:9202, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33136] Another function of GAM281 is therefore inhibition of Discs, large homolog 2, chapsyn-110 (drosophila) (DLG2, Accession NP_001355.1), a gene which may mediate organized clustering of NMDA receptors . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLG2.

[33137] The function of DLG2 has been established by previous studies. The proper distribution of voltage- gated and ligand- gated ion channels on the neuronal surface is critical for the processing and transmission of electrical signals in neurons. Kim et al. (1995) hypothesized that potential an-

choring molecules bind to the C- terminal intracellular tail of Shaker subfamily potassium channels. Using a yeast 2-hybrid screen with the C terminus of the rat Shaker sub-family member Kv1.4 (see OMIM Ref. No. KCNA4; 176266) as bait, they isolated partial human brain cDNAs encoding PSD95 (OMIM Ref. No. 602887), SAP97 (OMIM Ref. No. 601014), and DLG2. All 3 proteins are members of the 'membrane- associated guanylate kinase' (MAGUK) family. Kim et al. (1996) isolated additional cDNAs corresponding to the entire coding region of DLG2, which they called 'channel- associated protein of synapses- 110' (chapsyn-110). Like PSD95 and SAP97, the predicted 870- amino acid chapsyn- 110 protein contains 3 PDZ domains, an SH3 domain, and a guanylate kinase homology region. The chapsyn- 110 protein is 78%, 71%, and 57% identical to SAP97, PSD95, and the Drosophila 'discs large' protein, respectively. Using immunohistochemical analysis of rat brain, these authors found that chapsyn- 110 has a so-matodendritic expression pattern that overlaps partly with PSD95 but that contrasts with the axonal distribution of SAP97. When expressed in mammalian cells, chapsyn-110 and PSD95 each mediated the clustering of both NMDA receptors (e.g., 138249) and potassium channels.

Chapsyn- 110 and PSD95 heteromultimerized with each other and were recruited into the same NMDA receptor and potassium channel clusters. Kim et al. (1996) suggested that these 2 MAGUK proteins may interact at postsynaptic sites to form a multimeric scaffold for the clustering of receptors, ion channels, and associated signaling proteins. Northern blot analysis indicated that chapsyn-110 is expressed predominantly in the rat brain, where a major 6- kb mRNA and a minor 5- kb mRNA were detected.

[33138]

[33139] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[33140] Kim, E.; Cho, K.- O.; Rothschild, A.; Sheng, M. : Heteromultimerization and NMDA receptor- clustering activity of Chapsyn- 110, a member of the PSD- 95 family of proteins. Neuron 17: 103- 113, 1996. ; and

[33141] Kim, E.; Niethammer, M.; Rothschild, A.; Jan, Y. N.; Sheng, M. : Clustering of Shaker- type K+ channels by interaction with a family of membrane- associated guanylate kinases. Nature 378:.

[33142] Further studies establishing the function and utilities of

DLG2 are found in John Hopkins OMIM database record ID 603583, and in cited publications listed in Table 5, which are hereby incorporated by reference.Dynein, axonemal, heavy polypeptide 11 (DNAH11, Accession NP_003768.1) is another GAM281 target gene, herein designated TARGET GENE. DNAH11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DNAH11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DNAH11 BINDING SITE, designated SEQ ID:1214, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33143] Another function of GAM281 is therefore inhibition of Dynein, axonemal, heavy polypeptide 11 (DNAH11, Accession NP_003768.1), a gene which may function as a motor protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAH11.

[33144] The function of DNAH11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Dnaj (hsp40) homolog, subfamily b, member

5 (DNAJB5, Accession NP_036398.2) is another GAM281 target gene, herein designated TARGET GENE. DNAJB5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DNAJB5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DNAJB5 BINDING SITE, designated SEQ ID:5815, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33145] Another function of GAM281 is therefore inhibition of Dnaj (hsp40) homolog, subfamily b, member 5 (DNAJB5, Accession NP_036398.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAJB5.

[33146] Dynein, cytoplasmic, light polypeptide 2a (DNCL2A, Accession NP_808853.1) is another GAM281 target gene, herein designated TARGET GENE. DNCL2A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DNCL2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of DNCL2A BINDING SITE, designated SEQ ID:949, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33147] Another function of GAM281 is therefore inhibition of Dynein, cytoplasmic, light polypeptide 2a (DNCL2A, Accession NP_808853.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNCL2A.

[33148] Dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit (DPM2, Accession NP_689903.1) is another GAM281 target gene, herein designated TARGET GENE. DPM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DPM2 BINDING SITE, designated SEQ ID:3466, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33149] Another function of GAM281 is therefore inhibition of Dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit (DPM2, Accession NP_689903.1) . Ac-

cordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPM2.

[33150] DRIM (Accession NP_055318.1) is another GAM281 target gene, herein designated TARGET GENE. DRIM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DRIM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DRIM BINDING SITE, designated SEQ ID:6633, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33151] Another function of GAM281 is therefore inhibition of DRIM (Accession NP_055318.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRIM.

[33152] Dentatorubral-pallidoluysian atrophy (atrophin-1) (DRPLA, Accession NP_001931.1) is another GAM281 target gene, herein designated TARGET GENE. DRPLA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DRPLA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DRPLA BINDING SITE, designated SEQ ID:9796, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33153] Another function of GAM281 is therefore inhibition of Dentatorubral-pallidoluysian atrophy (atrophin-1) (DRPLA, Accession NP_001931.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRPLA.

[33154] Desmocollin 3 (DSC3, Accession NP_001932.1) is another GAM281 target gene, herein designated TARGET GENE. DSC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE, designated SEQ ID:7559, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33155] Another function of GAM281 is therefore inhibition of Desmocollin 3 (DSC3, Accession NP_001932.1), a gene which is a component of intercellular desmosome junc-

tions. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC3.

[33156] The function of DSC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Desmocollin 3 (DSC3, Accession NP_077741.1) is another GAM281 target gene, herein designated TARGET GENE. DSC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE, designated SEQ ID:7559, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33157] Another function of GAM281 is therefore inhibition of Desmocollin 3 (DSC3, Accession NP_077741.1), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC3.

[33158] The function of DSC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Down syndrome critical region gene 6 (DSCR6, Accession NP_061835.1) is another GAM281 target gene, herein designated TARGET GENE. DSCR6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSCR6 BINDING SITE, designated SEQ ID:14954, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33159] Another function of GAM281 is therefore inhibition of Down syndrome critical region gene 6 (DSCR6, Accession NP_061835.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSCR6.

[33160] DUPLIN (Accession XP_208760.3) is another GAM281 target gene, herein designated TARGET GENE. DUPLIN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DUPLIN, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUPLIN BINDING SITE, designated SEQ ID:6863, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33161] Another function of GAM281 is therefore inhibition of DUPLIN (Accession XP_208760.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUPLIN.

[33162] Dual specificity phosphatase 19 (DUSP19, Accession NP_543152.1) is another GAM281 target gene, herein designated TARGET GENE. DUSP19 BINDING SITE1 and DUSP19 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DUSP19, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP19 BINDING SITE1 and DUSP19 BINDING SITE2, designated SEQ ID:5768 and SEQ ID:15367 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33163] Another function of GAM281 is therefore inhibition of

Dual specificity phosphatase 19 (DUSP19, Accession NP_543152.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP19.

[33164] Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NP_567824.1) is another GAM281 target gene, herein designated TARGET GENE. DYRK1A BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by DYRK1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DYRK1A BINDING SITE, designated SEQ ID:10913, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33165] Another function of GAM281 is therefore inhibition of Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NP_567824.1), a gene which regulates cell proliferation and may be involved in brain development . and therefore may be associated with Down syndrome. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Down syndrome,

and of other diseases and clinical conditions associated with DYRK1A.

[33166] The function of DYRK1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Endometrial bleeding associated factor (left-right determination, factor a; transforming growth factor beta superfamily) (EBAF, Accession NP_003231.2) is another GAM281 target gene, herein designated TARGET GENE. EBAF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EBAF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EBAF BINDING SITE, designated SEQ ID:18275, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33167] Another function of GAM281 is therefore inhibition of Endometrial bleeding associated factor (left-right determination, factor a; transforming growth factor beta superfamily) (EBAF, Accession NP_003231.2), a gene which LEFT- RIGHT AXIS MALFORMATIONS and therefore is associated with Left- right axis malformations. Accordingly,

utilities of GAM281 include diagnosis, prevention and treatment of Left- right axis malformations, and of other diseases and clinical conditions associated with EBAF.

[33168] The function of EBAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Endothelial differentiation, sphingolipid g-protein-coupled receptor, 8 (EDG8, Accession NP_110387.1) is another GAM281 target gene, herein designated TARGET GENE. EDG8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EDG8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDG8 BINDING SITE, designated SEQ ID:12263, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33169] Another function of GAM281 is therefore inhibition of Endothelial differentiation, sphingolipid g-protein-coupled receptor, 8 (EDG8, Accession NP_110387.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with EDG8.

[33170] EEF2K (Accession NP_037434.1) is another GAM281 target gene, herein designated TARGET GENE. EEF2K BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EEF2K, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EEF2K BINDING SITE, designated SEQ ID:2595, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33171] Another function of GAM281 is therefore inhibition of EEF2K (Accession NP_037434.1), a gene which phosphorylates serine or threonine on the eukaryotic elongation factor- 2 and therefore may be associated with Systemic lupus erythematosus and cancer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Systemic lupus erythematosus and cancer, and of other diseases and clinical conditions associated with EEF2K.

[33172] The function of EEF2K and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Egf-like-domain, multiple 4 (EGFL4, Acces-

sion XP_290821.1) is another GAM281 target gene, herein designated TARGET GENE. EGFL4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by EGFL4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EGFL4 BINDING SITE, designated SEQ ID:5780, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33173] Another function of GAM281 is therefore inhibition of Egf-like-domain, multiple 4 (EGFL4, Accession XP_290821.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGFL4.

[33174] Eh-domain containing 1 (EHD1, Accession NP_006786.2) is another GAM281 target gene, herein designated TARGET GENE. EHD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EHD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EHD1 BINDING SITE, designated SEQ ID:7065, to the nucleotide sequence of GAM281 RNA,

herein designated GAM RNA, also designated SEQ ID:278.

[33175] Another function of GAM281 is therefore inhibition of Eh-domain containing 1 (EHD1, Accession NP_006786.2), a gene which may be involved in ligand- initiated endocytosis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHD1.

[33176] The function of EHD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.Eh-domain containing 2 (EHD2, Accession NP_055416.2) is another GAM281 target gene, herein designated TARGET GENE. EHD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EHD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EHD2 BINDING SITE, designated SEQ ID:4837, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33177] Another function of GAM281 is therefore inhibition of Eh-domain containing 2 (EHD2, Accession NP_055416.2) . Accordingly, utilities of GAM281 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with EHD2.

[33178] Eukaryotic translation initiation factor 2c, 1 (EIF2C1, Accession NP_036331.1) is another GAM281 target gene, herein designated TARGET GENE. EIF2C1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF2C1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF2C1 BINDING SITE, designated SEQ ID:2761, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33179] Another function of GAM281 is therefore inhibition of Eukaryotic translation initiation factor 2c, 1 (EIF2C1, Accession NP_036331.1), a gene which plays an important role in the eukaryotic peptide chain initiation process. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2C1.

[33180] The function of EIF2C1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM223.1.Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kda (EIF2S3, Accession NP_001406.1) is another GAM281 target gene, herein designated TARGET GENE. EIF2S3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF2S3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF2S3 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33181] Another function of GAM281 is therefore inhibition of Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kda (EIF2S3, Accession NP_001406.1), a gene which functions in the early steps of protein synthesis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2S3.

[33182] The function of EIF2S3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Eukaryotic translation initiation factor 5a2 (EIF5A2, Accession NP_065123.1) is another GAM281 tar-

get gene, herein designated TARGET GENE. EIF5A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF5A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF5A2 BINDING SITE, designated SEQ ID:8340, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33183] Another function of GAM281 is therefore inhibition of Eukaryotic translation initiation factor 5a2 (EIF5A2, Accession NP_065123.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF5A2.

[33184] ELP3 (Accession NP_060561.3) is another GAM281 target gene, herein designated TARGET GENE. ELP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ELP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ELP3 BINDING SITE, designated SEQ ID:14236, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[33185] Another function of GAM281 is therefore inhibition of ELP3 (Accession NP_060561.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELP3.

[33186] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690881.1) is another GAM281 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:13462, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33187] Another function of GAM281 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690881.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[33188] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_038475.2) is another GAM281 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:13462, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33189] Another function of GAM281 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_038475.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[33190] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690885.1) is another GAM281 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of

mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:13462, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33191] Another function of GAM281 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690885.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[33192] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690883.1) is another GAM281 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:13462, to the nucleotide sequence of

GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33193] Another function of GAM281 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690883.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[33194] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690882.1) is another GAM281 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:13462, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33195] Another function of GAM281 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690882.1) . Ac-

cordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[33196] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690884.1) is another GAM281 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:13462, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33197] Another function of GAM281 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690884.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[33198] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690880.1) is

another GAM281 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:13462, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33199] Another function of GAM281 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690880.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[33200] Endonuclease g-like 1 (ENDOGL1, Accession NP_005098.1) is another GAM281 target gene, herein designated TARGET GENE. ENDOGL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ENDOGL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of ENDOGL1 BINDING SITE, designated SEQ ID:5031, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33201] Another function of GAM281 is therefore inhibition of Endonuclease g-like 1 (ENDOGL1, Accession NP_005098.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENDOGL1.

[33202] Epiregulin (EREG, Accession NP_001423.1) is another GAM281 target gene, herein designated TARGET GENE. EREG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EREG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EREG BINDING SITE, designated SEQ ID:17956, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33203] Another function of GAM281 is therefore inhibition of Epiregulin (EREG, Accession NP_001423.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with EREG.

[33204] ERN2 (Accession NP_150296.1) is another GAM281 target gene, herein designated TARGET GENE. ERN2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ERN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ERN2 BINDING SITE, designated SEQ ID:12665, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33205] Another function of GAM281 is therefore inhibition of ERN2 (Accession NP_150296.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERN2.

[33206] Ero1-like (s. cerevisiae) (ERO1L, Accession NP_055399.1) is another GAM281 target gene, herein designated TARGET GENE. ERO1L BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ERO1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ERO1L BINDING SITE, designated

SEQ ID:11477, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33207] Another function of GAM281 is therefore inhibition of Ero1-like (s. cerevisiae) (ERO1L, Accession NP_055399.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERO1L.

[33208] Extra spindle poles like 1 (s. cerevisiae) (ESPL1, Accession NP_036423.1) is another GAM281 target gene, herein designated TARGET GENE. ESPL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ESPL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ESPL1 BINDING SITE, designated SEQ ID:20090, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33209] Another function of GAM281 is therefore inhibition of Extra spindle poles like 1 (s. cerevisiae) (ESPL1, Accession NP_036423.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with ESPL1.

[33210] Ellis van creveld syndrome (EVC, Accession NP_714928.1) is another GAM281 target gene, herein designated TARGET GENE. EVC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EVC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:18115, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33211] Another function of GAM281 is therefore inhibition of Ellis van creveld syndrome (EVC, Accession NP_714928.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC.

[33212] Ellis van creveld syndrome (EVC, Accession NP_055371.1) is another GAM281 target gene, herein designated TARGET GENE. EVC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EVC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:18115, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33213] Another function of GAM281 is therefore inhibition of Ellis van creveld syndrome (EVC, Accession NP_055371.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC.

[33214] EVER1 (Accession NP_009198.3) is another GAM281 target gene, herein designated TARGET GENE. EVER1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EVER1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVER1 BINDING SITE, designated SEQ ID:14255, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33215] Another function of GAM281 is therefore inhibition of EVER1 (Accession NP_009198.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with EVER1.

[33216] Ecotropic viral integration site 5 (EVI5, Accession NP_005656.2) is another GAM281 target gene, herein designated TARGET GENE. EVI5 BINDING SITE1 and EVI5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by EVI5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVI5 BINDING SITE1 and EVI5 BINDING SITE2, designated SEQ ID:11607 and SEQ ID:7219 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33217] Another function of GAM281 is therefore inhibition of Ecotropic viral integration site 5 (EVI5, Accession NP_005656.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVI5.

[33218] F11R (Accession NP_058642.1) is another GAM281 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:2664, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33219] Another function of GAM281 is therefore inhibition of F11R (Accession NP_058642.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[33220] F11R (Accession NP_653087.1) is another GAM281 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:2664, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33221] Another function of GAM281 is therefore inhibition of F11R (Accession NP_653087.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[33222] F11R (Accession NP_653086.1) is another GAM281 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:2664, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33223] Another function of GAM281 is therefore inhibition of F11R (Accession NP_653086.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[33224] F11R (Accession NP_653085.1) is another GAM281 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:2664, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[33225] Another function of GAM281 is therefore inhibition of F11R (Accession NP_653085.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[33226] Coagulation factor ii (thrombin) receptor-like 2 (F2RL2, Accession NP_004092.1) is another GAM281 target gene, herein designated TARGET GENE. F2RL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F2RL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F2RL2 BINDING SITE, designated SEQ ID:10122, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33227] Another function of GAM281 is therefore inhibition of Coagulation factor ii (thrombin) receptor-like 2 (F2RL2, Accession NP_004092.1), a gene which receptor for activated thrombin coupled to g proteins that stimulate phosphoinositide hydrolysis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2RL2.

[33228] The function of F2RL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Coagulation factor ii (thrombin) receptor-like 3 (F2RL3, Accession NP_003941.1) is another GAM281 target gene, herein designated TARGET GENE. F2RL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F2RL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F2RL3 BINDING SITE, designated SEQ ID:4234, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33229] Another function of GAM281 is therefore inhibition of Coagulation factor ii (thrombin) receptor-like 3 (F2RL3, Accession NP_003941.1), a gene which Protease- activated receptor 4; G protein- coupled receptor that increases phosphoinositide hydrolysis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2RL3.

[33230] The function of F2RL3 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM72.1.Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1) is another GAM281 target gene, herein designated TARGET GENE. F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F3 BINDING SITE, designated SEQ ID:18492, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33231] Another function of GAM281 is therefore inhibition of Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1), a gene which functions in normal hemostasis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F3.

[33232] The function of F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Coagulation factor v (proaccelerin, labile factor) (F5, Accession NP_000121.1) is another GAM281

target gene, herein designated TARGET GENE. F5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by F5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F5 BINDING SITE, designated SEQ ID:7269, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33233] Another function of GAM281 is therefore inhibition of Coagulation factor v (proaccelerin, labile factor) (F5, Accession NP_000121.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F5.

[33234] Fatty acid binding protein 2, intestinal (FABP2, Accession NP_000125.1) is another GAM281 target gene, herein designated TARGET GENE. FABP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FABP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FABP2 BINDING SITE, designated SEQ ID:2195, to the nucleotide sequence of GAM281 RNA,

herein designated GAM RNA, also designated SEQ ID:278.

[33235] Another function of GAM281 is therefore inhibition of Fatty acid binding protein 2, intestinal (FABP2, Accession NP_000125.1), a gene which may have a role in dietary fat uptake or processing. and therefore may be associated with Cardiovascular disease and type 2 diabetes. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Cardiovascular disease and type 2 diabetes., and of other diseases and clinical conditions associated with FABP2.

[33236] The function of FABP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Family with sequence similarity 13, member a1 (FAM13A1, Accession NP_055698.1) is another GAM281 target gene, herein designated TARGET GENE. FAM13A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FAM13A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FAM13A1 BINDING SITE, designated SEQ ID:9972, to the nucleotide sequence of GAM281 RNA,

herein designated GAM RNA, also designated SEQ ID:278.

[33237] Another function of GAM281 is therefore inhibition of Family with sequence similarity 13, member a1 (FAM13A1, Accession NP_055698.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAM13A1.

[33238] Fanconi anemia, complementation group c (FANCC, Accession NP_000127.1) is another GAM281 target gene, herein designated TARGET GENE. FANCC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCC BINDING SITE, designated SEQ ID:15368, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33239] Another function of GAM281 is therefore inhibition of Fanconi anemia, complementation group c (FANCC, Accession NP_000127.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCC.

[33240] Fanconi anemia, complementation group e (FANCE, Ac-

cession NP_068741.1) is another GAM281 target gene, herein designated TARGET GENE. FANCE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCE BINDING SITE, designated SEQ ID:5597, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33241] Another function of GAM281 is therefore inhibition of Fanconi anemia, complementation group e (FANCE, Accession NP_068741.1), a gene which is a possible regulator of lymphocyte and platelet function. and therefore is associated with Fanconi anemia, complementation group e. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Fanconi anemia, complementation group e., and of other diseases and clinical conditions associated with FANCE.

[33242] The function of FANCE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Fanconi anemia, complementation group f

(FANCF, Accession NP_073562.1) is another GAM281 target gene, herein designated TARGET GENE. FANCF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCF BINDING SITE, designated SEQ ID:5816, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33243] Another function of GAM281 is therefore inhibition of Fanconi anemia, complementation group f (FANCF, Accession NP_073562.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCF.

[33244] FAT3 (Accession XP_061871.5) is another GAM281 target gene, herein designated TARGET GENE. FAT3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FAT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FAT3 BINDING SITE, designated SEQ ID:8236, to the nucleotide sequence

of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33245] Another function of GAM281 is therefore inhibition of FAT3 (Accession XP_061871.5) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAT3.

[33246] F-box and leucine-rich repeat protein 7 (FBXL7, Accession NP_036436.1) is another GAM281 target gene, herein designated TARGET GENE. FBXL7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FBXL7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXL7 BINDING SITE, designated SEQ ID:11584, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33247] Another function of GAM281 is therefore inhibition of F-box and leucine-rich repeat protein 7 (FBXL7, Accession NP_036436.1), a gene which may be involved in in phosphorylation- dependent ubiquitination. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FBXL7.

[33248] The function of FBXL7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.F-box only protein 27 (FBXO27, Accession XP_059045.1) is another GAM281 target gene, herein designated TARGET GENE. FBXO27 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXO27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXO27 BINDING SITE, designated SEQ ID:16526, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33249] Another function of GAM281 is therefore inhibition of F-box only protein 27 (FBXO27, Accession XP_059045.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO27.

[33250] F-box only protein 27 (FBXO27, Accession NP_849142.1) is another GAM281 target gene, herein designated TARGET GENE. FBXO27 BINDING SITE is a target binding site

found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXO27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXO27 BINDING SITE, designated SEQ ID:16526, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33251] Another function of GAM281 is therefore inhibition of F-box only protein 27 (FBXO27, Accession NP_849142.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO27.

[33252] Fc fragment of iga, receptor for (FCAR, Accession NP_579811.1) is another GAM281 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:10448, SEQ

ID:10448 and SEQ ID:10448 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33253] Another function of GAM281 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579811.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[33254] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Accession NP_579803.1) is another GAM281 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:10448, SEQ ID:10448 and SEQ ID:10448 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33255] Another function of GAM281 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579803.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[33256] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Accession NP_001991.1) is another GAM281 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding

sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:3819, SEQ ID:17643 and SEQ ID:17643 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33257] Another function of GAM281 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_001991.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[33258] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Accession NP_579807.1) is another GAM281 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites

found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:10448, SEQ ID:497 and SEQ ID:2141 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33259] Another function of GAM281 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579807.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[33260] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) is another GAM281 target gene, herein

designated TARGET GENE. FER1L4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FER1L4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FER1L4 BINDING SITE, designated SEQ ID:11291, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33261] Another function of GAM281 is therefore inhibition of Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER1L4.

[33262] Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) is another GAM281 target gene, herein designated TARGET GENE. FER1L4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FER1L4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FER1L4 BINDING SITE, designated SEQ ID:11291, to the nucleotide sequence of GAM281

RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33263] Another function of GAM281 is therefore inhibition of Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER1L4.

[33264] Fasciculation and elongation protein zeta 1 (zygin i) (FEZ1, Accession NP_072043.1) is another GAM281 target gene, herein designated TARGET GENE. FEZ1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FEZ1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FEZ1 BINDING SITE, designated SEQ ID:5204, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33265] Another function of GAM281 is therefore inhibition of Fasciculation and elongation protein zeta 1 (zygin i) (FEZ1, Accession NP_072043.1), a gene which Zygin 1; may have a role in axonal outgrowth; has similarity to C. elegans UNC- 76. Accordingly, utilities of GAM281 include diag-

nosis, prevention and treatment of diseases and clinical conditions associated with FEZ1.

[33266] The function of FEZ1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Fibroblast growth factor 2 (basic) (FGF2, Accession NP_001997.3) is another GAM281 target gene, herein designated TARGET GENE. FGF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FGF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF2 BINDING SITE, designated SEQ ID:11604, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33267] Another function of GAM281 is therefore inhibition of Fibroblast growth factor 2 (basic) (FGF2, Accession NP_001997.3), a gene which the Basic fibroblast growth factor 2; is mitogenic, angiogenic, and neurotrophic factor. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF2.

[33268] The function of FGF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM36.1.Fibroblast growth factor 5 (FGF5, Accession NP_004455.1) is another GAM281 target gene, herein designated TARGET GENE. FGF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE, designated SEQ ID:14382, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33269] Another function of GAM281 is therefore inhibition of Fibroblast growth factor 5 (FGF5, Accession NP_004455.1), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5.

[33270] The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM106.1.Fibroblast growth factor 5 (FGF5, Accession NP_149134.1) is another GAM281 target gene, herein designated TARGET GENE. FGF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE, designated SEQ ID:14382, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33271] Another function of GAM281 is therefore inhibition of Fibroblast growth factor 5 (FGF5, Accession NP_149134.1), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5.

[33272] The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.1.Four and a half lim domains 2 (FHL2, Accession NP_001441.2) is another GAM281 target gene, herein designated TARGET GENE. FHL2 BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FHL2 BINDING SITE, designated SEQ ID:16589, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33273] Another function of GAM281 is therefore inhibition of Four and a half lim domains 2 (FHL2, Accession NP_001441.2), a gene which Contains four LIM domains and an additional zinc finger. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHL2.

[33274] The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.FISH (Accession NP_055446.1) is another GAM281 target gene, herein designated TARGET GENE. FISH BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FISH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FISH BINDING SITE, designated SEQ ID:13261, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33275] Another function of GAM281 is therefore inhibition of FISH (Accession NP_055446.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FISH.

[33276] Fk506 binding protein 9, 63 kda (FKBP9, Accession NP_009201.1) is another GAM281 target gene, herein designated TARGET GENE. FKBP9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FKBP9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FKBP9 BINDING SITE, designated SEQ ID:7851, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33277] Another function of GAM281 is therefore inhibition of Fk506 binding protein 9, 63 kda (FKBP9, Accession NP_009201.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKBP9.

[33278] FLJ00060 (Accession XP_028154.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ00060 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ00060, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ00060 BINDING SITE, designated SEQ ID:11528, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33279] Another function of GAM281 is therefore inhibition of FLJ00060 (Accession XP_028154.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00060.

[33280] FLJ10101 (Accession NP_078994.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10101 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10101 BINDING SITE, designated SEQ ID:9189, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33281] Another function of GAM281 is therefore inhibition of FLJ10101 (Accession NP_078994.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10101.

[33282] FLJ10232 (Accession NP_060503.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10232 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10232, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10232 BINDING SITE, designated SEQ ID:19236, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33283] Another function of GAM281 is therefore inhibition of FLJ10232 (Accession NP_060503.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10232.

[33284] FLJ10298 (Accession NP_060520.2) is another GAM281

target gene, herein designated TARGET GENE. FLJ10298 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10298, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10298 BINDING SITE, designated SEQ ID:2615, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33285] Another function of GAM281 is therefore inhibition of FLJ10298 (Accession NP_060520.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10298.

[33286] FLJ10346 (Accession NP_060535.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10346 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10346 BINDING SITE, designated SEQ ID:19219, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[33287] Another function of GAM281 is therefore inhibition of FLJ10346 (Accession NP_060535.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10346.

[33288] FLJ10520 (Accession NP_060594.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ10520 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10520, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10520 BINDING SITE, designated SEQ ID:4272, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33289] Another function of GAM281 is therefore inhibition of FLJ10520 (Accession NP_060594.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10520.

[33290] FLJ10535 (Accession NP_060599.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10535

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10535, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10535 BINDING SITE, designated SEQ ID:9543, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33291] Another function of GAM281 is therefore inhibition of FLJ10535 (Accession NP_060599.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10535.

[33292] FLJ10560 (Accession NP_060608.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10560 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10560, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10560 BINDING SITE, designated SEQ ID:15591, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33293] Another function of GAM281 is therefore inhibition of FLJ10560 (Accession NP_060608.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10560.

[33294] FLJ10569 (Accession NP_060612.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10569 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10569, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10569 BINDING SITE, designated SEQ ID:11899, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33295] Another function of GAM281 is therefore inhibition of FLJ10569 (Accession NP_060612.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10569.

[33296] FLJ10640 (Accession NP_061896.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10640 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by FLJ10640, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10640 BINDING SITE, designated SEQ ID:18109, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33297] Another function of GAM281 is therefore inhibition of FLJ10640 (Accession NP_061896.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10640.

[33298] FLJ10713 (Accession NP_060659.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10713 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10713, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10713 BINDING SITE, designated SEQ ID:7909, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33299] Another function of GAM281 is therefore inhibition of

FLJ10713 (Accession NP_060659.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10713.

[33300] FLJ10769 (Accession NP_060680.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10769 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10769, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10769 BINDING SITE, designated SEQ ID:12257, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33301] Another function of GAM281 is therefore inhibition of FLJ10769 (Accession NP_060680.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10769.

[33302] FLJ10846 (Accession NP_060711.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10846 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10846, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10846 BINDING SITE, designated SEQ ID:11528, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33303] Another function of GAM281 is therefore inhibition of FLJ10846 (Accession NP_060711.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10846.

[33304] FLJ10847 (Accession NP_060712.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ10847 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10847, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10847 BINDING SITE, designated SEQ ID:19357, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33305] Another function of GAM281 is therefore inhibition of FLJ10847 (Accession NP_060712.2) . Accordingly, utilities

of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10847.

[33306] FLJ10898 (Accession NP_060733.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10898 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10898, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10898 BINDING SITE, designated SEQ ID:7243, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33307] Another function of GAM281 is therefore inhibition of FLJ10898 (Accession NP_060733.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10898.

[33308] FLJ10922 (Accession NP_060743.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10922 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10922, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10922 BINDING SITE, designated SEQ ID:18818, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33309] Another function of GAM281 is therefore inhibition of FLJ10922 (Accession NP_060743.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10922.

[33310] FLJ10932 (Accession NP_060747.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ10932 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10932, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10932 BINDING SITE, designated SEQ ID:4934, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33311] Another function of GAM281 is therefore inhibition of FLJ10932 (Accession NP_060747.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ10932.

[33312] FLJ10936 (Accession NP_060749.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ10936 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10936, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10936 BINDING SITE, designated SEQ ID:7238, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33313] Another function of GAM281 is therefore inhibition of FLJ10936 (Accession NP_060749.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10936.

[33314] FLJ11029 (Accession NP_060774.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ11029 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11029, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ11029 BINDING SITE, designated SEQ ID:3089, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33315] Another function of GAM281 is therefore inhibition of FLJ11029 (Accession NP_060774.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11029.

[33316] FLJ11323 (Accession NP_060860.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ11323 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ11323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11323 BINDING SITE, designated SEQ ID:2044, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33317] Another function of GAM281 is therefore inhibition of FLJ11323 (Accession NP_060860.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ11323.

[33318] FLJ11467 (Accession NP_079239.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ11467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11467 BINDING SITE, designated SEQ ID:834, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33319] Another function of GAM281 is therefore inhibition of FLJ11467 (Accession NP_079239.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11467.

[33320] FLJ11710 (Accession NP_079122.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ11710 BINDING SITE1 and FLJ11710 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ11710, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of FLJ11710 BINDING SITE1 and FLJ11710 BINDING SITE2, designated SEQ ID:9688 and SEQ ID:2245 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33321] Another function of GAM281 is therefore inhibition of FLJ11710 (Accession NP_079122.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11710.

[33322] FLJ11715 (Accession NP_078840.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ11715 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11715, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11715 BINDING SITE, designated SEQ ID:3305, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33323] Another function of GAM281 is therefore inhibition of FLJ11715 (Accession NP_078840.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ11715.

[33324] FLJ11800 (Accession NP_079250.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ11800 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11800, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11800 BINDING SITE, designated SEQ ID:10847, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33325] Another function of GAM281 is therefore inhibition of FLJ11800 (Accession NP_079250.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11800.

[33326] FLJ12076 (Accession NP_079463.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ12076 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12076, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ12076 BINDING SITE, designated SEQ ID:8886, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33327] Another function of GAM281 is therefore inhibition of FLJ12076 (Accession NP_079463.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12076.

[33328] FLJ12363 (Accession NP_115543.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ12363 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12363, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12363 BINDING SITE, designated SEQ ID:17722, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33329] Another function of GAM281 is therefore inhibition of FLJ12363 (Accession NP_115543.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ12363.

[33330] FLJ12448 (Accession NP_075046.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ12448 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12448, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12448 BINDING SITE, designated SEQ ID:8405, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33331] Another function of GAM281 is therefore inhibition of FLJ12448 (Accession NP_075046.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12448.

[33332] FLJ12572 (Accession NP_075056.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ12572 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ12572, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ12572 BINDING SITE, designated SEQ ID:17515, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33333] Another function of GAM281 is therefore inhibition of FLJ12572 (Accession NP_075056.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12572.

[33334] FLJ12586 (Accession NP_078896.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ12586 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ12586, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12586 BINDING SITE, designated SEQ ID:10410, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33335] Another function of GAM281 is therefore inhibition of FLJ12586 (Accession NP_078896.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12586.

[33336] FLJ12649 (Accession XP_291344.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ12649 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12649, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12649 BINDING SITE, designated SEQ ID:3686, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33337] Another function of GAM281 is therefore inhibition of FLJ12649 (Accession XP_291344.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12649.

[33338] FLJ12687 (Accession NP_079193.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ12687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12687 BINDING SITE, designated SEQ ID:3324, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33339] Another function of GAM281 is therefore inhibition of FLJ12687 (Accession NP_079193.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12687.

[33340] FLJ12747 (Accession XP_290972.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ12747 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12747, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12747 BINDING SITE, designated SEQ ID:10683, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33341] Another function of GAM281 is therefore inhibition of FLJ12747 (Accession XP_290972.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12747.

[33342] FLJ12787 (Accession NP_115551.1) is another GAM281

target gene, herein designated TARGET GENE. FLJ12787 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12787, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12787 BINDING SITE, designated SEQ ID:14839, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33343] Another function of GAM281 is therefore inhibition of FLJ12787 (Accession NP_115551.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12787.

[33344] FLJ12800 (Accession NP_075054.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ12800 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12800, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12800 BINDING SITE, designated SEQ ID:4261, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[33345] Another function of GAM281 is therefore inhibition of FLJ12800 (Accession NP_075054.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12800.

[33346] FLJ12888 (Accession NP_079221.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ12888 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12888, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12888 BINDING SITE, designated SEQ ID:17723, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33347] Another function of GAM281 is therefore inhibition of FLJ12888 (Accession NP_079221.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12888.

[33348] FLJ12903 (Accession NP_073590.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ12903

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12903, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12903 BINDING SITE, designated SEQ ID:10224, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33349] Another function of GAM281 is therefore inhibition of FLJ12903 (Accession NP_073590.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12903.

[33350] FLJ12960 (Accession NP_078914.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ12960 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12960, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12960 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33351] Another function of GAM281 is therefore inhibition of FLJ12960 (Accession NP_078914.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12960.

[33352] FLJ12973 (Accession NP_079184.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ12973 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12973, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12973 BINDING SITE, designated SEQ ID:5230, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33353] Another function of GAM281 is therefore inhibition of FLJ12973 (Accession NP_079184.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12973.

[33354] FLJ12975 (Accession NP_079085.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ12975 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ12975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12975 BINDING SITE, designated SEQ ID:2409, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33355] Another function of GAM281 is therefore inhibition of FLJ12975 (Accession NP_079085.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12975.

[33356] FLJ12986 (Accession XP_290685.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ12986 BINDING SITE1 and FLJ12986 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ12986, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12986 BINDING SITE1 and FLJ12986 BINDING SITE2, designated SEQ ID:6037 and SEQ ID:11396 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[33357] Another function of GAM281 is therefore inhibition of FLJ12986 (Accession XP_290685.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12986.

[33358] FLJ13072 (Accession XP_117117.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ13072 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13072, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13072 BINDING SITE, designated SEQ ID:2223, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33359] Another function of GAM281 is therefore inhibition of FLJ13072 (Accession XP_117117.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13072.

[33360] FLJ13114 (Accession NP_078817.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ13114

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13114 BINDING SITE, designated SEQ ID:11919, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33361] Another function of GAM281 is therefore inhibition of FLJ13114 (Accession NP_078817.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13114.

[33362] FLJ13189 (Accession NP_079158.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ13189 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13189, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13189 BINDING SITE, designated SEQ ID:4530, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33363] Another function of GAM281 is therefore inhibition of FLJ13189 (Accession NP_079158.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13189.

[33364] FLJ13197 (Accession NP_078890.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ13197 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13197, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13197 BINDING SITE, designated SEQ ID:8231, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33365] Another function of GAM281 is therefore inhibition of FLJ13197 (Accession NP_078890.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13197.

[33366] FLJ13441 (Accession NP_076413.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ13441 BINDING SITE1 and FLJ13441 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by FLJ13441, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13441 BINDING SITE1 and FLJ13441 BINDING SITE2, designated SEQ ID:3478 and SEQ ID:12452 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33367] Another function of GAM281 is therefore inhibition of FLJ13441 (Accession NP_076413.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13441.

[33368] FLJ13456 (Accession XP_038291.5) is another GAM281 target gene, herein designated TARGET GENE. FLJ13456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13456 BINDING SITE, designated SEQ ID:8163, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[33369] Another function of GAM281 is therefore inhibition of FLJ13456 (Accession XP_038291.5) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13456.

[33370] FLJ13590 (Accession NP_079116.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ13590 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13590, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13590 BINDING SITE, designated SEQ ID:7813, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33371] Another function of GAM281 is therefore inhibition of FLJ13590 (Accession NP_079116.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13590.

[33372] FLJ13744 (Accession NP_079287.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ13744

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13744, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13744 BINDING SITE, designated SEQ ID:6185, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33373] Another function of GAM281 is therefore inhibition of FLJ13744 (Accession NP_079287.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13744.

[33374] FLJ13910 (Accession NP_073617.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ13910 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13910, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13910 BINDING SITE, designated SEQ ID:7691, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33375] Another function of GAM281 is therefore inhibition of FLJ13910 (Accession NP_073617.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13910.

[33376] FLJ13984 (Accession NP_079046.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ13984 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13984, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13984 BINDING SITE, designated SEQ ID:10809, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33377] Another function of GAM281 is therefore inhibition of FLJ13984 (Accession NP_079046.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13984.

[33378] FLJ14100 (Accession NP_079301.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ14100 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ14100, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14100 BINDING SITE, designated SEQ ID:12143, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33379] Another function of GAM281 is therefore inhibition of FLJ14100 (Accession NP_079301.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14100.

[33380] FLJ14351 (Accession NP_079008.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ14351 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14351, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14351 BINDING SITE, designated SEQ ID:8586, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33381] Another function of GAM281 is therefore inhibition of

FLJ14351 (Accession NP_079008.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14351.

[33382] FLJ14442 (Accession NP_116174.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ14442 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14442 BINDING SITE, designated SEQ ID:16259, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33383] Another function of GAM281 is therefore inhibition of FLJ14442 (Accession NP_116174.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14442.

[33384] FLJ14675 (Accession NP_116212.3) is another GAM281 target gene, herein designated TARGET GENE. FLJ14675 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14675, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14675 BINDING SITE, designated SEQ ID:16071, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33385] Another function of GAM281 is therefore inhibition of FLJ14675 (Accession NP_116212.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14675.

[33386] FLJ14803 (Accession NP_116231.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ14803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14803 BINDING SITE, designated SEQ ID:939, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33387] Another function of GAM281 is therefore inhibition of FLJ14803 (Accession NP_116231.1) . Accordingly, utilities

of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14803.

[33388] FLJ14957 (Accession NP_116255.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ14957 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14957, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14957 BINDING SITE, designated SEQ ID:13527, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33389] Another function of GAM281 is therefore inhibition of FLJ14957 (Accession NP_116255.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14957.

[33390] FLJ20045 (Accession NP_060108.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20045 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20045, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20045 BINDING SITE, designated SEQ ID:12557, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33391] Another function of GAM281 is therefore inhibition of FLJ20045 (Accession NP_060108.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20045.

[33392] FLJ20079 (Accession NP_060126.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20079 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20079, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20079 BINDING SITE, designated SEQ ID:14265, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33393] Another function of GAM281 is therefore inhibition of FLJ20079 (Accession NP_060126.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20079.

[33394] FLJ20095 (Accession NP_060136.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20095 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20095, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20095 BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33395] Another function of GAM281 is therefore inhibition of FLJ20095 (Accession NP_060136.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20095.

[33396] FLJ20123 (Accession NP_060144.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20123 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ20123 BINDING SITE, designated SEQ ID:17513, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33397] Another function of GAM281 is therefore inhibition of FLJ20123 (Accession NP_060144.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20123.

[33398] FLJ20136 (Accession NP_060154.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20136 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20136 BINDING SITE, designated SEQ ID:4536, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33399] Another function of GAM281 is therefore inhibition of FLJ20136 (Accession NP_060154.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20136.

[33400] FLJ20147 (Accession NP_060157.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20147 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20147, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20147 BINDING SITE, designated SEQ ID:2624, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33401] Another function of GAM281 is therefore inhibition of FLJ20147 (Accession NP_060157.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20147.

[33402] FLJ20207 (Accession NP_060181.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ20207 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20207, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ20207 BINDING SITE, designated SEQ ID:14870, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33403] Another function of GAM281 is therefore inhibition of FLJ20207 (Accession NP_060181.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20207.

[33404] FLJ20245 (Accession NP_060193.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20245 BINDING SITE1 and FLJ20245 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ20245, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20245 BINDING SITE1 and FLJ20245 BINDING SITE2, designated SEQ ID:5275 and SEQ ID:8581 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33405] Another function of GAM281 is therefore inhibition of FLJ20245 (Accession NP_060193.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20245.

[33406] FLJ20257 (Accession NP_062552.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20257 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20257, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20257 BINDING SITE, designated SEQ ID:7206, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33407] Another function of GAM281 is therefore inhibition of FLJ20257 (Accession NP_062552.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20257.

[33408] FLJ20308 (Accession NP_060228.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20308 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20308, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ20308 BINDING SITE, designated SEQ ID:5413, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33409] Another function of GAM281 is therefore inhibition of FLJ20308 (Accession NP_060228.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20308.

[33410] FLJ20320 (Accession NP_060235.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20320 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20320, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20320 BINDING SITE, designated SEQ ID:16994, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33411] Another function of GAM281 is therefore inhibition of FLJ20320 (Accession NP_060235.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20320.

[33412] FLJ20344 (Accession NP_060246.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20344 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20344, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20344 BINDING SITE, designated SEQ ID:4079, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33413] Another function of GAM281 is therefore inhibition of FLJ20344 (Accession NP_060246.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20344.

[33414] FLJ20359 (Accession NP_060251.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20359 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20359, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ20359 BINDING SITE, designated SEQ ID:11024, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33415] Another function of GAM281 is therefore inhibition of FLJ20359 (Accession NP_060251.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20359.

[33416] FLJ20375 (Accession NP_060264.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ20375 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20375, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20375 BINDING SITE, designated SEQ ID:9357, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33417] Another function of GAM281 is therefore inhibition of FLJ20375 (Accession NP_060264.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20375.

[33418] FLJ20507 (Accession NP_060319.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20507 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20507 BINDING SITE, designated SEQ ID:3211, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33419] Another function of GAM281 is therefore inhibition of FLJ20507 (Accession NP_060319.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20507.

[33420] FLJ20511 (Accession NP_060323.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20511 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20511, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20511 BINDING SITE, designated SEQ ID:17759, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33421] Another function of GAM281 is therefore inhibition of FLJ20511 (Accession NP_060323.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20511.

[33422] FLJ20671 (Accession NP_060394.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20671 BINDING SITE1 and FLJ20671 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ20671, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20671 BINDING SITE1 and FLJ20671 BINDING SITE2, designated SEQ ID:16491 and SEQ ID:13041 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33423] Another function of GAM281 is therefore inhibition of FLJ20671 (Accession NP_060394.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20671.

[33424] FLJ20700 (Accession NP_060402.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20700 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20700, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20700 BINDING SITE, designated SEQ ID:18943, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33425] Another function of GAM281 is therefore inhibition of FLJ20700 (Accession NP_060402.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20700.

[33426] FLJ20813 (Accession NP_060431.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20813 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ20813 BINDING SITE, designated SEQ ID:10574, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33427] Another function of GAM281 is therefore inhibition of FLJ20813 (Accession NP_060431.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20813.

[33428] FLJ20825 (Accession NP_060432.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20825 BINDING SITE1 and FLJ20825 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ20825, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20825 BINDING SITE1 and FLJ20825 BINDING SITE2, designated SEQ ID:3016 and SEQ ID:19008 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33429] Another function of GAM281 is therefore inhibition of FLJ20825 (Accession NP_060432.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20825.

[33430] FLJ20886 (Accession NP_079475.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ20886 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20886, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20886 BINDING SITE, designated SEQ ID:5155, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33431] Another function of GAM281 is therefore inhibition of FLJ20886 (Accession NP_079475.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20886.

[33432] FLJ21128 (Accession NP_079359.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ21128 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ21128 BINDING SITE, designated SEQ ID:17516, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33433] Another function of GAM281 is therefore inhibition of FLJ21128 (Accession NP_079359.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21128.

[33434] FLJ21603 (Accession NP_079038.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ21603 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21603 BINDING SITE, designated SEQ ID:15047, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33435] Another function of GAM281 is therefore inhibition of FLJ21603 (Accession NP_079038.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ21603.

[33436] FLJ21673 (Accession NP_112160.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ21673 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ21673, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21673 BINDING SITE, designated SEQ ID:1435, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33437] Another function of GAM281 is therefore inhibition of FLJ21673 (Accession NP_112160.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21673.

[33438] FLJ21777 (Accession NP_115585.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ21777 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21777, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ21777 BINDING SITE, designated SEQ ID:4203, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33439] Another function of GAM281 is therefore inhibition of FLJ21777 (Accession NP_115585.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21777.

[33440] FLJ21865 (Accession NP_073596.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ21865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21865 BINDING SITE, designated SEQ ID:13223, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33441] Another function of GAM281 is therefore inhibition of FLJ21865 (Accession NP_073596.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21865.

[33442] FLJ22029 (Accession NP_079225.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ22029 BINDING SITE1 through FLJ22029 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ22029, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22029 BINDING SITE1 through FLJ22029 BINDING SITE3, designated SEQ ID:5439, SEQ ID:19447 and SEQ ID:1727 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33443] Another function of GAM281 is therefore inhibition of FLJ22029 (Accession NP_079225.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22029.

[33444] FLJ22167 (Accession NP_078809.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ22167 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ22167 BINDING SITE, designated SEQ ID:15971, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33445] Another function of GAM281 is therefore inhibition of FLJ22167 (Accession NP_078809.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22167.

[33446] FLJ22329 (Accession NP_078932.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ22329 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22329 BINDING SITE, designated SEQ ID:9543, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33447] Another function of GAM281 is therefore inhibition of FLJ22329 (Accession NP_078932.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ22329.

[33448] FLJ22531 (Accession NP_078926.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ22531 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22531, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22531 BINDING SITE, designated SEQ ID:5636, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33449] Another function of GAM281 is therefore inhibition of FLJ22531 (Accession NP_078926.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22531.

[33450] FLJ22693 (Accession NP_073587.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ22693 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22693, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ22693 BINDING SITE, designated SEQ ID:4200, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33451] Another function of GAM281 is therefore inhibition of FLJ22693 (Accession NP_073587.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22693.

[33452] FLJ22794 (Accession NP_071357.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ22794 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22794, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22794 BINDING SITE, designated SEQ ID:5559, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33453] Another function of GAM281 is therefore inhibition of FLJ22794 (Accession NP_071357.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22794.

[33454] FLJ22955 (Accession NP_079095.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ22955 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22955, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22955 BINDING SITE, designated SEQ ID:19507, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33455] Another function of GAM281 is therefore inhibition of FLJ22955 (Accession NP_079095.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22955.

[33456] FLJ22965 (Accession NP_071384.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ22965 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22965, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22965 BINDING SITE, designated SEQ ID:2808, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33457] Another function of GAM281 is therefore inhibition of FLJ22965 (Accession NP_071384.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22965.

[33458] FLJ23024 (Accession NP_079212.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ23024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23024 BINDING SITE, designated SEQ ID:9682, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33459] Another function of GAM281 is therefore inhibition of FLJ23024 (Accession NP_079212.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23024.

[33460] FLJ23040 (Accession NP_079450.1) is another GAM281

target gene, herein designated TARGET GENE. FLJ23040 BINDING SITE1 and FLJ23040 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ23040, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23040 BINDING SITE1 and FLJ23040 BINDING SITE2, designated SEQ ID:18256 and SEQ ID:14760 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33461] Another function of GAM281 is therefore inhibition of FLJ23040 (Accession NP_079450.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23040.

[33462] FLJ23053 (Accession NP_075058.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ23053 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23053, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ23053 BINDING SITE, designated SEQ ID:8693, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33463] Another function of GAM281 is therefore inhibition of FLJ23053 (Accession NP_075058.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23053.

[33464] FLJ23186 (Accession NP_078892.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ23186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23186 BINDING SITE, designated SEQ ID:1340, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33465] Another function of GAM281 is therefore inhibition of FLJ23186 (Accession NP_078892.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23186.

[33466] FLJ23263 (Accession NP_079391.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ23263 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ23263, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23263 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33467] Another function of GAM281 is therefore inhibition of FLJ23263 (Accession NP_079391.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23263.

[33468] FLJ23356 (Accession NP_115613.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ23356 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23356 BINDING SITE, designated SEQ ID:12273, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33469] Another function of GAM281 is therefore inhibition of FLJ23356 (Accession NP_115613.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23356.

[33470] FLJ23392 (Accession NP_079060.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ23392 BINDING SITE1 through FLJ23392 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ23392, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23392 BINDING SITE1 through FLJ23392 BINDING SITE3, designated SEQ ID:20052, SEQ ID:9148 and SEQ ID:5554 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33471] Another function of GAM281 is therefore inhibition of FLJ23392 (Accession NP_079060.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ23392.

[33472] FLJ23416 (Accession NP_115614.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ23416 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23416, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23416 BINDING SITE, designated SEQ ID:2152, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33473] Another function of GAM281 is therefore inhibition of FLJ23416 (Accession NP_115614.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23416.

[33474] FLJ23556 (Accession NP_079156.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ23556 BINDING SITE1 and FLJ23556 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ23556, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of FLJ23556 BINDING SITE1 and FLJ23556 BINDING SITE2, designated SEQ ID:17969 and SEQ ID:11323 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33475] Another function of GAM281 is therefore inhibition of FLJ23556 (Accession NP_079156.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23556.

[33476] FLJ23563 (Accession XP_041701.4) is another GAM281 target gene, herein designated TARGET GENE. FLJ23563 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23563 BINDING SITE, designated SEQ ID:15048, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33477] Another function of GAM281 is therefore inhibition of FLJ23563 (Accession XP_041701.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ23563.

[33478] FLJ25416 (Accession NP_659455.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ25416 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ25416, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25416 BINDING SITE, designated SEQ ID:16915, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33479] Another function of GAM281 is therefore inhibition of FLJ25416 (Accession NP_659455.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25416.

[33480] FLJ25421 (Accession NP_689725.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ25421 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ25421, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ25421 BINDING SITE, designated SEQ ID:12127, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33481] Another function of GAM281 is therefore inhibition of FLJ25421 (Accession NP_689725.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25421.

[33482] FLJ25795 (Accession NP_689633.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ25795 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25795, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25795 BINDING SITE, designated SEQ ID:934, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33483] Another function of GAM281 is therefore inhibition of FLJ25795 (Accession NP_689633.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ25795.

[33484] FLJ30507 (Accession NP_694555.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ30507 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ30507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30507 BINDING SITE, designated SEQ ID:17957, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33485] Another function of GAM281 is therefore inhibition of FLJ30507 (Accession NP_694555.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30507.

[33486] FLJ30532 (Accession NP_653325.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ30532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ30532 BINDING SITE, designated SEQ ID:19834, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33487] Another function of GAM281 is therefore inhibition of FLJ30532 (Accession NP_653325.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30532.

[33488] FLJ31139 (Accession NP_775928.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ31139 BINDING SITE1 through FLJ31139 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ31139, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31139 BINDING SITE1 through FLJ31139 BINDING SITE3, designated SEQ ID:15200, SEQ ID:18868 and SEQ ID:3952 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33489] Another function of GAM281 is therefore inhibition of FLJ31139 (Accession NP_775928.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ31139.

[33490] FLJ31153 (Accession NP_653201.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ31153 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31153, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31153 BINDING SITE, designated SEQ ID:7373, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33491] Another function of GAM281 is therefore inhibition of FLJ31153 (Accession NP_653201.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31153.

[33492] FLJ31166 (Accession NP_694567.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ31166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ31166 BINDING SITE, designated SEQ ID:19301, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33493] Another function of GAM281 is therefore inhibition of FLJ31166 (Accession NP_694567.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31166.

[33494] FLJ31322 (Accession NP_689600.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ31322 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31322, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31322 BINDING SITE, designated SEQ ID:17683, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33495] Another function of GAM281 is therefore inhibition of FLJ31322 (Accession NP_689600.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ31322.

[33496] FLJ31338 (Accession NP_689682.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ31338 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31338, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31338 BINDING SITE, designated SEQ ID:1672, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33497] Another function of GAM281 is therefore inhibition of FLJ31338 (Accession NP_689682.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31338.

[33498] FLJ31384 (Accession NP_689685.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ31384 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31384, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ31384 BINDING SITE, designated SEQ ID:14326, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33499] Another function of GAM281 is therefore inhibition of FLJ31384 (Accession NP_689685.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31384.

[33500] FLJ31393 (Accession NP_694569.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ31393 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ31393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31393 BINDING SITE, designated SEQ ID:9670, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33501] Another function of GAM281 is therefore inhibition of FLJ31393 (Accession NP_694569.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31393.

[33502] FLJ31401 (Accession NP_689877.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ31401 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31401, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31401 BINDING SITE, designated SEQ ID:16543, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33503] Another function of GAM281 is therefore inhibition of FLJ31401 (Accession NP_689877.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31401.

[33504] FLJ31434 (Accession NP_689709.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ31434 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31434, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31434 BINDING SITE, designated SEQ ID:9290, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33505] Another function of GAM281 is therefore inhibition of FLJ31434 (Accession NP_689709.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31434.

[33506] FLJ32096 (Accession NP_776156.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ32096 BINDING SITE1 and FLJ32096 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ32096, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32096 BINDING SITE1 and FLJ32096 BINDING SITE2, designated SEQ ID:1025 and SEQ ID:16043 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33507] Another function of GAM281 is therefore inhibition of FLJ32096 (Accession NP_776156.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ32096.

[33508] FLJ32130 (Accession NP_689671.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ32130 BINDING SITE1 through FLJ32130 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ32130, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32130 BINDING SITE1 through FLJ32130 BINDING SITE3, designated SEQ ID:4630, SEQ ID:15049 and SEQ ID:2061 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33509] Another function of GAM281 is therefore inhibition of FLJ32130 (Accession NP_689671.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32130.

[33510] FLJ32206 (Accession NP_689710.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ32206 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32206, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32206 BINDING SITE, designated SEQ ID:3860, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33511] Another function of GAM281 is therefore inhibition of FLJ32206 (Accession NP_689710.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32206.

[33512] FLJ32332 (Accession NP_653242.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ32332 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32332, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32332 BINDING SITE, designated SEQ ID:12917, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33513] Another function of GAM281 is therefore inhibition of FLJ32332 (Accession NP_653242.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ32332.

[33514] FLJ32334 (Accession NP_653166.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ32334 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32334 BINDING SITE, designated SEQ ID:8493, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33515] Another function of GAM281 is therefore inhibition of FLJ32334 (Accession NP_653166.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32334.

[33516] FLJ32499 (Accession NP_653208.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ32499 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32499, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ32499 BINDING SITE, designated SEQ ID:4681, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33517] Another function of GAM281 is therefore inhibition of FLJ32499 (Accession NP_653208.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32499.

[33518] FLJ32731 (Accession NP_689632.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ32731 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32731, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32731 BINDING SITE, designated SEQ ID:16099, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33519] Another function of GAM281 is therefore inhibition of FLJ32731 (Accession NP_689632.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ32731.

[33520] FLJ32803 (Accession NP_694584.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ32803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32803 BINDING SITE, designated SEQ ID:1856, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33521] Another function of GAM281 is therefore inhibition of FLJ32803 (Accession NP_694584.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32803.

[33522] FLJ32865 (Accession NP_653214.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ32865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ32865 BINDING SITE, designated SEQ ID:2146, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33523] Another function of GAM281 is therefore inhibition of FLJ32865 (Accession NP_653214.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865.

[33524] FLJ32894 (Accession NP_653268.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ32894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32894 BINDING SITE, designated SEQ ID:7467, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33525] Another function of GAM281 is therefore inhibition of FLJ32894 (Accession NP_653268.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32894.

[33526] FLJ32932 (Accession NP_690873.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ32932 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32932, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32932 BINDING SITE, designated SEQ ID:9555, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33527] Another function of GAM281 is therefore inhibition of FLJ32932 (Accession NP_690873.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32932.

[33528] FLJ33505 (Accession NP_689530.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ33505 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33505, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33505 BINDING SITE, designated SEQ ID:13693, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33529] Another function of GAM281 is therefore inhibition of FLJ33505 (Accession NP_689530.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33505.

[33530] FLJ33655 (Accession NP_775912.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ33655 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33655, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33655 BINDING SITE, designated SEQ ID:16113, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33531] Another function of GAM281 is therefore inhibition of FLJ33655 (Accession NP_775912.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33655.

[33532] FLJ34817 (Accession NP_689516.1) is another GAM281

target gene, herein designated TARGET GENE. FLJ34817 BINDING SITE1 and FLJ34817 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ34817, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34817 BINDING SITE1 and FLJ34817 BINDING SITE2, designated SEQ ID:7075 and SEQ ID:4004 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33533] Another function of GAM281 is therefore inhibition of FLJ34817 (Accession NP_689516.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34817.

[33534] FLJ34922 (Accession NP_689483.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ34922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ34922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ34922 BINDING SITE, designated SEQ ID:18132, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33535] Another function of GAM281 is therefore inhibition of FLJ34922 (Accession NP_689483.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34922.

[33536] FLJ34969 (Accession XP_114353.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ34969 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ34969, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34969 BINDING SITE, designated SEQ ID:581, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33537] Another function of GAM281 is therefore inhibition of FLJ34969 (Accession XP_114353.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34969.

[33538] FLJ35105 (Accession NP_689890.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ35105 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ35105, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35105 BINDING SITE, designated SEQ ID:18938, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33539] Another function of GAM281 is therefore inhibition of FLJ35105 (Accession NP_689890.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35105.

[33540] FLJ35487 (Accession NP_776181.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ35487 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35487, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35487 BINDING SITE, designated SEQ ID:12556, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33541] Another function of GAM281 is therefore inhibition of FLJ35487 (Accession NP_776181.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35487.

[33542] FLJ35681 (Accession NP_787096.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ35681 BINDING SITE1 and FLJ35681 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ35681, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35681 BINDING SITE1 and FLJ35681 BINDING SITE2, designated SEQ ID:1653 and SEQ ID:11521 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33543] Another function of GAM281 is therefore inhibition of FLJ35681 (Accession NP_787096.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ35681.

[33544] FLJ35848 (Accession XP_290755.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ35848 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35848, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35848 BINDING SITE, designated SEQ ID:14986, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33545] Another function of GAM281 is therefore inhibition of FLJ35848 (Accession XP_290755.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35848.

[33546] FLJ36112 (Accession NP_775950.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ36112 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36112, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ36112 BINDING SITE, designated SEQ ID:6601, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33547] Another function of GAM281 is therefore inhibition of FLJ36112 (Accession NP_775950.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36112.

[33548] FLJ36445 (Accession NP_694965.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ36445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36445 BINDING SITE, designated SEQ ID:2147, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33549] Another function of GAM281 is therefore inhibition of FLJ36445 (Accession NP_694965.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36445.

[33550] FLJ37045 (Accession NP_787085.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ37045 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37045 BINDING SITE, designated SEQ ID:9497, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33551] Another function of GAM281 is therefore inhibition of FLJ37045 (Accession NP_787085.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37045.

[33552] FLJ37078 (Accession NP_694588.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ37078 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ37078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37078 BINDING SITE, designated SEQ ID:11528, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33553] Another function of GAM281 is therefore inhibition of FLJ37078 (Accession NP_694588.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37078.

[33554] FLJ37266 (Accession NP_787088.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ37266 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37266, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37266 BINDING SITE, designated SEQ ID:4602, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33555] Another function of GAM281 is therefore inhibition of FLJ37266 (Accession NP_787088.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37266.

[33556] FLJ37433 (Accession NP_848612.1) is another GAM281

target gene, herein designated TARGET GENE. FLJ37433 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37433, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37433 BINDING SITE, designated SEQ ID:8582, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33557] Another function of GAM281 is therefore inhibition of FLJ37433 (Accession NP_848612.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37433.

[33558] FLJ37543 (Accession NP_775938.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ37543 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37543, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37543 BINDING SITE, designated SEQ ID:5495, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[33559] Another function of GAM281 is therefore inhibition of FLJ37543 (Accession NP_775938.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37543.

[33560] FLJ38101 (Accession NP_694993.2) is another GAM281 target gene, herein designated TARGET GENE. FLJ38101 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38101 BINDING SITE, designated SEQ ID:5589, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33561] Another function of GAM281 is therefore inhibition of FLJ38101 (Accession NP_694993.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38101.

[33562] FLJ38149 (Accession XP_091919.5) is another GAM281 target gene, herein designated TARGET GENE. FLJ38149

BINDING SITE1 through FLJ38149 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ38149, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38149 BINDING SITE1 through FLJ38149 BINDING SITE3, designated SEQ ID:15044, SEQ ID:18971 and SEQ ID:9373 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33563] Another function of GAM281 is therefore inhibition of FLJ38149 (Accession XP_091919.5) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38149.

[33564] FLJ38281 (Accession NP_689814.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ38281 BINDING SITE1 and FLJ38281 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38281, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38281 BINDING SITE1 and

FLJ38281 BINDING SITE2, designated SEQ ID:9492 and SEQ ID:6885 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33565] Another function of GAM281 is therefore inhibition of FLJ38281 (Accession NP_689814.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38281.

[33566] FLJ38607 (Accession NP_689867.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ38607 BINDING SITE1 and FLJ38607 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38607, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38607 BINDING SITE1 and FLJ38607 BINDING SITE2, designated SEQ ID:16688 and SEQ ID:7382 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33567] Another function of GAM281 is therefore inhibition of FLJ38607 (Accession NP_689867.1) . Accordingly, utilities

of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38607.

[33568] FLJ38792 (Accession NP_848615.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ38792 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38792, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38792 BINDING SITE, designated SEQ ID:14861, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33569] Another function of GAM281 is therefore inhibition of FLJ38792 (Accession NP_848615.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38792.

[33570] FLJ38819 (Accession NP_665872.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ38819 BINDING SITE1 and FLJ38819 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38819, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38819 BINDING SITE1 and FLJ38819 BINDING SITE2, designated SEQ ID:18642 and SEQ ID:9791 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33571] Another function of GAM281 is therefore inhibition of FLJ38819 (Accession NP_665872.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38819.

[33572] FLJ38991 (Accession NP_776188.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ38991 BINDING SITE1 and FLJ38991 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38991, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38991 BINDING SITE1 and FLJ38991 BINDING SITE2, designated SEQ ID:14236 and SEQ ID:10356 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[33573] Another function of GAM281 is therefore inhibition of FLJ38991 (Accession NP_776188.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38991.

[33574] FLJ39415 (Accession NP_775952.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ39415 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39415, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39415 BINDING SITE, designated SEQ ID:11673, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33575] Another function of GAM281 is therefore inhibition of FLJ39415 (Accession NP_775952.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39415.

[33576] FLJ39441 (Accession XP_084736.6) is another GAM281 target gene, herein designated TARGET GENE. FLJ39441

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39441, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39441 BINDING SITE, designated SEQ ID:7388, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33577] Another function of GAM281 is therefore inhibition of FLJ39441 (Accession XP_084736.6) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39441.

[33578] FLJ39599 (Accession NP_776164.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ39599 BINDING SITE1 through FLJ39599 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ39599, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39599 BINDING SITE1 through FLJ39599 BINDING SITE3, designated SEQ ID:8232, SEQ ID:16001 and SEQ ID:2845 respectively, to the nucleotide

sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33579] Another function of GAM281 is therefore inhibition of FLJ39599 (Accession NP_776164.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39599.

[33580] FLJ39639 (Accession XP_290687.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ39639 BINDING SITE1 and FLJ39639 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ39639, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39639 BINDING SITE1 and FLJ39639 BINDING SITE2, designated SEQ ID:6883 and SEQ ID:9190 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33581] Another function of GAM281 is therefore inhibition of FLJ39639 (Accession XP_290687.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ39639.

[33582] FLJ39821 (Accession NP_775971.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ39821 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39821, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39821 BINDING SITE, designated SEQ ID:17406, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33583] Another function of GAM281 is therefore inhibition of FLJ39821 (Accession NP_775971.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39821.

[33584] FLJ90231 (Accession NP_775852.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ90231 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90231, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ90231 BINDING SITE, designated SEQ ID:10357, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33585] Another function of GAM281 is therefore inhibition of FLJ90231 (Accession NP_775852.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90231.

[33586] FLJ90586 (Accession NP_699176.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ90586 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90586, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90586 BINDING SITE, designated SEQ ID:2786, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33587] Another function of GAM281 is therefore inhibition of FLJ90586 (Accession NP_699176.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90586.

[33588] FLJ90723 (Accession NP_787115.1) is another GAM281 target gene, herein designated TARGET GENE. FLJ90723 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90723, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90723 BINDING SITE, designated SEQ ID:19889, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33589] Another function of GAM281 is therefore inhibition of FLJ90723 (Accession NP_787115.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90723.

[33590] Formin binding protein 1 (FNBP1, Accession XP_052666.3) is another GAM281 target gene, herein designated TARGET GENE. FNBP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FNBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FNBP1 BINDING SITE, designated

SEQ ID:16354, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33591] Another function of GAM281 is therefore inhibition of Formin binding protein 1 (FNBP1, Accession XP_052666.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FNBP1.

[33592] Forkhead box e2 (FOXE2, Accession NP_036317.1) is another GAM281 target gene, herein designated TARGET GENE. FOXE2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FOXE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXE2 BINDING SITE, designated SEQ ID:15626, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33593] Another function of GAM281 is therefore inhibition of Forkhead box e2 (FOXE2, Accession NP_036317.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXE2.

[33594] Forkhead box o1a (rhabdomyosarcoma) (FOXO1A, Accession NP_002006.2) is another GAM281 target gene, herein designated TARGET GENE. FOXO1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOXO1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXO1A BINDING SITE, designated SEQ ID:736, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33595] Another function of GAM281 is therefore inhibition of Forkhead box o1a (rhabdomyosarcoma) (FOXO1A, Accession NP_002006.2), a gene which is a probable transcription factor. and therefore may be associated with Alveolar rhabdomyosarcoma- 2. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Alveolar rhabdomyosarcoma- 2., and of other diseases and clinical conditions associated with FOXO1A.

[33596] The function of FOXO1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Fsh primary response (lrpr1 homolog, rat) 1

(FSHPRH1, Accession NP_006724.1) is another GAM281 target gene, herein designated TARGET GENE. FSHPRH1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FSHPRH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FSHPRH1 BINDING SITE, designated SEQ ID:11528, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33597] Another function of GAM281 is therefore inhibition of Fsh primary response (lrpr1 homolog, rat) 1 (FSHPRH1, Accession NP_006724.1), a gene which is involved in the response of gonadal tissues to follicle- stimulating hormone. and therefore may be associated with Hypergonadotropic ovarian dysgenesis (odg), x- linked disorders of gonadal development. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Hypergonadotropic ovarian dysgenesis (odg), x- linked disorders of gonadal development, and of other diseases and clinical conditions associated with FSHPRH1.

[33598] The function of FSHPRH1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM189.1.Follistatin-like 1 (FSTL1, Accession NP_009016.1) is another GAM281 target gene, herein designated TARGET GENE. FSTL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FSTL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FSTL1 BINDING SITE, designated SEQ ID:11213, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33599] Another function of GAM281 is therefore inhibition of Follistatin-like 1 (FSTL1, Accession NP_009016.1), a gene which may modulate the action of some growth factors on cell proliferation and differentiation. and therefore may be associated with Rheumatoid arthritis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Rheumatoid arthritis., and of other diseases and clinical conditions associated with FSTL1.

[33600] The function of FSTL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM279.1.Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) is another GAM281 target gene, herein designated TARGET GENE. FUT1 BINDING SITE1 and FUT1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FUT1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FUT1 BINDING SITE1 and FUT1 BINDING SITE2, designated SEQ ID:11525 and SEQ ID:16365 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33601] Another function of GAM281 is therefore inhibition of Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUT1.

[33602] Frizzled homolog 4 (drosophila) (FZD4, Accession NP_036325.2) is another GAM281 target gene, herein

designated TARGET GENE. FZD4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FZD4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FZD4 BINDING SITE, designated SEQ ID:4487, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33603] Another function of GAM281 is therefore inhibition of Frizzled homolog 4 (drosophila) (FZD4, Accession NP_036325.2), a gene which may function in cell polarity, cell fate specification and cancer; similar to frizzled receptor family, has seven transmembrane domains and therefore may be associated with Familial exudative vitreoretinopathy. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Familial exudative vitreoretinopathy., and of other diseases and clinical conditions associated with FZD4.

[33604] The function of FZD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.1.Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075010.1) is another GAM281

target gene, herein designated TARGET GENE. G1P3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by G1P3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G1P3 BINDING SITE, designated SEQ ID:724, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33605] Another function of GAM281 is therefore inhibition of Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075010.1), a gene which is an interferon-stimulated gene (ISG). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G1P3.

[33606] The function of G1P3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_002029.3) is another GAM281 target gene, herein designated TARGET GENE. G1P3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA en-

coded by G1P3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G1P3 BINDING SITE, designated SEQ ID:724, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33607] Another function of GAM281 is therefore inhibition of Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_002029.3), a gene which is an interferon-stimulated gene (ISG). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G1P3.

[33608] The function of G1P3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075011.1) is another GAM281 target gene, herein designated TARGET GENE. G1P3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by G1P3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of G1P3 BINDING SITE, designated SEQ ID:724, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33609] Another function of GAM281 is therefore inhibition of Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075011.1), a gene which is an interferon-stimulated gene (ISG). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G1P3.

[33610] The function of G1P3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.G2A (Accession NP_037477.1) is another GAM281 target gene, herein designated TARGET GENE. G2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G2A BINDING SITE, designated SEQ ID:8714, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33611] Another function of GAM281 is therefore inhibition of G2A

(Accession NP_037477.1), a gene which may mediate some of the effects of extracellular atp on insulin secretion. and therefore may be associated with Autoimmune disease. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Autoimmune disease., and of other diseases and clinical conditions associated with G2A.

[33612] The function of G2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Glucose-6-phosphatase, catalytic (glycogen storage disease type i, von gierke disease) (G6PC, Accession NP_000142.1) is another GAM281 target gene, herein designated TARGET GENE. G6PC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G6PC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G6PC BINDING SITE, designated SEQ ID:4204, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33613] Another function of GAM281 is therefore inhibition of Glucose-6-phosphatase, catalytic (glycogen storage dis-

ease type i, von gierke disease) (G6PC, Accession NP_000142.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G6PC.

[33614] GAL3ST-4 (Accession NP_078913.3) is another GAM281 target gene, herein designated TARGET GENE. GAL3ST-4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAL3ST-4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAL3ST-4 BINDING SITE, designated SEQ ID:4518, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33615] Another function of GAM281 is therefore inhibition of GAL3ST-4 (Accession NP_078913.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAL3ST-4.

[33616] Gata binding protein 2 (GATA2, Accession NP_116027.2) is another GAM281 target gene, herein designated TARGET GENE. GATA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

GATA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GATA2 BINDING SITE, designated SEQ ID:16014, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33617] Another function of GAM281 is therefore inhibition of Gata binding protein 2 (GATA2, Accession NP_116027.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GATA2.

[33618] GBP4 (Accession NP_443173.2) is another GAM281 target gene, herein designated TARGET GENE. GBP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GBP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GBP4 BINDING SITE, designated SEQ ID:15052, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33619] Another function of GAM281 is therefore inhibition of

GBP4 (Accession NP_443173.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GBP4.

[33620] Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) is another GAM281 target gene, herein designated TARGET GENE. GGA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE, designated SEQ ID:5631, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33621] Another function of GAM281 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[33622] Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) is another GAM281 target gene, herein designated TARGET GENE.

GGA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE, designated SEQ ID:5631, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33623] Another function of GAM281 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[33624] Gamma-glutamyltransferase 1 (GGT1, Accession NP_005256.1) is another GAM281 target gene, herein designated TARGET GENE. GGT1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by GGT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGT1 BINDING SITE, designated SEQ ID:13688, to the nucleotide

sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33625] Another function of GAM281 is therefore inhibition of Gamma-glutamyltransferase 1 (GGT1, Accession NP_005256.1), a gene which catalyzes the transfer of the glutamyl moiety of glutathione to a variety of amino acids and dipeptide acceptors and therefore is associated with Glutathionuria. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Glutathionuria, and of other diseases and clinical conditions associated with GGT1.

[33626] The function of GGT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Gamma-glutamyltransferase 1 (GGT1, Accession NP_038265.1) is another GAM281 target gene, herein designated TARGET GENE. GGT1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by GGT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGT1 BINDING SITE, designated SEQ ID:13688, to the nu-

cleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33627] Another function of GAM281 is therefore inhibition of Gamma-glutamyltransferase 1 (GGT1, Accession NP_038265.1), a gene which catalyzes the transfer of the glutamyl moiety of glutathione to a variety of amino acids and dipeptide acceptors and therefore is associated with Glutathionuria. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Glutathionuria, and of other diseases and clinical conditions associated with GGT1.

[33628] The function of GGT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Gamma-glutamyltransferase 1 (GGT1, Accession NP_038347.1) is another GAM281 target gene, herein designated TARGET GENE. GGT1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by GGT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGT1 BINDING SITE, designated SEQ ID:13688, to the nu-

cleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33629] Another function of GAM281 is therefore inhibition of Gamma-glutamyltransferase 1 (GGT1, Accession NP_038347.1), a gene which catalyzes the transfer of the glutamyl moiety of glutathione to a variety of amino acids and dipeptide acceptors and therefore is associated with Glutathionuria. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Glutathionuria, and of other diseases and clinical conditions associated with GGT1.

[33630] The function of GGT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Gamma-glutamyltransferase 2 (GGT2, Accession XP_290331.1) is another GAM281 target gene, herein designated TARGET GENE. GGT2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GGT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGT2 BINDING SITE, designated SEQ ID:13688, to the nucleotide sequence of

GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33631] Another function of GAM281 is therefore inhibition of Gamma-glutamyltransferase 2 (GGT2, Accession XP_290331.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGT2.

[33632] Gm2 ganglioside activator protein (GM2A, Accession NP_000396.1) is another GAM281 target gene, herein designated TARGET GENE. GM2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GM2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GM2A BINDING SITE, designated SEQ ID:11286, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33633] Another function of GAM281 is therefore inhibition of Gm2 ganglioside activator protein (GM2A, Accession NP_000396.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GM2A.

[33634] GNE (Accession NP_005467.1) is another GAM281 target gene, herein designated TARGET GENE. GNE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNE BINDING SITE, designated SEQ ID:8367, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33635] Another function of GAM281 is therefore inhibition of GNE (Accession NP_005467.1), a gene which has roles in sialic acid biosynthesis and regulates cell surface sialylation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNE.

[33636] The function of GNE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Guanine nucleotide binding protein (g protein), gamma 4 (GNG4, Accession NP_004476.1) is another GAM281 target gene, herein designated TARGET GENE. GNG4 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by GNG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNG4 BINDING SITE, designated SEQ ID:559, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33637] Another function of GAM281 is therefore inhibition of Guanine nucleotide binding protein (g protein), gamma 4 (GNG4, Accession NP_004476.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNG4.

[33638] GNPNAT1 (Accession XP_085119.1) is another GAM281 target gene, herein designated TARGET GENE. GNPNAT1 BINDING SITE1 and GNPNAT1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GNPNAT1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNPNAT1 BINDING SITE1 and GNPNAT1 BINDING SITE2, designated SEQ ID:8464 and SEQ ID:854 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[33639] Another function of GAM281 is therefore inhibition of GNPNAT1 (Accession XP_085119.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNPNAT1.

[33640] GNRPX (Accession NP_060519.1) is another GAM281 target gene, herein designated TARGET GENE. GNRPX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNRPX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNRPX BINDING SITE, designated SEQ ID:12243, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33641] Another function of GAM281 is therefore inhibition of GNRPX (Accession NP_060519.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNRPX.

[33642] Golgi autoantigen, golgin subfamily a, 1 (GOLGA1, Accession NP_002068.1) is another GAM281 target gene, herein designated TARGET GENE. GOLGA1 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by GOLGA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GOLGA1 BINDING SITE, designated SEQ ID:12206, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33643] Another function of GAM281 is therefore inhibition of Golgi autoantigen, golgin subfamily a, 1 (GOLGA1, Accession NP_002068.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLGA1.

[33644] Golgi autoantigen, golgin subfamily a, 3 (GOLGA3, Accession NP_005886.2) is another GAM281 target gene, herein designated TARGET GENE. GOLGA3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GOLGA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GOLGA3 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[33645] Another function of GAM281 is therefore inhibition of Golgi autoantigen, golgin subfamily a, 3 (GOLGA3, Accession NP_005886.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLGA3.

[33646] GOLGIN-67 (Accession NP_851421.1) is another GAM281 target gene, herein designated TARGET GENE. GOLGIN-67 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by GOLGIN-67, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GOLGIN-67 BINDING SITE, designated SEQ ID:4244, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33647] Another function of GAM281 is therefore inhibition of GOLGIN-67 (Accession NP_851421.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLGIN-67.

[33648] Glycoprotein v (platelet) (GP5, Accession NP_004479.1) is another GAM281 target gene, herein designated TARGET GENE. GP5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GP5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GP5 BINDING SITE, designated SEQ ID:5681, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33649] Another function of GAM281 is therefore inhibition of Glycoprotein v (platelet) (GP5, Accession NP_004479.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GP5.

[33650] GPP34R (Accession NP_060648.2) is another GAM281 target gene, herein designated TARGET GENE. GPP34R BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPP34R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPP34R BINDING SITE, designated SEQ ID:14203, to the nucleotide

sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33651] Another function of GAM281 is therefore inhibition of GPP34R (Accession NP_060648.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPP34R.

[33652] G protein-coupled receptor 114 (GPR114, Accession NP_722579.1) is another GAM281 target gene, herein designated TARGET GENE. GPR114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR114 BINDING SITE, designated SEQ ID:10636, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33653] Another function of GAM281 is therefore inhibition of G protein-coupled receptor 114 (GPR114, Accession NP_722579.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR114.

[33654] G protein-coupled receptor 26 (GPR26, Accession

NP_703143.1) is another GAM281 target gene, herein designated TARGET GENE. GPR26 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR26, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR26 BINDING SITE, designated SEQ ID:3010, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33655] Another function of GAM281 is therefore inhibition of G protein-coupled receptor 26 (GPR26, Accession NP_703143.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR26.

[33656] G protein-coupled receptor 4 (GPR4, Accession NP_005273.1) is another GAM281 target gene, herein designated TARGET GENE. GPR4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR4 BINDING SITE, designated SEQ ID:4965, to the nucleotide sequence of GAM281 RNA,

herein designated GAM RNA, also designated SEQ ID:278.

[33657] Another function of GAM281 is therefore inhibition of G protein-coupled receptor 4 (GPR4, Accession NP_005273.1), a gene which stimulates to produce increased calcium by both SPC and LPC . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR4.

[33658] The function of GPR4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.G protein-coupled receptor 56 (GPR56, Accession NP_005673.2) is another GAM281 target gene, herein designated TARGET GENE. GPR56 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GPR56, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR56 BINDING SITE, designated SEQ ID:8622, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33659] Another function of GAM281 is therefore inhibition of G

protein-coupled receptor 56 (GPR56, Accession NP_005673.2), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR56.

[33660] The function of GPR56 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.G protein-coupled receptor 61 (GPR61, Accession NP_114142.2) is another GAM281 target gene, herein designated TARGET GENE. GPR61 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR61, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR61 BINDING SITE, designated SEQ ID:15604, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33661] Another function of GAM281 is therefore inhibition of G protein-coupled receptor 61 (GPR61, Accession NP_114142.2), a gene which transduces extracellular sig-

nals through heterotrimeric G proteins. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR61.

[33662] The function of GPR61 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.2.G protein-coupled receptor 66 (GPR66, Accession NP_006047.2) is another GAM281 target gene, herein designated TARGET GENE. GPR66 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR66, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR66 BINDING SITE, designated SEQ ID:19237, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33663] Another function of GAM281 is therefore inhibition of G protein-coupled receptor 66 (GPR66, Accession NP_006047.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR66.

[33664] G protein-coupled receptor 81 (GPR81, Accession NP_115943.1) is another GAM281 target gene, herein designated TARGET GENE. GPR81 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR81, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR81 BINDING SITE, designated SEQ ID:13260, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33665] Another function of GAM281 is therefore inhibition of G protein-coupled receptor 81 (GPR81, Accession NP_115943.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR81.

[33666] GR6 (Accession NP_031380.1) is another GAM281 target gene, herein designated TARGET GENE. GR6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GR6 BINDING

SITE, designated SEQ ID:2604, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33667] Another function of GAM281 is therefore inhibition of GR6 (Accession NP_031380.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GR6.

[33668] GRAF (Accession NP_055886.1) is another GAM281 target gene, herein designated TARGET GENE. GRAF BINDING SITE1 and GRAF BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GRAF, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRAF BINDING SITE1 and GRAF BINDING SITE2, designated SEQ ID:13350 and SEQ ID:4362 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33669] Another function of GAM281 is therefore inhibition of GRAF (Accession NP_055886.1), a gene which ia a GTPase activating protein for p21- rac and therefore may be associated with Juvenile myelomonocytic leukemia. Accordingly, utilities of GAM281 include diagnosis, prevention

and treatment of Juvenile myelomonocytic leukemia, and of other diseases and clinical conditions associated with GRAF.

[33670] The function of GRAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.GREB1 (Accession NP_055483.2) is another GAM281 target gene, herein designated TARGET GENE. GREB1 BINDING SITE1 through GREB1 BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by GREB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GREB1 BINDING SITE1 through GREB1 BINDING SITE3, designated SEQ ID:14113, SEQ ID:14861 and SEQ ID:9792 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33671] Another function of GAM281 is therefore inhibition of GREB1 (Accession NP_055483.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GREB1.

[33672] Glutamate receptor, ionotropic, delta 1 (GRID1, Accession

XP_043613.8) is another GAM281 target gene, herein designated TARGET GENE. GRID1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRID1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRID1 BINDING SITE, designated SEQ ID:17390, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33673] Another function of GAM281 is therefore inhibition of Glutamate receptor, ionotropic, delta 1 (GRID1, Accession XP_043613.8) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRID1.

[33674] Glutamate receptor, ionotropic, n-methyl d-aspartate-like 1a (GRINL1A, Accession NP_056347.1) is another GAM281 target gene, herein designated TARGET GENE. GRINL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRINL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

GRINL1A BINDING SITE, designated SEQ ID:5433, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33675] Another function of GAM281 is therefore inhibition of Glutamate receptor, ionotropic, n-methyl d-aspartate-like 1a (GRINL1A, Accession NP_056347.1), a gene which plays a role in the development and function of the mammalian brain. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRINL1A.

[33676] The function of GRINL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Glutamate receptor, metabotropic 6 (GRM6, Accession NP_000834.1) is another GAM281 target gene, herein designated TARGET GENE. GRM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRM6 BINDING SITE, designated SEQ ID:10398, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[33677] Another function of GAM281 is therefore inhibition of Glutamate receptor, metabotropic 6 (GRM6, Accession NP_000834.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRM6.

[33678] GRWD (Accession NP_113673.2) is another GAM281 target gene, herein designated TARGET GENE. GRWD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRWD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRWD BINDING SITE, designated SEQ ID:7996, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33679] Another function of GAM281 is therefore inhibition of GRWD (Accession NP_113673.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRWD.

[33680] GSDM (Accession XP_209009.1) is another GAM281 target gene, herein designated TARGET GENE. GSDM BINDING SITE is a target binding site found in the 3` untranslated

region of multiple transcripts of mRNA encoded by GSDM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSDM BINDING SITE, designated SEQ ID:3199, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33681] Another function of GAM281 is therefore inhibition of GSDM (Accession XP_209009.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSDM.

[33682] GSDM (Accession NP_835465.1) is another GAM281 target gene, herein designated TARGET GENE. GSDM BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSDM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSDM BINDING SITE, designated SEQ ID:3199, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33683] Another function of GAM281 is therefore inhibition of GSDM (Accession NP_835465.1) . Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSDM.

[33684] Glutathione s-transferase m1 (GSTM1, Accession NP_000552.2) is another GAM281 target gene, herein designated TARGET GENE. GSTM1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSTM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSTM1 BINDING SITE, designated SEQ ID:12752, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33685] Another function of GAM281 is therefore inhibition of Glutathione s-transferase m1 (GSTM1, Accession NP_000552.2), a gene which is conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. and therefore may be associated with Aplastic anemia and cancer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Aplastic anemia and cancer, and of other diseases and clinical conditions associated with GSTM1.

[33686] The function of GSTM1 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Glutathione s-transferase m1 (GSTM1, Accession NP_666533.1) is another GAM281 target gene, herein designated TARGET GENE. GSTM1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSTM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSTM1 BINDING SITE, designated SEQ ID:12752, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33687] Another function of GAM281 is therefore inhibition of Glutathione s-transferase m1 (GSTM1, Accession NP_666533.1), a gene which is conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. and therefore may be associated with Aplastic anemia and cancer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Aplastic anemia and cancer, and of other diseases and clinical conditions associated with GSTM1.

[33688] The function of GSTM1 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Glutathione s-transferase m2 (muscle) (GSTM2, Accession NP_000839.1) is another GAM281 target gene, herein designated TARGET GENE. GSTM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GSTM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSTM2 BINDING SITE, designated SEQ ID:12752, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33689] Another function of GAM281 is therefore inhibition of Glutathione s-transferase m2 (muscle) (GSTM2, Accession NP_000839.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSTM2.

[33690] Glutathione s-transferase m4 (GSTM4, Accession NP_671490.1) is another GAM281 target gene, herein designated TARGET GENE. GSTM4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSTM4, correspond-

ing to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSTM4 BINDING SITE, designated SEQ ID:12752, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33691] Another function of GAM281 is therefore inhibition of Glutathione s-transferase m4 (GSTM4, Accession NP_671490.1), a gene which conjugates reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSTM4.

[33692] The function of GSTM4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Glutathione s-transferase m4 (GSTM4, Accession NP_000841.1) is another GAM281 target gene, herein designated TARGET GENE. GSTM4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GSTM4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of GSTM4 BINDING SITE, designated SEQ ID:12752, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33693] Another function of GAM281 is therefore inhibition of Glutathione s-transferase m4 (GSTM4, Accession NP_000841.1), a gene which conjugates reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSTM4.

[33694] The function of GSTM4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.General transcription factor iie, polypeptide 1, alpha 56kda (GTF2E1, Accession NP_005504.1) is another GAM281 target gene, herein designated TARGET GENE. GTF2E1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GTF2E1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2E1 BINDING SITE, designated

SEQ ID:15661, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33695] Another function of GAM281 is therefore inhibition of General transcription factor iie, polypeptide 1, alpha 56kda (GTF2E1, Accession NP_005504.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2E1.

[33696] GTF2IRD2 (Accession NP_775808.1) is another GAM281 target gene, herein designated TARGET GENE. GTF2IRD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GTF2IRD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2IRD2 BINDING SITE, designated SEQ ID:11522, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33697] Another function of GAM281 is therefore inhibition of GTF2IRD2 (Accession NP_775808.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with GTF2IRD2.

[33698] GTF2IRD2 (Accession NP_115579.3) is another GAM281 target gene, herein designated TARGET GENE. GTF2IRD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GTF2IRD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2IRD2 BINDING SITE, designated SEQ ID:11522, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33699] Another function of GAM281 is therefore inhibition of GTF2IRD2 (Accession NP_115579.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2IRD2.

[33700] GTPBG3 (Accession NP_116009.1) is another GAM281 target gene, herein designated TARGET GENE. GTPBG3 BINDING SITE1 and GTPBG3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GTPBG3, corresponding to target binding sites such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTPBG3 BINDING SITE1 and GTPBG3 BINDING SITE2, designated SEQ ID:7812 and SEQ ID:10292 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33701] Another function of GAM281 is therefore inhibition of GTPBG3 (Accession NP_116009.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTPBG3.

[33702] Glycogenin (GYG, Accession NP_004121.2) is another GAM281 target gene, herein designated TARGET GENE. GYG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GYG BINDING SITE, designated SEQ ID:4258, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33703] Another function of GAM281 is therefore inhibition of Glycogenin (GYG, Accession NP_004121.2), a gene which

primes de novo glycogen synthesis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GYG.

[33704] The function of GYG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.H-plk (Accession NP_056936.1) is another GAM281 target gene, herein designated TARGET GENE. H-plk BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by H-plk, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H-plk BINDING SITE, designated SEQ ID:12753, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33705] Another function of GAM281 is therefore inhibition of H-plk (Accession NP_056936.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H-plk.

[33706] H2AV (Accession NP_619541.1) is another GAM281 target gene, herein designated TARGET GENE. H2AV BINDING SITE is a target binding site found in the 3` untranslated

region of multiple transcripts of mRNA encoded by H2AV, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H2AV BINDING SITE, designated SEQ ID:18864, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33707] Another function of GAM281 is therefore inhibition of H2AV (Accession NP_619541.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H2AV.

[33708] H63 (Accession NP_612432.2) is another GAM281 target gene, herein designated TARGET GENE. H63 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H63, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H63 BINDING SITE, designated SEQ ID:4554, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33709] Another function of GAM281 is therefore inhibition of H63 (Accession NP_612432.2) . Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H63.

[33710] H63 (Accession NP_816929.1) is another GAM281 target gene, herein designated TARGET GENE. H63 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H63, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H63 BINDING SITE, designated SEQ ID:4554, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33711] Another function of GAM281 is therefore inhibition of H63 (Accession NP_816929.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H63.

[33712] Hepatitis a virus cellular receptor 2 (HAVCR2, Accession NP_116171.2) is another GAM281 target gene, herein designated TARGET GENE. HAVCR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HAVCR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of HAVCR2 BINDING SITE, designated SEQ ID:16260, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33713] Another function of GAM281 is therefore inhibition of Hepatitis a virus cellular receptor 2 (HAVCR2, Accession NP_116171.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAVCR2.

[33714] Hemopoietic cell kinase (HCK, Accession NP_002101.2) is another GAM281 target gene, herein designated TARGET GENE. HCK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HCK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HCK BINDING SITE, designated SEQ ID:7142, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33715] Another function of GAM281 is therefore inhibition of Hemopoietic cell kinase (HCK, Accession NP_002101.2), a gene which is non- receptor protein tyrosine kinase. and therefore may be associated with Leukemias. Accordingly,

utilities of GAM281 include diagnosis, prevention and treatment of Leukemias., and of other diseases and clinical conditions associated with HCK.

[33716] The function of HCK has been established by previous studies. During a search for a cDNA clone representing human SRC (OMIM Ref. No. 190090), Quintrell et al. (1987) encountered a previously unrecognized gene that appeared to encode a protein- tyrosine kinase similar to SRC. Ziegler et al. (1987) found the same gene by a different route. Expression of this gene may be limited to certain hemopoietic cells and is especially prominent in cells of myeloid lineage, particularly mature granulocytes and monocytes. Therefore, Quintrell et al. (1987) designated the gene HCK (pronounced 'hick') for hemopoietic cell kinase. They described the nucleotide sequence of a cDNA clone that represents most or all of the mRNA for HCK, the deduced amino acid sequence of the protein encoded by HCK, and the distribution of RNA transcribed from HCK among various hemopoietic cells. By spot- blot analysis of sorted chromosomes and by in situ hybridization, Quintrell et al. (1987) assigned the HCK gene to 20q11- q12. Since this region is affected by interstitial deletions in some acute myeloid leukemias and myeloproliferative dis-

orders, they suggested that damage to HCK may contribute to the pathogenesis of these conditions.

[33717]

[33718] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[33719] Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J. M.; Pettenati, M. J.; Le Beau, M. M.; Diaz, M. O.; Rowley, J. D. : Identification of a human gene (HCK) that encodes a protein- tyrosine kinase and is expressed in hemopoietic cells. Molec. Cell. Biol. 7: 2267- 2275, 1987. ; and

[33720] Ziegler, S. F.; Marth, J. D.; Lewis, D. B.; Perlmutter, R. M. : Novel protein- tyrosine kinase gene (hck) preferentially expressed in cells of hematopoietic origin. Molec. Cell. Biol. 7:.

[33721] Further studies establishing the function and utilities of HCK are found in John Hopkins OMIM database record ID 142370, and in cited publications listed in Table 5, which are hereby incorporated by reference.HE9 (Accession NP_741997.1) is another GAM281 target gene, herein designated TARGET GENE. HE9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HE9, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HE9 BINDING SITE, designated SEQ ID:7942, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33722] Another function of GAM281 is therefore inhibition of HE9 (Accession NP_741997.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HE9.

[33723] HECA (Accession NP_057301.1) is another GAM281 target gene, herein designated TARGET GENE. HECA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HECA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HECA BINDING SITE, designated SEQ ID:17954, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33724] Another function of GAM281 is therefore inhibition of HECA (Accession NP_057301.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HECA.

[33725] HEMK (Accession NP_057257.1) is another GAM281 target gene, herein designated TARGET GENE. HEMK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HEMK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HEMK BINDING SITE, designated SEQ ID:6468, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33726] Another function of GAM281 is therefore inhibition of HEMK (Accession NP_057257.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEMK.

[33727] Hephaestin (HEPH, Accession NP_055614.1) is another GAM281 target gene, herein designated TARGET GENE. HEPH BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by HEPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HEPH BINDING SITE, designated SEQ ID:15338, to the nucleotide sequence of GAM281

RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33728] Another function of GAM281 is therefore inhibition of Hephaestin (HEPH, Accession NP_055614.1), a gene which is thought to be a membrane- bound protein responsible for transport of dietary iron from epithelial cells of the intestinal lumen into the circulatory system. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEPH.

[33729] The function of HEPH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Hexosaminidase a (alpha polypeptide) (HEXA, Accession NP_000511.1) is another GAM281 target gene, herein designated TARGET GENE. HEXA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HEXA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HEXA BINDING SITE, designated SEQ ID:14035, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[33730] Another function of GAM281 is therefore inhibition of Hexosaminidase a (alpha polypeptide) (HEXA, Accession NP_000511.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEXA.

[33731] Herv-h ltr-associating 3 (HHLA3, Accession XP_294968.1) is another GAM281 target gene, herein designated TARGET GENE. HHLA3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by HHLA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HHLA3 BINDING SITE, designated SEQ ID:13713, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33732] Another function of GAM281 is therefore inhibition of Herv-h ltr-associating 3 (HHLA3, Accession XP_294968.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HHLA3.

[33733] Herv-h ltr-associating 3 (HHLA3, Accession NP_009002.1)

is another GAM281 target gene, herein designated TARGET GENE. HHLA3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by HHLA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HHLA3 BINDING SITE, designated SEQ ID:13713, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33734] Another function of GAM281 is therefore inhibition of Herv-h ltr-associating 3 (HHLA3, Accession NP_009002.1). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HHLA3.

[33735] HIC (Accession XP_041273.1) is another GAM281 target gene, herein designated TARGET GENE. HIC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HIC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIC BINDING SITE, designated SEQ ID:488, to the nucleotide sequence

of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33736] Another function of GAM281 is therefore inhibition of HIC (Accession XP_041273.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIC.

[33737] Holocarboxylase synthetase (biotin-[proprionyl-coenzyme a-carboxylase (atp-hydrolysing)] ligase) (HLCS, Accession NP_000402.2) is another GAM281 target gene, herein designated TARGET GENE. HLCS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HLCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:2142, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33738] Another function of GAM281 is therefore inhibition of Holocarboxylase synthetase (biotin-[proprionyl-coenzyme a-carboxylase (atp-hydrolysing)] ligase) (HLCS, Accession NP_000402.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLCS.

[33739] High-mobility group 20a (HMG20A, Accession NP_060670.1) is another GAM281 target gene, herein designated TARGET GENE. HMG20A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HMG20A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HMG20A BINDING SITE, designated SEQ ID:5040, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33740] Another function of GAM281 is therefore inhibition of High-mobility group 20a (HMG20A, Accession NP_060670.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMG20A.

[33741] HPRN (Accession NP_071938.1) is another GAM281 target gene, herein designated TARGET GENE. HPRN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HPRN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HPRN BIND-

ING SITE, designated SEQ ID:12916, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33742] Another function of GAM281 is therefore inhibition of HPRN (Accession NP_071938.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HPRN.

[33743] Histamine receptor h4 (HRH4, Accession NP_067637.2) is another GAM281 target gene, herein designated TARGET GENE. HRH4 BINDING SITE1 through HRH4 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by HRH4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HRH4 BINDING SITE1 through HRH4 BINDING SITE3, designated SEQ ID:5301, SEQ ID:5358 and SEQ ID:3116 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33744] Another function of GAM281 is therefore inhibition of Histamine receptor h4 (HRH4, Accession NP_067637.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with HRH4.

[33745] HSC3 (Accession NP_660157.1) is another GAM281 target gene, herein designated TARGET GENE. HSC3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSC3 BINDING SITE, designated SEQ ID:1095, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33746] Another function of GAM281 is therefore inhibition of HSC3 (Accession NP_660157.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSC3.

[33747] HSD3B7 (Accession NP_079469.2) is another GAM281 target gene, herein designated TARGET GENE. HSD3B7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSD3B7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSD3B7 BINDING SITE, designated SEQ ID:2674, to the nucleotide

sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33748] Another function of GAM281 is therefore inhibition of HSD3B7 (Accession NP_079469.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSD3B7.

[33749] HSMPP8 (Accession XP_167894.1) is another GAM281 target gene, herein designated TARGET GENE. HSMPP8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSMPP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSMPP8 BINDING SITE, designated SEQ ID:7797, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33750] Another function of GAM281 is therefore inhibition of HSMPP8 (Accession XP_167894.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSMPP8.

[33751] HSNOV1 (Accession NP_059985.2) is another GAM281

target gene, herein designated TARGET GENE. HSNOV1 BINDING SITE1 and HSNOV1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HSNOV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSNOV1 BINDING SITE1 and HSNOV1 BINDING SITE2, designated SEQ ID:849 and SEQ ID:12942 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33752] Another function of GAM281 is therefore inhibition of HSNOV1 (Accession NP_059985.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSNOV1.

[33753] HSPC065 (Accession NP_054876.2) is another GAM281 target gene, herein designated TARGET GENE. HSPC065 BINDING SITE1 and HSPC065 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HSPC065, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of HSPC065 BINDING SITE1 and HSPC065 BINDING SITE2, designated SEQ ID:4676 and SEQ ID:713 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33754] Another function of GAM281 is therefore inhibition of HSPC065 (Accession NP_054876.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC065.

[33755] 5-hydroxytryptamine (serotonin) receptor 1d (HTR1D, Accession NP_000855.1) is another GAM281 target gene, herein designated TARGET GENE. HTR1D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR1D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR1D BINDING SITE, designated SEQ ID:2563, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33756] Another function of GAM281 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 1d (HTR1D, Ac-

cession NP_000855.1), a gene which belongs to g- protein coupled receptor. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR1D.

[33757] The function of HTR1D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.5-hydroxytryptamine (serotonin) receptor 1e (HTR1E, Accession NP_000856.1) is another GAM281 target gene, herein designated TARGET GENE. HTR1E BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR1E, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR1E BINDING SITE, designated SEQ ID:538, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33758] Another function of GAM281 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 1e (HTR1E, Accession NP_000856.1), a gene which belongs to g- protein coupled receptors. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with HTR1E.

[33759] The function of HTR1E and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.5-hydroxytryptamine (serotonin) receptor 3b (HTR3B, Accession NP_006019.1) is another GAM281 target gene, herein designated TARGET GENE. HTR3B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR3B BINDING SITE, designated SEQ ID:656, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33760] Another function of GAM281 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 3b (HTR3B, Accession NP_006019.1), a gene which is a component of ligand gated ion channels. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR3B.

[33761] The function of HTR3B has been established by previous studies. Serotonin mediates rapid excitatory responses

through ligand- gated channels (HTR3 receptors). When expressed as a homomeric unit, HTR3A (OMIM Ref. No. 182139) is a functional receptor but displays rather weak conductance. By searching human genome sequence data, Davies et al. (1999) identified a homolog of the HTR3A subunit in a PAC clone from 11q23.1, the same chromosomal location of HTR3A. Using anchored PCR to screen brain and kidney cDNA libraries, they obtained a cDNA clone, which they designated HTR3B, that encodes a 441-amino acid protein with 41% sequence identity to HTR3A. Northern blot analysis revealed expression of a 4.4- kb transcript in kidney and brain, specifically in caudate nucleus, hippocampus, and thalamus, and particularly in amygdala. These regions of the brain also express 2.4- kb transcripts for HTR3A. HTR3B was absent from heart, placenta, lung, liver, skeletal muscle, and pancreas. The authors determined that HTR3B cannot assemble as a homomeric HTR3 receptor but that heteromeric HTR3A/HTR3B receptors display a large single- channel conductance (16 pS), low permeability to calcium ions, and a current- voltage relationship resembling that of characterized neuronal HTR3 channels. By RT- PCR in situ hybridization, Dubin et al. (1999) found that HTR3A and

HTR3B colocalize in amygdala, telencephalon, and entorhinal cortex, as well as in small monocytes of spleen and tonsil, and in uterus, prostate, ovary, placenta, and intestine. Hydropathy analysis indicated that the HTR3B protein has 4 putative transmembrane domains. In contrast to HTR3A, HTR3B lacks the 3 negatively charged residues bracketing the second transmembrane domain that are thought to be critical for the rate of ion transport in acetylcholine receptors (see OMIM Ref. No. CHRNA1, 100690). It also contains 5 potential glycosylation and 4 potential phosphorylation sites.

[33762]

[33763] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[33764] Davies, P. A.; Pistis, M.; Hanna, M. C.; Peters, J. A.; Lambert, J. J.; Hales, T. G.; Kirkness, E. F. : The 5- HT(3B) subunit is a major determinant of serotonin- receptor function. Nature 397: 359- 363, 1999. ; and

[33765] Dubin, A. E.; Huvar, R.; D'Andrea, M. R.; Pyati, J.; Zhu, J. Y.; Joy, K. C.; Wilson, S. J.; Galindo, J. E.; Glass, C. A.; Luo, L.; Jackson, M. R.; Lovenberg, T. W.; Erlander, M. G. : Th.

[33766] Further studies establishing the function and utilities of

HTR3B are found in John Hopkins OMIM database record ID 604654, and in cited publications listed in Table 5, which are hereby incorporated by reference.Hormonally upregulated neu-associated kinase (HUNK, Accession NP_055401.1) is another GAM281 target gene, herein designated TARGET GENE. HUNK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HUNK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUNK BINDING SITE, designated SEQ ID:17952, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33767] Another function of GAM281 is therefore inhibition of Hormonally upregulated neu-associated kinase (HUNK, Accession NP_055401.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUNK.

[33768] Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1) is another GAM281 target gene, herein designated TARGET GENE. HUS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by HUS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUS1 BINDING SITE, designated SEQ ID:14238, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33769] Another function of GAM281 is therefore inhibition of Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1), a gene which May form DNA damage- responsive protein complex . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUS1.

[33770] The function of HUS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Hyaluronoglucosaminidase 1 (HYAL1, Accession NP_695018.1) is another GAM281 target gene, herein designated TARGET GENE. HYAL1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by HYAL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of HYAL1 BINDING SITE, designated SEQ ID:1192, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33771] Another function of GAM281 is therefore inhibition of Hyaluronoglucosaminidase 1 (HYAL1, Accession NP_695018.1), a gene which plays a role in cell proliferation, migration and differentiation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HYAL1.

[33772] The function of HYAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM180.2.Hyaluronoglucosaminidase 4 (HYAL4, Accession NP_036401.1) is another GAM281 target gene, herein designated TARGET GENE. HYAL4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HYAL4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HYAL4 BINDING SITE, designated SEQ ID:2143, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[33773] Another function of GAM281 is therefore inhibition of Hyaluronoglucosaminidase 4 (HYAL4, Accession NP_036401.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HYAL4.

[33774] Intercellular adhesion molecule 1 (cd54), human rhinovirus receptor (ICAM1, Accession NP_000192.1) is another GAM281 target gene, herein designated TARGET GENE. ICAM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ICAM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICAM1 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33775] Another function of GAM281 is therefore inhibition of Intercellular adhesion molecule 1 (cd54), human rhinovirus receptor (ICAM1, Accession NP_000192.1), a gene which binds the integrin LFA- 1 (ITGB2) and promotes adhesion; member of the immunoglobulin superfamily and therefore may be associated with Malaria, cerebral, susceptibility to.

Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Malaria, cerebral, susceptibility to, and of other diseases and clinical conditions associated with ICAM1.

[33776] The function of ICAM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.ICK (Accession NP_057597.2) is another GAM281 target gene, herein designated TARGET GENE. ICK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ICK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33777] Another function of GAM281 is therefore inhibition of ICK (Accession NP_057597.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK.

[33778] ICK (Accession NP_055735.1) is another GAM281 target gene, herein designated TARGET GENE. ICK BINDING SITE

is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ICK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33779] Another function of GAM281 is therefore inhibition of ICK (Accession NP_055735.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK.

[33780] Insulin-like growth factor 1 (somatomedin c) (IGF1, Accession NP_000609.1) is another GAM281 target gene, herein designated TARGET GENE. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IGF1 BINDING SITE, designated SEQ ID:6279, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33781] Another function of GAM281 is therefore inhibition of Insulin-like growth factor 1 (somatomedin c) (IGF1, Accession NP_000609.1), a gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore may be associated with Growth retardation with sensorineural deafness and mental retardation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Growth retardation with sensorineural deafness and mental retardation, and of other diseases and clinical conditions associated with IGF1.

[33782] The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Interleukin 11 (IL11, Accession NP_000632.1) is another GAM281 target gene, herein designated TARGET GENE. IL11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL11 BINDING SITE, designated SEQ ID:11544, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[33783] Another function of GAM281 is therefore inhibition of Interleukin 11 (IL11, Accession NP_000632.1), a gene which stimulates the proliferation of hematopoietic stem cells and megakaryocyte progenitor cells and induces megakaryocyte maturation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL11.

[33784] The function of IL11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM41.1.Interleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NP_757366.1) is another GAM281 target gene, herein designated TARGET GENE. IL16 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by IL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL16 BINDING SITE, designated SEQ ID:19554, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33785] Another function of GAM281 is therefore inhibition of In-

terleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NP_757366.1), a gene which modulates T- cell activation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL16.

[33786] The function of IL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Interleukin 21 receptor (IL21R, Accession NP_068570.1) is another GAM281 target gene, herein designated TARGET GENE. IL21R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL21R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL21R BINDING SITE, designated SEQ ID:498, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33787] Another function of GAM281 is therefore inhibition of Interleukin 21 receptor (IL21R, Accession NP_068570.1), a gene which is involved in receptor mediated endocytosis and transduces the mitogenic signals of il- 2. Accordingly,

utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL21R.

[33788] The function of IL21R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Interleukin 21 receptor (IL21R, Accession NP_851565.1) is another GAM281 target gene, herein designated TARGET GENE. IL21R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL21R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL21R BINDING SITE, designated SEQ ID:498, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33789] Another function of GAM281 is therefore inhibition of Interleukin 21 receptor (IL21R, Accession NP_851565.1), a gene which is involved in receptor mediated endocytosis and transduces the mitogenic signals of il- 2. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with IL21R.

[33790] The function of IL21R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Interleukin 21 receptor (IL21R, Accession NP_851564.1) is another GAM281 target gene, herein designated TARGET GENE. IL21R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL21R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL21R BINDING SITE, designated SEQ ID:498, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33791] Another function of GAM281 is therefore inhibition of Interleukin 21 receptor (IL21R, Accession NP_851564.1), a gene which is involved in receptor mediated endocytosis and transduces the mitogenic signals of il- 2. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL21R.

[33792] The function of IL21R and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Interleukin 28 receptor, alpha (IL28RA, Accession NP_775087.1) is another GAM281 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:7046, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33793] Another function of GAM281 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_775087.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[33794] Interleukin 28 receptor, alpha (IL28RA, Accession NP_775088.1) is another GAM281 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, correspond-

ing to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:7046, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33795] Another function of GAM281 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_775088.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[33796] Interleukin 28 receptor, alpha (IL28RA, Accession NP_734464.1) is another GAM281 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:7046, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33797] Another function of GAM281 is therefore inhibition of In-

terleukin 28 receptor, alpha (IL28RA, Accession NP_734464.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[33798] IMPACT (Accession NP_060909.1) is another GAM281 target gene, herein designated TARGET GENE. IMPACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IMPACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IMPACT BINDING SITE, designated SEQ ID:8975, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33799] Another function of GAM281 is therefore inhibition of IMPACT (Accession NP_060909.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMPACT.

[33800] INHBE (Accession NP_113667.1) is another GAM281 target gene, herein designated TARGET GENE. INHBE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INHBE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INHBE BINDING SITE, designated SEQ ID:16283, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33801] Another function of GAM281 is therefore inhibition of INHBE (Accession NP_113667.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INHBE.

[33802] Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) is another GAM281 target gene, herein designated TARGET GENE. INMT BINDING SITE1 and INMT BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by INMT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INMT BINDING SITE1 and INMT BINDING SITE2, designated SEQ ID:9149 and SEQ ID:11523 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33803] Another function of GAM281 is therefore inhibition of Indolethylamine n-methyltransferase (INMT, Accession

NP_006765.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INMT.

[33804] Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) is another GAM281 target gene, herein designated TARGET GENE. IRF4 BINDING SITE1 and IRF4 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IRF4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRF4 BINDING SITE1 and IRF4 BINDING SITE2, designated SEQ ID:2698 and SEQ ID:1517 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33805] Another function of GAM281 is therefore inhibition of Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRF4.

[33806] IRTA2 (Accession NP_112571.1) is another GAM281 target gene, herein designated TARGET GENE. IRTA2 BINDING SITE is a target binding site found in the 5` untranslated

region of mRNA encoded by IRTA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRTA2 BINDING SITE, designated SEQ ID:19371, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33807] Another function of GAM281 is therefore inhibition of IRTA2 (Accession NP_112571.1), a gene which binds to the fc region of immunoglobulins gamma low affinity receptor. and therefore may be associated with Burkitt lymphoma. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Burkitt lymphoma, and of other diseases and clinical conditions associated with IRTA2.

[33808] The function of IRTA2 has been established by previous studies. Chromosomal abnormalities involving translocation breakpoints at 1q21- q23 are frequent in B- cell non- Hodgkin lymphoma (see OMIM Ref. No. BCL9; 602597) and multiple myeloma (MM; OMIM Ref. No. 254500). By cloning the breakpoints of a (1;14)(q21;q32) chromosomal translocation in the FR4 multiple myeloma cell line, followed by exon trapping and screening a

spleen cDNA library, Hatzivassiliou et al. (2001) obtained cDNAs encoding 3 isoforms of IRTA1 (OMIM Ref. No. 605876) and 4 isoforms of IRTA2. The 3 major IRTA2 mRNA isoforms (ITRA2A, ITRA2B, and ITRA2C) each have their own unique 3- prime untranslated region, and the proteins they encode share a common amino acid sequence until residue 560, including a signal peptide and 6 extracellular Ig- type domains. Sequence analysis predicted that IRTA2A is a 759- amino acid secreted glycoprotein with 8 total extracellular Ig- type domains followed by 13 unique, predominantly polar residues at its C terminus. After the common 560 amino acids, IRTA2B has only 32 additional residues, whose hydrophobicity is compatible with its docking to the plasma membrane via a GPI anchor. The 977- amino acid IRTA2C protein shares the first 746 amino acids with IRTA2A. IRTA2C has a total of 9 extracellular Ig- type domains with 8 potential N-linked glycosylation sites; a 23- residue transmembrane region; and a 104- residue cytoplasmic domain with 3 consensus SH2- binding domains, all of which exhibit features of ITIMs (immune- receptor tyrosine- based inhibition motifs) and are encoded by separate exons. The fourth isoform, IRTA2D, encodes a peptide of 152 amino

acids. Northern blot analysis detected 2.8-, 4.4-, 5.3-, and 0.6- kb IRTA2 transcripts in lymph node, spleen, bone marrow, and small intestine, with a preponderance of the IRTA2A isoform. In situ hybridization analysis detected IRTA2 expression in tonsillar germinal center centrocytes, but not in centroblasts, as well as in intraepithelial and interfollicular regions. Nakayama et al. (2001) independently cloned IRTA2, which they called BXMAS1, by representational difference analysis of genes activated by anti- IgM crosslinking of a human B- cell line. The deduced 977- amino acid protein contains 8 ITIMs and 8 potential N- linked glycosylation sites. Northern blot analysis detected a 6.7- kb transcript and a larger transcript between 14- and 17- kb in B cells 24 to 36 hours after activation. Northern blot analysis of tissues detected expression only in spleen In situ hybridization analysis demonstrated expression of IRTA2 in the mantle zone of tonsil tissue but not in germinal center cells

[33809]

[33810] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[33811] Hatzivassiliou, G.; Miller, I.; Takizawa, J.; Palanisamy, N.;

Rao, P. H.; Iida, S.; Tagawa, S.; Taniwaki, M.; Russo, J.; Neri, A.; Cattoretti, G.; Clynes, R.; Mendelsohn, C.; Chaganti, R. S. K.; Dalla- Favera, R. : IRTA1 and IRTA2, novel immunoglobulin superfamily receptors expressed in B cells and involved in chromosome 1q21 abnormalities in B cell malignancy. Immunity 14: 277- 289, 2001. ; and

[33812] Nakayama, Y.; Weissman, S. M.; Bothwell, A. L. M. : BX-MAS1 identifies a cluster of homologous genes differentially expressed in B cells. Biochem. Biophys. Res. Commun. 285: 830- 837, 200.

[33813] Further studies establishing the function and utilities of IRTA2 are found in John Hopkins OMIM database record ID 605877, and in cited publications listed in Table 5, which are hereby incorporated by reference.Integrin, alpha d (ITGAD, Accession XP_113880.1) is another GAM281 target gene, herein designated TARGET GENE. ITGAD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITGAD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITGAD BINDING SITE, designated SEQ ID:2749, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[33814] Another function of GAM281 is therefore inhibition of Integrin, alpha d (ITGAD, Accession XP_113880.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAD.

[33815] Integrin, alpha m (complement component receptor 3, alpha; also known as cd11b (p170), macrophage antigen alpha polypeptide) (ITGAM, Accession NP_000623.1) is another GAM281 target gene, herein designated TARGET GENE. ITGAM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITGAM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITGAM BINDING SITE, designated SEQ ID:5922, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33816] Another function of GAM281 is therefore inhibition of Integrin, alpha m (complement component receptor 3, alpha; also known as cd11b (p170), macrophage antigen alpha polypeptide) (ITGAM, Accession NP_000623.1), a gene which is invovled in various adhesive interactions of

monocytes, macrophages and granulocytes as well as in mediating the uptake of complement- coated particles. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAM.

[33817] The function of ITGAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Integrin, alpha x (antigen cd11c (p150), alpha polypeptide) (ITGAX, Accession NP_000878.1) is another GAM281 target gene, herein designated TARGET GENE. ITGAX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITGAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITGAX BINDING SITE, designated SEQ ID:559, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33818] Another function of GAM281 is therefore inhibition of Integrin, alpha x (antigen cd11c (p150), alpha polypeptide) (ITGAX, Accession NP_000878.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with ITGAX.

[33819] Inositol 1,4,5-triphosphate receptor, type 2 (ITPR2, Accession NP_002214.1) is another GAM281 target gene, herein designated TARGET GENE. ITPR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITPR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITPR2 BINDING SITE, designated SEQ ID:20047, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33820] Another function of GAM281 is therefore inhibition of Inositol 1,4,5-triphosphate receptor, type 2 (ITPR2, Accession NP_002214.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPR2.

[33821] Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3, Accession NP_000206.1) is another GAM281 target gene, herein designated TARGET GENE. JAK3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JAK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JAK3 BINDING SITE, designated SEQ ID:18060, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33822] Another function of GAM281 is therefore inhibition of Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3, Accession NP_000206.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAK3.

[33823] JDP2 (Accession NP_569736.1) is another GAM281 target gene, herein designated TARGET GENE. JDP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JDP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JDP2 BINDING SITE, designated SEQ ID:2088, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33824] Another function of GAM281 is therefore inhibition of JDP2 (Accession NP_569736.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with JDP2.

[33825] JM11 (Accession NP_296375.1) is another GAM281 target gene, herein designated TARGET GENE. JM11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JM11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JM11 BINDING SITE, designated SEQ ID:10197, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33826] Another function of GAM281 is therefore inhibition of JM11 (Accession NP_296375.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JM11.

[33827] Jerky homolog (mouse) (JRK, Accession NP_003715.1) is another GAM281 target gene, herein designated TARGET GENE. JRK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JRK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JRK BINDING SITE, designated SEQ ID:3927, to the nu-

cleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33828] Another function of GAM281 is therefore inhibition of Jerky homolog (mouse) (JRK, Accession NP_003715.1), a gene which might function as a DNA- binding protein. and therefore may be associated with Absence epilepsy. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Absence epilepsy, and of other diseases and clinical conditions associated with JRK.

[33829] The function of JRK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.2.JWA (Accession NP_006398.1) is another GAM281 target gene, herein designated TARGET GENE. JWA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JWA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JWA BINDING SITE, designated SEQ ID:8446, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33830] Another function of GAM281 is therefore inhibition of JWA

(Accession NP_006398.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JWA.

[33831] Potassium inwardly-rectifying channel, subfamily j, member 11 (KCNJ11, Accession NP_000516.2) is another GAM281 target gene, herein designated TARGET GENE. KCNJ11 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KCNJ11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ11 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33832] Another function of GAM281 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 11 (KCNJ11, Accession NP_000516.2), a gene which is controlled by g proteins. inward rectifier k+ channels are characterized by a greater tendancy to allow potassium to flow into the cell rather than out of it. and therefore is associated with Persistent hyperinsulinemic hypoglycemia of infancy. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Persistent hyperinsuline-

mic hypoglycemia of infancy, and of other diseases and clinical conditions associated with KCNJ11.

[33833] The function of KCNJ11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733938.1) is another GAM281 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNJ16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:2456, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33834] Another function of GAM281 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733938.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[33835] Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_061128.1) is another GAM281 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNJ16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:2456, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33836] Another function of GAM281 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_061128.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[33837] Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733937.1) is another GAM281 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA

encoded by KCNJ16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:2456, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33838] Another function of GAM281 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733937.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[33839] Potassium channel, subfamily k, member 3 (KCNK3, Accession NP_002237.1) is another GAM281 target gene, herein designated TARGET GENE. KCNK3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KCNK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNK3 BINDING SITE, designated SEQ ID:16912, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[33840] Another function of GAM281 is therefore inhibition of Potassium channel, subfamily k, member 3 (KCNK3, Accession NP_002237.1), a gene which is a ph- dependent, voltage- insensitive, background potassium channel. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK3.

[33841] The function of KCNK3 has been established by previous studies. Potassium channels are ubiquitous multisubunit membrane proteins that regulate membrane potential in numerous cell types. One family of mammalian K+ channels is characterized by the presence of 4 transmembrane domains and 2 P domains per subunit; this family includes TASK, TWIK (KCNK1; 601745), and TREK (KCNK2; 603219). Duprat et al. (1997) identified mouse expressed sequence tags with similarity to TREK and TWIK and cloned a corresponding cDNA from a mouse brain library. The mouse cDNA was used to clone the human counterpart from a kidney cDNA library. The human cDNA, designated TASK, encodes a 394- amino acid polypeptide with 85% identity to the mouse ortholog. The sequence contains consensus sites for N- linked glycosylation and for

phosphorylation at the C- terminal. Northern blot analysis showed that TASK is expressed in a variety of human tissues, with highest levels in pancreas and placenta. Expression of the TASK cDNA revealed that the functional protein creates currents that are K(+)- selective, instantaneous, and noninactivating. These currents showed an outward rectification when external K+ was low, but evinced absence of activation and inactivation kinetics as well as voltage independence, characteristics of so- called leak or background conductances. TASK currents were very sensitive to small changes in extracellular pH, suggesting that TASK has a role in cellular responses to changes in extracellular pH. Lesage and Lazdunski (1998) used a radiation hybrid mapping panel to map the human KCNK3 gene to chromosome 2p23 between markers WI13615 and WI11298. By fluorescence in situ hybridization, Manjunath et al. (1999) mapped the KCNK3 gene to 2p24.1- p23.3 and the mouse homolog to chromosome 5B.

[33842]

[33843] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[33844] Lesage, F.; Lazdunski, M. : Mapping of human potassium channel genes TREK- 1 (KCNK2) and TASK (KCNK3) to chromosomes 1q41 and 2p23. Genomics 51: 478- 479, 1998. ; and

[33845] Manjunath, N. A.; Bray- Ward, P.; Goldstein, S. A. N.; Gallagher, P. G. : Assignment of the 2P domain, acid- sensitive potassium channel OAT1 gene KCNK3 to human chromosome bands 2p24.1- p.

[33846] Further studies establishing the function and utilities of KCNK3 are found in John Hopkins OMIM database record ID 603220, and in cited publications listed in Table 5, which are hereby incorporated by reference.KENAE (Accession NP_789786.1) is another GAM281 target gene, herein designated TARGET GENE. KENAE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KENAE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KENAE BINDING SITE, designated SEQ ID:14862, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33847] Another function of GAM281 is therefore inhibition of KE-

NAE (Accession NP_789786.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KENAE.

[33848] KIAA0063 (Accession NP_055691.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0063 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0063, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0063 BINDING SITE, designated SEQ ID:5884, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33849] Another function of GAM281 is therefore inhibition of KIAA0063 (Accession NP_055691.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0063.

[33850] KIAA0082 (Accession NP_055865.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0082 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0082, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0082 BINDING SITE, designated SEQ ID:18751, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33851] Another function of GAM281 is therefore inhibition of KIAA0082 (Accession NP_055865.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0082.

[33852] KIAA0087 (Accession NP_055584.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0087 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0087, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0087 BINDING SITE, designated SEQ ID:10179, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33853] Another function of GAM281 is therefore inhibition of KIAA0087 (Accession NP_055584.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA0087.

[33854] KIAA0117 (Accession XP_290939.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0117 BINDING SITE, designated SEQ ID:9255, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33855] Another function of GAM281 is therefore inhibition of KIAA0117 (Accession XP_290939.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0117.

[33856] KIAA0182 (Accession XP_050495.4) is another GAM281 target gene, herein designated TARGET GENE. KIAA0182 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0182, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA0182 BINDING SITE, designated SEQ ID:2218, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33857] Another function of GAM281 is therefore inhibition of KIAA0182 (Accession XP_050495.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0182.

[33858] KIAA0186 (Accession NP_066545.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0186 BINDING SITE, designated SEQ ID:2625, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33859] Another function of GAM281 is therefore inhibition of KIAA0186 (Accession NP_066545.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0186.

[33860] KIAA0205 (Accession NP_055688.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0205 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0205, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0205 BINDING SITE, designated SEQ ID:3429, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33861] Another function of GAM281 is therefore inhibition of KIAA0205 (Accession NP_055688.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0205.

[33862] KIAA0237 (Accession NP_055562.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0237 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0237, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA0237 BINDING SITE, designated SEQ ID:17386, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33863] Another function of GAM281 is therefore inhibition of KIAA0237 (Accession NP_055562.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0237.

[33864] KIAA0258 (Accession NP_055600.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0258 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0258, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0258 BINDING SITE, designated SEQ ID:9416, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33865] Another function of GAM281 is therefore inhibition of KIAA0258 (Accession NP_055600.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0258.

[33866] KIAA0295 (Accession XP_042833.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA0295 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0295, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0295 BINDING SITE, designated SEQ ID:10742, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33867] Another function of GAM281 is therefore inhibition of KIAA0295 (Accession XP_042833.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0295.

[33868] KIAA0318 (Accession XP_044334.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0318 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0318 BINDING SITE, designated SEQ ID:13450, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33869] Another function of GAM281 is therefore inhibition of KIAA0318 (Accession XP_044334.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0318.

[33870] KIAA0435 (Accession NP_055616.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0435 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0435, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0435 BINDING SITE, designated SEQ ID:5041, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33871] Another function of GAM281 is therefore inhibition of KIAA0435 (Accession NP_055616.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0435.

[33872] KIAA0446 (Accession XP_044155.1) is another GAM281

target gene, herein designated TARGET GENE. KIAA0446 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0446, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0446 BINDING SITE, designated SEQ ID:1475, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33873] Another function of GAM281 is therefore inhibition of KIAA0446 (Accession XP_044155.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0446.

[33874] KIAA0459 (Accession XP_027862.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:4531, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[33875] Another function of GAM281 is therefore inhibition of KIAA0459 (Accession XP_027862.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459.

[33876] KIAA0469 (Accession NP_055666.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0469 BINDING SITE1 and KIAA0469 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0469, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0469 BINDING SITE1 and KIAA0469 BINDING SITE2, designated SEQ ID:9147 and SEQ ID:9493 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33877] Another function of GAM281 is therefore inhibition of KIAA0469 (Accession NP_055666.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469.

[33878] KIAA0475 (Accession NP_055679.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0475 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:16940, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33879] Another function of GAM281 is therefore inhibition of KIAA0475 (Accession NP_055679.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475.

[33880] KIAA0493 (Accession XP_034717.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0493 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0493 BINDING SITE, designated SEQ ID:17206, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33881] Another function of GAM281 is therefore inhibition of KIAA0493 (Accession XP_034717.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0493.

[33882] KIAA0495 (Accession XP_031397.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0495 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0495, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0495 BINDING SITE, designated SEQ ID:14759, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33883] Another function of GAM281 is therefore inhibition of KIAA0495 (Accession XP_031397.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0495.

[33884] KIAA0513 (Accession NP_055547.1) is another GAM281

target gene, herein designated TARGET GENE. KIAA0513 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0513, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE, designated SEQ ID:3931, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33885] Another function of GAM281 is therefore inhibition of KIAA0513 (Accession NP_055547.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513.

[33886] KIAA0527 (Accession XP_171054.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0527 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0527, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0527 BINDING SITE, designated SEQ ID:19745, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[33887] Another function of GAM281 is therefore inhibition of KIAA0527 (Accession XP_171054.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0527.

[33888] KIAA0532 (Accession XP_047659.6) is another GAM281 target gene, herein designated TARGET GENE. KIAA0532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0532 BINDING SITE, designated SEQ ID:12455, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33889] Another function of GAM281 is therefore inhibition of KIAA0532 (Accession XP_047659.6) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0532.

[33890] KIAA0555 (Accession NP_055605.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0555

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0555, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0555 BINDING SITE, designated SEQ ID:5555, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33891] Another function of GAM281 is therefore inhibition of KIAA0555 (Accession NP_055605.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0555.

[33892] KIAA0557 (Accession XP_085507.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0557 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0557, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0557 BINDING SITE, designated SEQ ID:2234, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33893] Another function of GAM281 is therefore inhibition of KIAA0557 (Accession XP_085507.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0557.

[33894] KIAA0561 (Accession XP_038150.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA0561 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0561, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0561 BINDING SITE, designated SEQ ID:9629, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33895] Another function of GAM281 is therefore inhibition of KIAA0561 (Accession XP_038150.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0561.

[33896] KIAA0562 (Accession NP_055519.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0562 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA0562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0562 BINDING SITE, designated SEQ ID:16544, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33897] Another function of GAM281 is therefore inhibition of KIAA0562 (Accession NP_055519.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0562.

[33898] KIAA0563 (Accession NP_055649.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0563 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0563 BINDING SITE, designated SEQ ID:16377, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33899] Another function of GAM281 is therefore inhibition of

KIAA0563 (Accession NP_055649.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0563.

[33900] KIAA0682 (Accession NP_055667.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0682 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA0682, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0682 BINDING SITE, designated SEQ ID:6522, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33901] Another function of GAM281 is therefore inhibition of KIAA0682 (Accession NP_055667.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0682.

[33902] KIAA0683 (Accession NP_057195.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0683 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0683, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0683 BINDING SITE, designated SEQ ID:18206, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33903] Another function of GAM281 is therefore inhibition of KIAA0683 (Accession NP_057195.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0683.

[33904] KIAA0831 (Accession NP_055739.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0831 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0831, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0831 BINDING SITE, designated SEQ ID:3260, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33905] Another function of GAM281 is therefore inhibition of KIAA0831 (Accession NP_055739.1) . Accordingly, utilities

of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0831.

[33906] KIAA0841 (Accession XP_049237.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0841 BINDING SITE1 and KIAA0841 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0841, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0841 BINDING SITE1 and KIAA0841 BINDING SITE2, designated SEQ ID:8185 and SEQ ID:5490 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33907] Another function of GAM281 is therefore inhibition of KIAA0841 (Accession XP_049237.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0841.

[33908] KIAA0861 (Accession NP_055893.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA0861 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA0861, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0861 BINDING SITE, designated SEQ ID:2153, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33909] Another function of GAM281 is therefore inhibition of KIAA0861 (Accession NP_055893.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0861.

[33910] KIAA0889 (Accession NP_056192.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0889 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA0889, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0889 BINDING SITE, designated SEQ ID:13271, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33911] Another function of GAM281 is therefore inhibition of KIAA0889 (Accession NP_056192.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0889.

[33912] KIAA0924 (Accession NP_055712.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0924 BINDING SITE1 and KIAA0924 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0924, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0924 BINDING SITE1 and KIAA0924 BINDING SITE2, designated SEQ ID:13297 and SEQ ID:7655 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33913] Another function of GAM281 is therefore inhibition of KIAA0924 (Accession NP_055712.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0924.

[33914] KIAA0931 (Accession XP_041191.2) is another GAM281

target gene, herein designated TARGET GENE. KIAA0931 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0931, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0931 BINDING SITE, designated SEQ ID:14272, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33915] Another function of GAM281 is therefore inhibition of KIAA0931 (Accession XP_041191.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0931.

[33916] KIAA0935 (Accession XP_052620.6) is another GAM281 target gene, herein designated TARGET GENE. KIAA0935 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0935, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0935 BINDING SITE, designated SEQ ID:11958, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[33917] Another function of GAM281 is therefore inhibition of KIAA0935 (Accession XP_052620.6) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0935.

[33918] KIAA0962 (Accession XP_290942.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA0962 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0962, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0962 BINDING SITE, designated SEQ ID:8976, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33919] Another function of GAM281 is therefore inhibition of KIAA0962 (Accession XP_290942.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0962.

[33920] KIAA1002 (Accession XP_290584.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1002

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1002, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1002 BINDING SITE, designated SEQ ID:12518, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33921] Another function of GAM281 is therefore inhibition of KIAA1002 (Accession XP_290584.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1002.

[33922] KIAA1032 (Accession XP_038604.4) is another GAM281 target gene, herein designated TARGET GENE. KIAA1032 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1032, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1032 BINDING SITE, designated SEQ ID:1326, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33923] Another function of GAM281 is therefore inhibition of KIAA1032 (Accession XP_038604.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1032.

[33924] KIAA1040 (Accession XP_051091.3) is another GAM281 target gene, herein designated TARGET GENE. KIAA1040 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1040, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1040 BINDING SITE, designated SEQ ID:11846, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33925] Another function of GAM281 is therefore inhibition of KIAA1040 (Accession XP_051091.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1040.

[33926] KIAA1041 (Accession NP_055762.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1041 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1041, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1041 BINDING SITE, designated SEQ ID:3653, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33927] Another function of GAM281 is therefore inhibition of KIAA1041 (Accession NP_055762.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1041.

[33928] KIAA1052 (Accession NP_055771.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1052 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1052 BINDING SITE, designated SEQ ID:919, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33929] Another function of GAM281 is therefore inhibition of

KIAA1052 (Accession NP_055771.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1052.

[33930] KIAA1054 (Accession XP_043493.5) is another GAM281 target gene, herein designated TARGET GENE. KIAA1054 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1054, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1054 BINDING SITE, designated SEQ ID:14832, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33931] Another function of GAM281 is therefore inhibition of KIAA1054 (Accession XP_043493.5) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1054.

[33932] KIAA1115 (Accession NP_055746.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1115 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1115, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1115 BINDING SITE, designated SEQ ID:9842, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33933] Another function of GAM281 is therefore inhibition of KIAA1115 (Accession NP_055746.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1115.

[33934] KIAA1126 (Accession XP_050325.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1126 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1126, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1126 BINDING SITE, designated SEQ ID:10583, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33935] Another function of GAM281 is therefore inhibition of KIAA1126 (Accession XP_050325.1) . Accordingly, utilities

of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1126.

[33936] KIAA1128 (Accession NP_061872.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1128 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1128 BINDING SITE, designated SEQ ID:5783, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33937] Another function of GAM281 is therefore inhibition of KIAA1128 (Accession NP_061872.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1128.

[33938] KIAA1143 (Accession XP_044014.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1143, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1143 BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33939] Another function of GAM281 is therefore inhibition of KIAA1143 (Accession XP_044014.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1143.

[33940] KIAA1155 (Accession XP_030864.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA1155 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1155, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1155 BINDING SITE, designated SEQ ID:2664, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33941] Another function of GAM281 is therefore inhibition of KIAA1155 (Accession XP_030864.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA1155.

[33942] KIAA1170 (Accession XP_045907.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA1170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1170 BINDING SITE, designated SEQ ID:10162, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33943] Another function of GAM281 is therefore inhibition of KIAA1170 (Accession XP_045907.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1170.

[33944] KIAA1185 (Accession NP_065761.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1185 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1185, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA1185 BINDING SITE, designated SEQ ID:5755, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33945] Another function of GAM281 is therefore inhibition of KIAA1185 (Accession NP_065761.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1185.

[33946] KIAA1193 (Accession XP_041843.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1193, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1193 BINDING SITE, designated SEQ ID:17517, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33947] Another function of GAM281 is therefore inhibition of KIAA1193 (Accession XP_041843.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1193.

[33948] KIAA1198 (Accession NP_065765.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE5 are target binding sites found in untranslated regions of mRNA encoded by KIAA1198, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE5, designated SEQ ID:13749, SEQ ID:16088, SEQ ID:12389, SEQ ID:16471 and SEQ ID:12478 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33949] Another function of GAM281 is therefore inhibition of KIAA1198 (Accession NP_065765.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1198.

[33950] KIAA1210 (Accession XP_172801.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1210 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1210, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1210 BINDING SITE, designated SEQ ID:9144, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33951] Another function of GAM281 is therefore inhibition of KIAA1210 (Accession XP_172801.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1210.

[33952] KIAA1257 (Accession XP_031577.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA1257 BINDING SITE1 through KIAA1257 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by KIAA1257, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1257 BINDING SITE1 through KIAA1257 BINDING SITE3, designated SEQ ID:8196, SEQ ID:11523 and SEQ ID:9032 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33953] Another function of GAM281 is therefore inhibition of KIAA1257 (Accession XP_031577.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1257.

[33954] KIAA1268 (Accession XP_291055.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1268 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1268 BINDING SITE, designated SEQ ID:3236, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33955] Another function of GAM281 is therefore inhibition of KIAA1268 (Accession XP_291055.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1268.

[33956] KIAA1273 (Accession XP_300760.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1273 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by KIAA1273, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1273 BINDING SITE, designated SEQ ID:7374, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33957] Another function of GAM281 is therefore inhibition of KIAA1273 (Accession XP_300760.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1273.

[33958] KIAA1287 (Accession NP_065799.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1287 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1287, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1287 BINDING SITE, designated SEQ ID:9573, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33959] Another function of GAM281 is therefore inhibition of

KIAA1287 (Accession NP_065799.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1287.

[33960] KIAA1393 (Accession XP_050793.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA1393 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1393 BINDING SITE, designated SEQ ID:10123, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33961] Another function of GAM281 is therefore inhibition of KIAA1393 (Accession XP_050793.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1393.

[33962] KIAA1443 (Accession NP_065885.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1443 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1443, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1443 BINDING SITE, designated SEQ ID:15171, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33963] Another function of GAM281 is therefore inhibition of KIAA1443 (Accession NP_065885.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1443.

[33964] KIAA1456 (Accession XP_040100.3) is another GAM281 target gene, herein designated TARGET GENE. KIAA1456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1456 BINDING SITE, designated SEQ ID:5529, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33965] Another function of GAM281 is therefore inhibition of KIAA1456 (Accession XP_040100.3) . Accordingly, utilities

of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1456.

[33966] KIAA1465 (Accession XP_027396.4) is another GAM281 target gene, herein designated TARGET GENE. KIAA1465 BINDING SITE1 and KIAA1465 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1465, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1465 BINDING SITE1 and KIAA1465 BINDING SITE2, designated SEQ ID:18992 and SEQ ID:18838 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33967] Another function of GAM281 is therefore inhibition of KIAA1465 (Accession XP_027396.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1465.

[33968] KIAA1493 (Accession XP_034415.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1493 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1493 BINDING SITE, designated SEQ ID:15045, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33969] Another function of GAM281 is therefore inhibition of KIAA1493 (Accession XP_034415.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1493.

[33970] KIAA1508 (Accession XP_290952.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1508 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1508, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1508 BINDING SITE, designated SEQ ID:8820, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33971] Another function of GAM281 is therefore inhibition of

KIAA1508 (Accession XP_290952.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1508.

[33972] KIAA1518 (Accession XP_170889.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1518 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA1518, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1518 BINDING SITE, designated SEQ ID:13383, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33973] Another function of GAM281 is therefore inhibition of KIAA1518 (Accession XP_170889.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1518.

[33974] KIAA1530 (Accession XP_042661.5) is another GAM281 target gene, herein designated TARGET GENE. KIAA1530 BINDING SITE1 through KIAA1530 BINDING SITE3 are tar-

get binding sites found in untranslated regions of mRNA encoded by KIAA1530, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1530 BINDING SITE1 through KIAA1530 BINDING SITE3, designated SEQ ID:4028, SEQ ID:12345 and SEQ ID:15284 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33975] Another function of GAM281 is therefore inhibition of KIAA1530 (Accession XP_042661.5) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1530.

[33976] KIAA1550 (Accession XP_039393.3) is another GAM281 target gene, herein designated TARGET GENE. KIAA1550 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1550, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1550 BINDING SITE, designated SEQ ID:3790, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[33977] Another function of GAM281 is therefore inhibition of KIAA1550 (Accession XP_039393.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1550.

[33978] KIAA1559 (Accession XP_054472.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA1559 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1559, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1559 BINDING SITE, designated SEQ ID:4029, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33979] Another function of GAM281 is therefore inhibition of KIAA1559 (Accession XP_054472.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1559.

[33980] KIAA1571 (Accession XP_027744.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1571

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1571, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1571 BINDING SITE, designated SEQ ID:14154, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33981] Another function of GAM281 is therefore inhibition of KIAA1571 (Accession XP_027744.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1571.

[33982] KIAA1615 (Accession NP_066002.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1615, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2, designated SEQ ID:8549 and SEQ ID:10111 respectively, to the nucleotide sequence of

GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33983] Another function of GAM281 is therefore inhibition of KIAA1615 (Accession NP_066002.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1615.

[33984] KIAA1671 (Accession XP_037809.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1671 BINDING SITE1 and KIAA1671 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1671, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1671 BINDING SITE1 and KIAA1671 BINDING SITE2, designated SEQ ID:7194 and SEQ ID:17191 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33985] Another function of GAM281 is therefore inhibition of KIAA1671 (Accession XP_037809.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1671.

[33986] KIAA1679 (Accession XP_046570.3) is another GAM281 target gene, herein designated TARGET GENE. KIAA1679 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1679, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1679 BINDING SITE, designated SEQ ID:5094, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33987] Another function of GAM281 is therefore inhibition of KIAA1679 (Accession XP_046570.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1679.

[33988] KIAA1712 (Accession XP_041497.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by KIAA1712, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2, designated SEQ ID:1142 and SEQ ID:14165 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33989] Another function of GAM281 is therefore inhibition of KIAA1712 (Accession XP_041497.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1712.

[33990] KIAA1712 (Accession NP_085136.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by KIAA1712, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2, designated SEQ ID:1142 and SEQ ID:14165 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33991] Another function of GAM281 is therefore inhibition of

KIAA1712 (Accession NP_085136.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1712.

[33992] KIAA1724 (Accession XP_040280.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA1724 BINDING SITE1 and KIAA1724 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1724, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1724 BINDING SITE1 and KIAA1724 BINDING SITE2, designated SEQ ID:14630 and SEQ ID:15040 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33993] Another function of GAM281 is therefore inhibition of KIAA1724 (Accession XP_040280.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1724.

[33994] KIAA1737 (Accession NP_219494.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1737

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1737, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1737 BINDING SITE, designated SEQ ID:10602, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33995] Another function of GAM281 is therefore inhibition of KIAA1737 (Accession NP_219494.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1737.

[33996] KIAA1775 (Accession NP_149091.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1775 BINDING SITE1 and KIAA1775 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1775, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1775 BINDING SITE1 and KIAA1775 BINDING SITE2, designated SEQ ID:17949 and SEQ ID:1618 respectively, to the nucleotide sequence of

GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33997] Another function of GAM281 is therefore inhibition of KIAA1775 (Accession NP_149091.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1775.

[33998] KIAA1784 (Accession NP_115820.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1784 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1784, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1784 BINDING SITE, designated SEQ ID:11058, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[33999] Another function of GAM281 is therefore inhibition of KIAA1784 (Accession NP_115820.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1784.

[34000] KIAA1822 (Accession XP_041566.2) is another GAM281

target gene, herein designated TARGET GENE. KIAA1822 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1822 BINDING SITE, designated SEQ ID:10095, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34001] Another function of GAM281 is therefore inhibition of KIAA1822 (Accession XP_041566.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1822.

[34002] KIAA1827 (Accession XP_290834.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1827 BINDING SITE1 and KIAA1827 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1827, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1827 BINDING SITE1 and KIAA1827 BINDING SITE2, designated SEQ ID:2143 and

SEQ ID:12636 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34003] Another function of GAM281 is therefore inhibition of KIAA1827 (Accession XP_290834.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1827.

[34004] KIAA1829 (Accession XP_030378.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA1829 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1829, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1829 BINDING SITE, designated SEQ ID:14863, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34005] Another function of GAM281 is therefore inhibition of KIAA1829 (Accession XP_030378.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1829.

[34006] KIAA1836 (Accession XP_114087.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA1836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1836 BINDING SITE, designated SEQ ID:12627, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34007] Another function of GAM281 is therefore inhibition of KIAA1836 (Accession XP_114087.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1836.

[34008] KIAA1853 (Accession XP_045184.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1853 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1853, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1853 BINDING SITE, designated SEQ ID:19095, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34009] Another function of GAM281 is therefore inhibition of KIAA1853 (Accession XP_045184.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1853.

[34010] KIAA1862 (Accession XP_044212.4) is another GAM281 target gene, herein designated TARGET GENE. KIAA1862 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1862, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1862 BINDING SITE, designated SEQ ID:16627, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34011] Another function of GAM281 is therefore inhibition of KIAA1862 (Accession XP_044212.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1862.

[34012] KIAA1904 (Accession XP_056282.1) is another GAM281

target gene, herein designated TARGET GENE. KIAA1904 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1904, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1904 BINDING SITE, designated SEQ ID:16492, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34013] Another function of GAM281 is therefore inhibition of KIAA1904 (Accession XP_056282.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1904.

[34014] KIAA1922 (Accession XP_057040.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1922 BINDING SITE, designated SEQ ID:7553, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[34015] Another function of GAM281 is therefore inhibition of KIAA1922 (Accession XP_057040.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1922.

[34016] KIAA1924 (Accession NP_694971.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA1924 BINDING SITE1 and KIAA1924 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1924, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1924 BINDING SITE1 and KIAA1924 BINDING SITE2, designated SEQ ID:8341 and SEQ ID:1857 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34017] Another function of GAM281 is therefore inhibition of KIAA1924 (Accession NP_694971.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1924.

[34018] KIAA1937 (Accession XP_057107.3) is another GAM281 target gene, herein designated TARGET GENE. KIAA1937 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1937, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1937 BINDING SITE, designated SEQ ID:2983, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34019] Another function of GAM281 is therefore inhibition of KIAA1937 (Accession XP_057107.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1937.

[34020] KIAA1971 (Accession XP_058720.4) is another GAM281 target gene, herein designated TARGET GENE. KIAA1971 BINDING SITE1 through KIAA1971 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by KIAA1971, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1971 BINDING SITE1

through KIAA1971 BINDING SITE3, designated SEQ ID:11506, SEQ ID:6902 and SEQ ID:5820 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34021] Another function of GAM281 is therefore inhibition of KIAA1971 (Accession XP_058720.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1971.

[34022] KIAA1987 (Accession XP_113870.1) is another GAM281 target gene, herein designated TARGET GENE. KIAA1987 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1987, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1987 BINDING SITE, designated SEQ ID:7554, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34023] Another function of GAM281 is therefore inhibition of KIAA1987 (Accession XP_113870.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1987.

[34024] KIAA2028 (Accession XP_059415.2) is another GAM281 target gene, herein designated TARGET GENE. KIAA2028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA2028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA2028 BINDING SITE, designated SEQ ID:12100, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34025] Another function of GAM281 is therefore inhibition of KIAA2028 (Accession XP_059415.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2028.

[34026] KIF25 (Accession NP_005346.2) is another GAM281 target gene, herein designated TARGET GENE. KIF25 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by KIF25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of KIF25 BINDING SITE, designated SEQ ID:17138, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34027] Another function of GAM281 is therefore inhibition of KIF25 (Accession NP_005346.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF25.

[34028] KIF25 (Accession NP_085118.1) is another GAM281 target gene, herein designated TARGET GENE. KIF25 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by KIF25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIF25 BINDING SITE, designated SEQ ID:17138, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34029] Another function of GAM281 is therefore inhibition of KIF25 (Accession NP_085118.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF25.

[34030] KIP2 (Accession NP_006374.1) is another GAM281 target gene, herein designated TARGET GENE. KIP2 BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by KIP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIP2 BINDING SITE, designated SEQ ID:4201, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34031] Another function of GAM281 is therefore inhibition of KIP2 (Accession NP_006374.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIP2.

[34032] Kruppel-like factor 12 (KLF12, Accession NP_009180.3) is another GAM281 target gene, herein designated TARGET GENE. KLF12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLF12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLF12 BINDING SITE, designated SEQ ID:1127, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34033] Another function of GAM281 is therefore inhibition of Kruppel-like factor 12 (KLF12, Accession NP_009180.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF12.

[34034] Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_002253.1) is another GAM281 target gene, herein designated TARGET GENE. KLRD1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLRD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLRD1 BINDING SITE, designated SEQ ID:2353, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34035] Another function of GAM281 is therefore inhibition of Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_002253.1), a gene which is a receptor for the recognition of mhc class i hla- e molecules by nk cells and some cytotoxic t- cells. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KLRD1.

[34036] The function of KLRD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_031360.1) is another GAM281 target gene, herein designated TARGET GENE. KLRD1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLRD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLRD1 BINDING SITE, designated SEQ ID:2353, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34037] Another function of GAM281 is therefore inhibition of Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_031360.1), a gene which is a receptor for the recognition of mhc class i hla- e molecules by nk cells and some cytotoxic t- cells. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLRD1.

[34038] The function of KLRD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NP_003670.1) is another GAM281 target gene, herein designated TARGET GENE. KMO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KMO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KMO BINDING SITE, designated SEQ ID:6338, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34039] Another function of GAM281 is therefore inhibition of Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NP_003670.1), a gene which may play a role in encephalic photoreception. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KMO.

[34040] The function of KMO and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM30.1.Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) is another GAM281 target gene, herein designated TARGET GENE. LAMP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAMP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMP3 BINDING SITE, designated SEQ ID:17760, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34041] Another function of GAM281 is therefore inhibition of Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP3.

[34042] Lipocalin 7 (LCN7, Accession NP_071447.1) is another GAM281 target gene, herein designated TARGET GENE. LCN7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCN7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of LCN7 BINDING SITE, designated SEQ ID:15937, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34043] Another function of GAM281 is therefore inhibition of Lipocalin 7 (LCN7, Accession NP_071447.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCN7.

[34044] LCX (Accession XP_167612.2) is another GAM281 target gene, herein designated TARGET GENE. LCX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCX BINDING SITE, designated SEQ ID:2891, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34045] Another function of GAM281 is therefore inhibition of LCX (Accession XP_167612.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCX.

[34046] Leptin receptor overlapping transcript-like 1 (LEPROTL1, Accession NP_056159.1) is another GAM281 target gene, herein designated TARGET GENE. LEPROTL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LEPROTL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LEPROTL1 BINDING SITE, designated SEQ ID:1871, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34047] Another function of GAM281 is therefore inhibition of Leptin receptor overlapping transcript-like 1 (LEPROTL1, Accession NP_056159.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LEPROTL1.

[34048] Leucine zipper-ef-hand containing transmembrane protein 1 (LETM1, Accession NP_036450.1) is another GAM281 target gene, herein designated TARGET GENE. LETM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LETM1, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LETM1 BINDING SITE, designated SEQ ID:18695, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34049] Another function of GAM281 is therefore inhibition of Leucine zipper-ef-hand containing transmembrane protein 1 (LETM1, Accession NP_036450.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LETM1.

[34050] LGP1 (Accession NP_115873.1) is another GAM281 target gene, herein designated TARGET GENE. LGP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LGP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LGP1 BINDING SITE, designated SEQ ID:16610, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34051] Another function of GAM281 is therefore inhibition of LGP1 (Accession NP_115873.1) . Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGP1.

[34052] LGP2 (Accession NP_077024.1) is another GAM281 target gene, herein designated TARGET GENE. LGP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LGP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LGP2 BINDING SITE, designated SEQ ID:8032, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34053] Another function of GAM281 is therefore inhibition of LGP2 (Accession NP_077024.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGP2.

[34054] LIN-28 (Accession NP_078950.1) is another GAM281 target gene, herein designated TARGET GENE. LIN-28 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LIN-28, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LIN-28

BINDING SITE, designated SEQ ID:4726, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34055] Another function of GAM281 is therefore inhibition of LIN-28 (Accession NP_078950.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIN-28.

[34056] Link-GEFII (Accession NP_057423.1) is another GAM281 target gene, herein designated TARGET GENE. Link-GEFII BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Link-GEFII, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Link-GEFII BINDING SITE, designated SEQ ID:19936, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34057] Another function of GAM281 is therefore inhibition of Link-GEFII (Accession NP_057423.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Link-GEFII.

[34058] Lipase, member h (LIPH, Accession NP_640341.1) is an-

other GAM281 target gene, herein designated TARGET GENE. LIPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LIPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LIPH BINDING SITE, designated SEQ ID:10379, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34059] Another function of GAM281 is therefore inhibition of Lipase, member h (LIPH, Accession NP_640341.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIPH.

[34060] LNK (Accession NP_005466.1) is another GAM281 target gene, herein designated TARGET GENE. LNK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LNK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LNK BINDING SITE, designated SEQ ID:13992, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[34061] Another function of GAM281 is therefore inhibition of LNK (Accession NP_005466.1), a gene which links T- cell receptor activation signal to phospholipase c- gamma- 1, grb- 2 and phosphatidylinositol 3- kinase (by similarity). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNK.

[34062] The function of LNK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.LOC112687 (Accession XP_053145.1) is another GAM281 target gene, herein designated TARGET GENE. LOC112687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112687 BINDING SITE, designated SEQ ID:16673, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34063] Another function of GAM281 is therefore inhibition of

LOC112687 (Accession XP_053145.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112687.

[34064] LOC112817 (Accession NP_612422.2) is another GAM281 target gene, herein designated TARGET GENE. LOC112817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112817 BINDING SITE, designated SEQ ID:16256, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34065] Another function of GAM281 is therefore inhibition of LOC112817 (Accession NP_612422.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112817.

[34066] LOC112868 (Accession XP_053402.1) is another GAM281 target gene, herein designated TARGET GENE. LOC112868 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC112868, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112868 BINDING SITE, designated SEQ ID:12772, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34067] Another function of GAM281 is therefore inhibition of LOC112868 (Accession XP_053402.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112868.

[34068] LOC113444 (Accession NP_612437.2) is another GAM281 target gene, herein designated TARGET GENE. LOC113444 BINDING SITE1 through LOC113444 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC113444, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC113444 BINDING SITE1 through LOC113444 BINDING SITE3, designated SEQ ID:15899, SEQ ID:5336 and SEQ ID:18294 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34069] Another function of GAM281 is therefore inhibition of LOC113444 (Accession NP_612437.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113444.

[34070] LOC113828 (Accession NP_612444.1) is another GAM281 target gene, herein designated TARGET GENE. LOC113828 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC113828, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC113828 BINDING SITE, designated SEQ ID:5632, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34071] Another function of GAM281 is therefore inhibition of LOC113828 (Accession NP_612444.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113828.

[34072] LOC115123 (Accession XP_055276.1) is another GAM281 target gene, herein designated TARGET GENE. LOC115123 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC115123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115123 BINDING SITE, designated SEQ ID:15271, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34073] Another function of GAM281 is therefore inhibition of LOC115123 (Accession XP_055276.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115123.

[34074] LOC115219 (Accession XP_055499.2) is another GAM281 target gene, herein designated TARGET GENE. LOC115219 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC115219, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115219 BINDING SITE, designated SEQ ID:12422, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34075] Another function of GAM281 is therefore inhibition of

LOC115219 (Accession XP_055499.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115219.

[34076] LOC115648 (Accession NP_663299.1) is another GAM281 target gene, herein designated TARGET GENE. LOC115648 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC115648, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115648 BINDING SITE, designated SEQ ID:7429, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34077] Another function of GAM281 is therefore inhibition of LOC115648 (Accession NP_663299.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115648.

[34078] LOC116411 (Accession XP_058095.1) is another GAM281 target gene, herein designated TARGET GENE. LOC116411 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC116411, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC116411 BINDING SITE, designated SEQ ID:14720, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34079] Another function of GAM281 is therefore inhibition of LOC116411 (Accession XP_058095.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116411.

[34080] LOC118490 (Accession XP_060981.3) is another GAM281 target gene, herein designated TARGET GENE. LOC118490 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC118490, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118490 BINDING SITE, designated SEQ ID:456, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34081] Another function of GAM281 is therefore inhibition of LOC118490 (Accession XP_060981.3) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118490.

[34082] LOC118812 (Accession NP_849154.1) is another GAM281 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:2649, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34083] Another function of GAM281 is therefore inhibition of LOC118812 (Accession NP_849154.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118812.

[34084] LOC118812 (Accession XP_058346.2) is another GAM281 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded

by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:2649, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34085] Another function of GAM281 is therefore inhibition of LOC118812 (Accession XP_058346.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118812.

[34086] LOC120526 (Accession XP_058475.1) is another GAM281 target gene, herein designated TARGET GENE. LOC120526 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC120526, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC120526 BINDING SITE, designated SEQ ID:17112, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34087] Another function of GAM281 is therefore inhibition of

LOC120526 (Accession XP_058475.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120526.

[34088] LOC121952 (Accession XP_062872.2) is another GAM281 target gene, herein designated TARGET GENE. LOC121952 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC121952, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC121952 BINDING SITE, designated SEQ ID:9891, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34089] Another function of GAM281 is therefore inhibition of LOC121952 (Accession XP_062872.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121952.

[34090] LOC124221 (Accession XP_058785.3) is another GAM281 target gene, herein designated TARGET GENE. LOC124221 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC124221, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC124221 BINDING SITE, designated SEQ ID:14576, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34091] Another function of GAM281 is therefore inhibition of LOC124221 (Accession XP_058785.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124221.

[34092] LOC125061 (Accession XP_058889.3) is another GAM281 target gene, herein designated TARGET GENE. LOC125061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC125061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC125061 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34093] Another function of GAM281 is therefore inhibition of LOC125061 (Accession XP_058889.3) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125061.

[34094] LOC126669 (Accession XP_060121.4) is another GAM281 target gene, herein designated TARGET GENE. LOC126669 BINDING SITE1 and LOC126669 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC126669, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126669 BINDING SITE1 and LOC126669 BINDING SITE2, designated SEQ ID:17906 and SEQ ID:3477 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34095] Another function of GAM281 is therefore inhibition of LOC126669 (Accession XP_060121.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126669.

[34096] LOC127253 (Accession XP_059122.1) is another GAM281 target gene, herein designated TARGET GENE. LOC127253 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC127253, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC127253 BINDING SITE, designated SEQ ID:18918, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34097] Another function of GAM281 is therefore inhibition of LOC127253 (Accession XP_059122.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127253.

[34098] LOC127841 (Accession XP_059184.1) is another GAM281 target gene, herein designated TARGET GENE. LOC127841 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC127841, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC127841 BINDING SITE, designated SEQ ID:18516, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34099] Another function of GAM281 is therefore inhibition of

LOC127841 (Accession XP_059184.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127841.

[34100] LOC128387 (Accession XP_059243.2) is another GAM281 target gene, herein designated TARGET GENE. LOC128387 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC128387, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC128387 BINDING SITE, designated SEQ ID:15173, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34101] Another function of GAM281 is therefore inhibition of LOC128387 (Accession XP_059243.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128387.

[34102] LOC130813 (Accession XP_065904.1) is another GAM281 target gene, herein designated TARGET GENE. LOC130813 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC130813, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:12052, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34103] Another function of GAM281 is therefore inhibition of LOC130813 (Accession XP_065904.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813.

[34104] LOC132241 (Accession XP_059583.1) is another GAM281 target gene, herein designated TARGET GENE. LOC132241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC132241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC132241 BINDING SITE, designated SEQ ID:509, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34105] Another function of GAM281 is therefore inhibition of LOC132241 (Accession XP_059583.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132241.

[34106] LOC135293 (Accession XP_072402.4) is another GAM281 target gene, herein designated TARGET GENE. LOC135293 BINDING SITE1 and LOC135293 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC135293, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135293 BINDING SITE1 and LOC135293 BINDING SITE2, designated SEQ ID:3512 and SEQ ID:10443 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34107] Another function of GAM281 is therefore inhibition of LOC135293 (Accession XP_072402.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135293.

[34108] LOC135763 (Accession NP_612639.1) is another GAM281 target gene, herein designated TARGET GENE. LOC135763 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC135763, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135763 BINDING SITE, designated SEQ ID:17207, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34109] Another function of GAM281 is therefore inhibition of LOC135763 (Accession NP_612639.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135763.

[34110] LOC135818 (Accession XP_059804.4) is another GAM281 target gene, herein designated TARGET GENE. LOC135818 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135818 BINDING SITE, designated SEQ ID:19136, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34111] Another function of GAM281 is therefore inhibition of

LOC135818 (Accession XP_059804.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135818.

[34112] LOC137886 (Accession XP_059929.3) is another GAM281 target gene, herein designated TARGET GENE. LOC137886 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC137886, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC137886 BINDING SITE, designated SEQ ID:19990, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34113] Another function of GAM281 is therefore inhibition of LOC137886 (Accession XP_059929.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137886.

[34114] LOC138428 (Accession XP_059972.1) is another GAM281 target gene, herein designated TARGET GENE. LOC138428 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC138428, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC138428 BINDING SITE, designated SEQ ID:3277, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34115] Another function of GAM281 is therefore inhibition of LOC138428 (Accession XP_059972.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138428.

[34116] LOC139422 (Accession XP_066687.2) is another GAM281 target gene, herein designated TARGET GENE. LOC139422 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC139422, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC139422 BINDING SITE, designated SEQ ID:9489, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34117] Another function of GAM281 is therefore inhibition of LOC139422 (Accession XP_066687.2) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139422.

[34118] LOC142946 (Accession XP_096365.1) is another GAM281 target gene, herein designated TARGET GENE. LOC142946 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC142946, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC142946 BINDING SITE, designated SEQ ID:2999, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34119] Another function of GAM281 is therefore inhibition of LOC142946 (Accession XP_096365.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142946.

[34120] LOC143241 (Accession NP_620167.1) is another GAM281 target gene, herein designated TARGET GENE. LOC143241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC143241, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143241 BINDING SITE, designated SEQ ID:15574, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34121] Another function of GAM281 is therefore inhibition of LOC143241 (Accession NP_620167.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143241.

[34122] LOC144248 (Accession XP_084786.1) is another GAM281 target gene, herein designated TARGET GENE. LOC144248 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144248 BINDING SITE, designated SEQ ID:3159, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34123] Another function of GAM281 is therefore inhibition of LOC144248 (Accession XP_084786.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC144248.

[34124] LOC144402 (Accession NP_705898.1) is another GAM281 target gene, herein designated TARGET GENE. LOC144402 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144402, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144402 BINDING SITE, designated SEQ ID:3665, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34125] Another function of GAM281 is therefore inhibition of LOC144402 (Accession NP_705898.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144402.

[34126] LOC144404 (Accession XP_084852.6) is another GAM281 target gene, herein designated TARGET GENE. LOC144404 BINDING SITE1 through LOC144404 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC144404, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144404 BINDING SITE1 through LOC144404 BINDING SITE3, designated SEQ ID:15352, SEQ ID:5897 and SEQ ID:1633 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34127] Another function of GAM281 is therefore inhibition of LOC144404 (Accession XP_084852.6) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144404.

[34128] LOC144481 (Accession XP_096611.2) is another GAM281 target gene, herein designated TARGET GENE. LOC144481 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144481, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144481 BINDING SITE, designated SEQ ID:19220, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34129] Another function of GAM281 is therefore inhibition of LOC144481 (Accession XP_096611.2) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144481.

[34130] LOC144667 (Accession XP_096648.1) is another GAM281 target gene, herein designated TARGET GENE. LOC144667 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144667, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144667 BINDING SITE, designated SEQ ID:12712, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34131] Another function of GAM281 is therefore inhibition of LOC144667 (Accession XP_096648.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144667.

[34132] LOC144742 (Accession XP_084949.1) is another GAM281 target gene, herein designated TARGET GENE. LOC144742 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144742, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144742 BINDING SITE, designated SEQ ID:17736, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34133] Another function of GAM281 is therefore inhibition of LOC144742 (Accession XP_084949.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144742.

[34134] LOC144747 (Accession XP_084954.1) is another GAM281 target gene, herein designated TARGET GENE. LOC144747 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144747, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144747 BINDING SITE, designated SEQ ID:12981, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34135] Another function of GAM281 is therefore inhibition of LOC144747 (Accession XP_084954.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC144747.

[34136] LOC144766 (Accession XP_084963.2) is another GAM281 target gene, herein designated TARGET GENE. LOC144766 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144766, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144766 BINDING SITE, designated SEQ ID:8972, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34137] Another function of GAM281 is therefore inhibition of LOC144766 (Accession XP_084963.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144766.

[34138] LOC144776 (Accession XP_084964.1) is another GAM281 target gene, herein designated TARGET GENE. LOC144776 BINDING SITE1 and LOC144776 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC144776, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144776 BINDING SITE1 and LOC144776 BINDING SITE2, designated SEQ ID:444 and SEQ ID:16275 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34139] Another function of GAM281 is therefore inhibition of LOC144776 (Accession XP_084964.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144776.

[34140] LOC144817 (Accession XP_084972.1) is another GAM281 target gene, herein designated TARGET GENE. LOC144817 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144817 BINDING SITE, designated SEQ ID:12065, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34141] Another function of GAM281 is therefore inhibition of LOC144817 (Accession XP_084972.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144817.

[34142] LOC144871 (Accession XP_096698.1) is another GAM281 target gene, herein designated TARGET GENE. LOC144871 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144871, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144871 BINDING SITE, designated SEQ ID:14506, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34143] Another function of GAM281 is therefore inhibition of LOC144871 (Accession XP_096698.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144871.

[34144] LOC144962 (Accession XP_084990.1) is another GAM281 target gene, herein designated TARGET GENE. LOC144962 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144962, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144962 BINDING SITE, designated SEQ ID:12130, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34145] Another function of GAM281 is therefore inhibition of LOC144962 (Accession XP_084990.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144962.

[34146] LOC145268 (Accession XP_085072.1) is another GAM281 target gene, herein designated TARGET GENE. LOC145268 BINDING SITE1 and LOC145268 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC145268, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145268 BINDING SITE1 and LOC145268 BINDING SITE2, designated SEQ ID:18805 and SEQ ID:6493 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34147] Another function of GAM281 is therefore inhibition of

LOC145268 (Accession XP_085072.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145268.

[34148] LOC145453 (Accession XP_085120.1) is another GAM281 target gene, herein designated TARGET GENE. LOC145453 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145453, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145453 BINDING SITE, designated SEQ ID:11939, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34149] Another function of GAM281 is therefore inhibition of LOC145453 (Accession XP_085120.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145453.

[34150] LOC145663 (Accession XP_096829.1) is another GAM281 target gene, herein designated TARGET GENE. LOC145663 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145663, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145663 BINDING SITE, designated SEQ ID:13897, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34151] Another function of GAM281 is therefore inhibition of LOC145663 (Accession XP_096829.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145663.

[34152] LOC145725 (Accession XP_085211.1) is another GAM281 target gene, herein designated TARGET GENE. LOC145725 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145725 BINDING SITE, designated SEQ ID:4773, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34153] Another function of GAM281 is therefore inhibition of LOC145725 (Accession XP_085211.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145725.

[34154] LOC145757 (Accession XP_085227.1) is another GAM281 target gene, herein designated TARGET GENE. LOC145757 BINDING SITE1 and LOC145757 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC145757, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145757 BINDING SITE1 and LOC145757 BINDING SITE2, designated SEQ ID:11523 and SEQ ID:7370 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34155] Another function of GAM281 is therefore inhibition of LOC145757 (Accession XP_085227.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145757.

[34156] LOC145783 (Accession XP_085231.2) is another GAM281 target gene, herein designated TARGET GENE. LOC145783 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC145783, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145783 BINDING SITE, designated SEQ ID:2196, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34157] Another function of GAM281 is therefore inhibition of LOC145783 (Accession XP_085231.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145783.

[34158] LOC145813 (Accession XP_096873.1) is another GAM281 target gene, herein designated TARGET GENE. LOC145813 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145813 BINDING SITE, designated SEQ ID:16256, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34159] Another function of GAM281 is therefore inhibition of

LOC145813 (Accession XP_096873.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145813.

[34160] LOC146177 (Accession NP_778229.1) is another GAM281 target gene, herein designated TARGET GENE. LOC146177 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146177 BINDING SITE, designated SEQ ID:16175, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34161] Another function of GAM281 is therefore inhibition of LOC146177 (Accession NP_778229.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146177.

[34162] LOC146229 (Accession XP_085387.1) is another GAM281 target gene, herein designated TARGET GENE. LOC146229 BINDING SITE1 through LOC146229 BINDING SITE4 are target binding sites found in untranslated regions of

mRNA encoded by LOC146229, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146229 BINDING SITE1 through LOC146229 BINDING SITE4, designated SEQ ID:5551, SEQ ID:5672, SEQ ID:8706 and SEQ ID:1644 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34163] Another function of GAM281 is therefore inhibition of LOC146229 (Accession XP_085387.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146229.

[34164] LOC146346 (Accession XP_085430.1) is another GAM281 target gene, herein designated TARGET GENE. LOC146346 BINDING SITE1 through LOC146346 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC146346, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146346 BINDING SITE1 through LOC146346 BINDING SITE3, des-

ignated SEQ ID:1901, SEQ ID:5798 and SEQ ID:17670 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34165] Another function of GAM281 is therefore inhibition of LOC146346 (Accession XP_085430.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146346.

[34166] LOC146429 (Accession XP_096998.2) is another GAM281 target gene, herein designated TARGET GENE. LOC146429 BINDING SITE1 and LOC146429 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC146429, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146429 BINDING SITE1 and LOC146429 BINDING SITE2, designated SEQ ID:2457 and SEQ ID:4769 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34167] Another function of GAM281 is therefore inhibition of LOC146429 (Accession XP_096998.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC146429.

[34168] LOC146443 (Accession XP_085461.6) is another GAM281 target gene, herein designated TARGET GENE. LOC146443 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146443, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146443 BINDING SITE, designated SEQ ID:813, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34169] Another function of GAM281 is therefore inhibition of LOC146443 (Accession XP_085461.6) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146443.

[34170] LOC146475 (Accession XP_097006.1) is another GAM281 target gene, herein designated TARGET GENE. LOC146475 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC146475 BINDING SITE, designated SEQ ID:9246, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34171] Another function of GAM281 is therefore inhibition of LOC146475 (Accession XP_097006.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146475.

[34172] LOC146513 (Accession XP_097013.1) is another GAM281 target gene, herein designated TARGET GENE. LOC146513 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146513, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146513 BINDING SITE, designated SEQ ID:3374, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34173] Another function of GAM281 is therefore inhibition of LOC146513 (Accession XP_097013.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC146513.

[34174] LOC146603 (Accession XP_085514.2) is another GAM281 target gene, herein designated TARGET GENE. LOC146603 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146603 BINDING SITE, designated SEQ ID:7382, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34175] Another function of GAM281 is therefore inhibition of LOC146603 (Accession XP_085514.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146603.

[34176] LOC146756 (Accession XP_097085.5) is another GAM281 target gene, herein designated TARGET GENE. LOC146756 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146756, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC146756 BINDING SITE, designated SEQ ID:5954, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34177] Another function of GAM281 is therefore inhibition of LOC146756 (Accession XP_097085.5) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146756.

[34178] LOC146784 (Accession XP_085588.1) is another GAM281 target gene, herein designated TARGET GENE. LOC146784 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146784, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146784 BINDING SITE, designated SEQ ID:13448, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34179] Another function of GAM281 is therefore inhibition of LOC146784 (Accession XP_085588.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146784.

[34180] LOC146839 (Accession XP_097107.1) is another GAM281 target gene, herein designated TARGET GENE. LOC146839 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146839, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146839 BINDING SITE, designated SEQ ID:1745, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34181] Another function of GAM281 is therefore inhibition of LOC146839 (Accession XP_097107.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146839.

[34182] LOC146894 (Accession NP_660316.1) is another GAM281 target gene, herein designated TARGET GENE. LOC146894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146894 BINDING SITE, designated SEQ ID:8315, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34183] Another function of GAM281 is therefore inhibition of LOC146894 (Accession NP_660316.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146894.

[34184] LOC146895 (Accession XP_097120.1) is another GAM281 target gene, herein designated TARGET GENE. LOC146895 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146895, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146895 BINDING SITE, designated SEQ ID:8232, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34185] Another function of GAM281 is therefore inhibition of LOC146895 (Accession XP_097120.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146895.

[34186] LOC146901 (Accession XP_097121.1) is another GAM281

target gene, herein designated TARGET GENE. LOC146901 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146901, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146901 BINDING SITE, designated SEQ ID:6392, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34187] Another function of GAM281 is therefore inhibition of LOC146901 (Accession XP_097121.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146901.

[34188] LOC146909 (Accession XP_085634.2) is another GAM281 target gene, herein designated TARGET GENE. LOC146909 BINDING SITE1 and LOC146909 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC146909, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146909 BINDING SITE1 and LOC146909 BINDING SITE2, designated SEQ ID:9492

and SEQ ID:19550 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34189] Another function of GAM281 is therefore inhibition of LOC146909 (Accession XP_085634.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146909.

[34190] LOC147071 (Accession XP_054031.5) is another GAM281 target gene, herein designated TARGET GENE. LOC147071 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147071, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147071 BINDING SITE, designated SEQ ID:16699, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34191] Another function of GAM281 is therefore inhibition of LOC147071 (Accession XP_054031.5) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147071.

[34192] LOC147080 (Accession XP_097182.1) is another GAM281 target gene, herein designated TARGET GENE. LOC147080 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147080, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147080 BINDING SITE, designated SEQ ID:12558, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34193] Another function of GAM281 is therefore inhibition of LOC147080 (Accession XP_097182.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147080.

[34194] LOC147166 (Accession XP_085722.2) is another GAM281 target gene, herein designated TARGET GENE. LOC147166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147166 BINDING SITE, designated SEQ ID:10618, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34195] Another function of GAM281 is therefore inhibition of LOC147166 (Accession XP_085722.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147166.

[34196] LOC147381 (Accession XP_097230.2) is another GAM281 target gene, herein designated TARGET GENE. LOC147381 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147381, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147381 BINDING SITE, designated SEQ ID:19915, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34197] Another function of GAM281 is therefore inhibition of LOC147381 (Accession XP_097230.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147381.

[34198] LOC147407 (Accession XP_084000.1) is another GAM281

target gene, herein designated TARGET GENE. LOC147407 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147407, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147407 BINDING SITE, designated SEQ ID:12065, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34199] Another function of GAM281 is therefore inhibition of LOC147407 (Accession XP_084000.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147407.

[34200] LOC147622 (Accession XP_097255.1) is another GAM281 target gene, herein designated TARGET GENE. LOC147622 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147622, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147622 BINDING SITE, designated SEQ ID:16101, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34201] Another function of GAM281 is therefore inhibition of LOC147622 (Accession XP_097255.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147622.

[34202] LOC147817 (Accession XP_085903.1) is another GAM281 target gene, herein designated TARGET GENE. LOC147817 BINDING SITE1 and LOC147817 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC147817, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147817 BINDING SITE1 and LOC147817 BINDING SITE2, designated SEQ ID:19233 and SEQ ID:1634 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34203] Another function of GAM281 is therefore inhibition of LOC147817 (Accession XP_085903.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147817.

[34204] LOC147841 (Accession XP_085924.2) is another GAM281 target gene, herein designated TARGET GENE. LOC147841 BINDING SITE1 and LOC147841 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC147841, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147841 BINDING SITE1 and LOC147841 BINDING SITE2, designated SEQ ID:12065 and SEQ ID:8642 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34205] Another function of GAM281 is therefore inhibition of LOC147841 (Accession XP_085924.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147841.

[34206] LOC147947 (Accession XP_085974.1) is another GAM281 target gene, herein designated TARGET GENE. LOC147947 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147947, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC147947 BINDING SITE, designated SEQ ID:17952, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34207] Another function of GAM281 is therefore inhibition of LOC147947 (Accession XP_085974.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147947.

[34208] LOC148137 (Accession NP_653293.1) is another GAM281 target gene, herein designated TARGET GENE. LOC148137 BINDING SITE1 and LOC148137 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC148137, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148137 BINDING SITE1 and LOC148137 BINDING SITE2, designated SEQ ID:17935 and SEQ ID:5784 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34209] Another function of GAM281 is therefore inhibition of LOC148137 (Accession NP_653293.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148137.

[34210] LOC148189 (Accession XP_086087.1) is another GAM281 target gene, herein designated TARGET GENE. LOC148189 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148189, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148189 BINDING SITE, designated SEQ ID:12666, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34211] Another function of GAM281 is therefore inhibition of LOC148189 (Accession XP_086087.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148189.

[34212] LOC148198 (Accession XP_047554.4) is another GAM281 target gene, herein designated TARGET GENE. LOC148198 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148198, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148198 BINDING SITE, designated SEQ ID:11563, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34213] Another function of GAM281 is therefore inhibition of LOC148198 (Accession XP_047554.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148198.

[34214] LOC148708 (Accession XP_086286.4) is another GAM281 target gene, herein designated TARGET GENE. LOC148708 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148708 BINDING SITE, designated SEQ ID:15671, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34215] Another function of GAM281 is therefore inhibition of LOC148708 (Accession XP_086286.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC148708.

[34216] LOC148709 (Accession XP_086281.1) is another GAM281 target gene, herein designated TARGET GENE. LOC148709 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148709, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148709 BINDING SITE, designated SEQ ID:9201, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34217] Another function of GAM281 is therefore inhibition of LOC148709 (Accession XP_086281.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148709.

[34218] LOC149149 (Accession XP_097598.1) is another GAM281 target gene, herein designated TARGET GENE. LOC149149 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC149149 BINDING SITE, designated SEQ ID:2184, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34219] Another function of GAM281 is therefore inhibition of LOC149149 (Accession XP_097598.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149149.

[34220] LOC149371 (Accession NP_787072.1) is another GAM281 target gene, herein designated TARGET GENE. LOC149371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149371 BINDING SITE, designated SEQ ID:13354, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34221] Another function of GAM281 is therefore inhibition of LOC149371 (Accession NP_787072.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC149371.

[34222] LOC149466 (Accession XP_086546.1) is another GAM281 target gene, herein designated TARGET GENE. LOC149466 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149466, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149466 BINDING SITE, designated SEQ ID:16260, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34223] Another function of GAM281 is therefore inhibition of LOC149466 (Accession XP_086546.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149466.

[34224] LOC149478 (Accession XP_086536.1) is another GAM281 target gene, herein designated TARGET GENE. LOC149478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149478, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC149478 BINDING SITE, designated SEQ ID:5016, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34225] Another function of GAM281 is therefore inhibition of LOC149478 (Accession XP_086536.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149478.

[34226] LOC149506 (Accession XP_097661.1) is another GAM281 target gene, herein designated TARGET GENE. LOC149506 BINDING SITE1 and LOC149506 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC149506, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE1 and LOC149506 BINDING SITE2, designated SEQ ID:2139 and SEQ ID:1489 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34227] Another function of GAM281 is therefore inhibition of LOC149506 (Accession XP_097661.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC149506.

[34228] LOC149692 (Accession XP_097706.1) is another GAM281 target gene, herein designated TARGET GENE. LOC149692 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149692, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149692 BINDING SITE, designated SEQ ID:11025, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34229] Another function of GAM281 is therefore inhibition of LOC149692 (Accession XP_097706.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149692.

[34230] LOC149703 (Accession XP_097719.1) is another GAM281 target gene, herein designated TARGET GENE. LOC149703 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149703, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC149703 BINDING SITE, designated SEQ ID:10508, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34231] Another function of GAM281 is therefore inhibition of LOC149703 (Accession XP_097719.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149703.

[34232] LOC150054 (Accession XP_097797.1) is another GAM281 target gene, herein designated TARGET GENE. LOC150054 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150054, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150054 BINDING SITE, designated SEQ ID:5157, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34233] Another function of GAM281 is therefore inhibition of LOC150054 (Accession XP_097797.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC150054.

[34234] LOC150150 (Accession XP_097820.1) is another GAM281 target gene, herein designated TARGET GENE. LOC150150 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150150, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150150 BINDING SITE, designated SEQ ID:8279, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34235] Another function of GAM281 is therefore inhibition of LOC150150 (Accession XP_097820.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150150.

[34236] LOC150157 (Accession XP_097823.1) is another GAM281 target gene, herein designated TARGET GENE. LOC150157 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150157, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC150157 BINDING SITE, designated SEQ ID:13000, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34237] Another function of GAM281 is therefore inhibition of LOC150157 (Accession XP_097823.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150157.

[34238] LOC150166 (Accession XP_097824.1) is another GAM281 target gene, herein designated TARGET GENE. LOC150166 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150166 BINDING SITE, designated SEQ ID:19856, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34239] Another function of GAM281 is therefore inhibition of LOC150166 (Accession XP_097824.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150166.

[34240] LOC150225 (Accession XP_097870.1) is another GAM281 target gene, herein designated TARGET GENE. LOC150225 BINDING SITE1 and LOC150225 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC150225, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150225 BINDING SITE1 and LOC150225 BINDING SITE2, designated SEQ ID:4400 and SEQ ID:7207 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34241] Another function of GAM281 is therefore inhibition of LOC150225 (Accession XP_097870.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150225.

[34242] LOC150356 (Accession XP_086884.2) is another GAM281 target gene, herein designated TARGET GENE. LOC150356 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC150356 BINDING SITE, designated SEQ ID:9922, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34243] Another function of GAM281 is therefore inhibition of LOC150356 (Accession XP_086884.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150356.

[34244] LOC150383 (Accession XP_086905.1) is another GAM281 target gene, herein designated TARGET GENE. LOC150383 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150383, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150383 BINDING SITE, designated SEQ ID:826, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34245] Another function of GAM281 is therefore inhibition of LOC150383 (Accession XP_086905.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC150383.

[34246] LOC150384 (Accession XP_097894.1) is another GAM281 target gene, herein designated TARGET GENE. LOC150384 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150384, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150384 BINDING SITE, designated SEQ ID:7485, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34247] Another function of GAM281 is therefore inhibition of LOC150384 (Accession XP_097894.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150384.

[34248] LOC150407 (Accession XP_086906.1) is another GAM281 target gene, herein designated TARGET GENE. LOC150407 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150407, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC150407 BINDING SITE, designated SEQ ID:5756, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34249] Another function of GAM281 is therefore inhibition of LOC150407 (Accession XP_086906.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150407.

[34250] LOC150587 (Accession XP_097917.1) is another GAM281 target gene, herein designated TARGET GENE. LOC150587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150587 BINDING SITE, designated SEQ ID:16940, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34251] Another function of GAM281 is therefore inhibition of LOC150587 (Accession XP_097917.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150587.

[34252] LOC150819 (Accession XP_097954.1) is another GAM281 target gene, herein designated TARGET GENE. LOC150819 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150819, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150819 BINDING SITE, designated SEQ ID:18257, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34253] Another function of GAM281 is therefore inhibition of LOC150819 (Accession XP_097954.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150819.

[34254] LOC151057 (Accession XP_097998.1) is another GAM281 target gene, herein designated TARGET GENE. LOC151057 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151057, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151057 BINDING SITE, designated SEQ ID:12075, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34255] Another function of GAM281 is therefore inhibition of LOC151057 (Accession XP_097998.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151057.

[34256] LOC151196 (Accession XP_098019.1) is another GAM281 target gene, herein designated TARGET GENE. LOC151196 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151196, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151196 BINDING SITE, designated SEQ ID:19774, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34257] Another function of GAM281 is therefore inhibition of LOC151196 (Accession XP_098019.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151196.

[34258] LOC151201 (Accession XP_098021.1) is another GAM281

target gene, herein designated TARGET GENE. LOC151201 BINDING SITE1 and LOC151201 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC151201, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE1 and LOC151201 BINDING SITE2, designated SEQ ID:12725 and SEQ ID:2572 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34259] Another function of GAM281 is therefore inhibition of LOC151201 (Accession XP_098021.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151201.

[34260] LOC151475 (Accession XP_098063.1) is another GAM281 target gene, herein designated TARGET GENE. LOC151475 BINDING SITE1 and LOC151475 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC151475, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC151475 BINDING SITE1 and LOC151475 BINDING SITE2, designated SEQ ID:4174 and SEQ ID:4371 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34261] Another function of GAM281 is therefore inhibition of LOC151475 (Accession XP_098063.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151475.

[34262] LOC151636 (Accession NP_612144.1) is another GAM281 target gene, herein designated TARGET GENE. LOC151636 BINDING SITE1 through LOC151636 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC151636, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151636 BINDING SITE1 through LOC151636 BINDING SITE3, designated SEQ ID:2693, SEQ ID:4151 and SEQ ID:14731 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34263] Another function of GAM281 is therefore inhibition of

LOC151636 (Accession NP_612144.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151636.

[34264] LOC151658 (Accession XP_098103.1) is another GAM281 target gene, herein designated TARGET GENE. LOC151658 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151658, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151658 BINDING SITE, designated SEQ ID:3130, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34265] Another function of GAM281 is therefore inhibition of LOC151658 (Accession XP_098103.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151658.

[34266] LOC151877 (Accession XP_098132.1) is another GAM281 target gene, herein designated TARGET GENE. LOC151877 BINDING SITE1 and LOC151877 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by LOC151877, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151877 BINDING SITE1 and LOC151877 BINDING SITE2, designated SEQ ID:17499 and SEQ ID:4677 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34267] Another function of GAM281 is therefore inhibition of LOC151877 (Accession XP_098132.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151877.

[34268] LOC151878 (Accession XP_087329.1) is another GAM281 target gene, herein designated TARGET GENE. LOC151878 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151878, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151878 BINDING SITE, designated SEQ ID:15127, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34269] Another function of GAM281 is therefore inhibition of LOC151878 (Accession XP_087329.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151878.

[34270] LOC152245 (Accession XP_098182.1) is another GAM281 target gene, herein designated TARGET GENE. LOC152245 BINDING SITE1 and LOC152245 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC152245, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152245 BINDING SITE1 and LOC152245 BINDING SITE2, designated SEQ ID:9470 and SEQ ID:3559 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34271] Another function of GAM281 is therefore inhibition of LOC152245 (Accession XP_098182.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152245.

[34272] LOC152445 (Accession XP_098231.1) is another GAM281

target gene, herein designated TARGET GENE. LOC152445 BINDING SITE1 and LOC152445 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC152445, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE1 and LOC152445 BINDING SITE2, designated SEQ ID:6147 and SEQ ID:2922 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34273] Another function of GAM281 is therefore inhibition of LOC152445 (Accession XP_098231.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152445.

[34274] LOC152620 (Accession XP_011108.2) is another GAM281 target gene, herein designated TARGET GENE. LOC152620 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152620, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC152620 BINDING SITE, designated SEQ ID:1745, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34275] Another function of GAM281 is therefore inhibition of LOC152620 (Accession XP_011108.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152620.

[34276] LOC152719 (Accession XP_098257.1) is another GAM281 target gene, herein designated TARGET GENE. LOC152719 BINDING SITE1 and LOC152719 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC152719, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152719 BINDING SITE1 and LOC152719 BINDING SITE2, designated SEQ ID:11919 and SEQ ID:17637 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34277] Another function of GAM281 is therefore inhibition of LOC152719 (Accession XP_098257.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC152719.

[34278] LOC152765 (Accession XP_087519.1) is another GAM281 target gene, herein designated TARGET GENE. LOC152765 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152765, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152765 BINDING SITE, designated SEQ ID:18605, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34279] Another function of GAM281 is therefore inhibition of LOC152765 (Accession XP_087519.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152765.

[34280] LOC152794 (Accession XP_087525.1) is another GAM281 target gene, herein designated TARGET GENE. LOC152794 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152794, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC152794 BINDING SITE, designated SEQ ID:2010, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34281] Another function of GAM281 is therefore inhibition of LOC152794 (Accession XP_087525.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152794.

[34282] LOC152804 (Accession XP_098266.2) is another GAM281 target gene, herein designated TARGET GENE. LOC152804 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152804, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152804 BINDING SITE, designated SEQ ID:9568, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34283] Another function of GAM281 is therefore inhibition of LOC152804 (Accession XP_098266.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC152804.

[34284] LOC153027 (Accession XP_041221.1) is another GAM281 target gene, herein designated TARGET GENE. LOC153027 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153027, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153027 BINDING SITE, designated SEQ ID:1646, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34285] Another function of GAM281 is therefore inhibition of LOC153027 (Accession XP_041221.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153027.

[34286] LOC153077 (Accession XP_098307.1) is another GAM281 target gene, herein designated TARGET GENE. LOC153077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC153077 BINDING SITE, designated SEQ ID:5304, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34287] Another function of GAM281 is therefore inhibition of LOC153077 (Accession XP_098307.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153077.

[34288] LOC153811 (Accession XP_087779.2) is another GAM281 target gene, herein designated TARGET GENE. LOC153811 BINDING SITE1 through LOC153811 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC153811, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153811 BINDING SITE1 through LOC153811 BINDING SITE4, designated SEQ ID:19665, SEQ ID:9683, SEQ ID:9170 and SEQ ID:17512 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34289] Another function of GAM281 is therefore inhibition of LOC153811 (Accession XP_087779.2) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153811.

[34290] LOC153883 (Accession XP_087798.1) is another GAM281 target gene, herein designated TARGET GENE. LOC153883 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153883, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153883 BINDING SITE, designated SEQ ID:15929, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34291] Another function of GAM281 is therefore inhibition of LOC153883 (Accession XP_087798.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153883.

[34292] LOC153910 (Accession XP_087801.1) is another GAM281 target gene, herein designated TARGET GENE. LOC153910 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153910, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153910 BINDING SITE, designated SEQ ID:2882, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34293] Another function of GAM281 is therefore inhibition of LOC153910 (Accession XP_087801.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153910.

[34294] LOC154282 (Accession XP_098505.1) is another GAM281 target gene, herein designated TARGET GENE. LOC154282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154282 BINDING SITE, designated SEQ ID:4307, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34295] Another function of GAM281 is therefore inhibition of LOC154282 (Accession XP_098505.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC154282.

[34296] LOC154822 (Accession XP_098618.3) is another GAM281 target gene, herein designated TARGET GENE. LOC154822 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154822 BINDING SITE, designated SEQ ID:19205, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34297] Another function of GAM281 is therefore inhibition of LOC154822 (Accession XP_098618.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154822.

[34298] LOC154877 (Accession XP_098626.1) is another GAM281 target gene, herein designated TARGET GENE. LOC154877 BINDING SITE1 through LOC154877 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC154877, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE1 through LOC154877 BINDING SITE4, designated SEQ ID:17731, SEQ ID:3200, SEQ ID:12700 and SEQ ID:16089 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34299] Another function of GAM281 is therefore inhibition of LOC154877 (Accession XP_098626.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877.

[34300] LOC155066 (Accession XP_088142.4) is another GAM281 target gene, herein designated TARGET GENE. LOC155066 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC155066, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC155066 BINDING SITE, designated SEQ ID:17980, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34301] Another function of GAM281 is therefore inhibition of

LOC155066 (Accession XP_088142.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155066.

[34302] LOC157931 (Accession XP_098845.1) is another GAM281 target gene, herein designated TARGET GENE. LOC157931 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC157931, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157931 BINDING SITE, designated SEQ ID:9709, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34303] Another function of GAM281 is therefore inhibition of LOC157931 (Accession XP_098845.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157931.

[34304] LOC158014 (Accession XP_088442.1) is another GAM281 target gene, herein designated TARGET GENE. LOC158014 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158014, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158014 BINDING SITE, designated SEQ ID:2542, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34305] Another function of GAM281 is therefore inhibition of LOC158014 (Accession XP_088442.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158014.

[34306] LOC158228 (Accession XP_098903.4) is another GAM281 target gene, herein designated TARGET GENE. LOC158228 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158228, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158228 BINDING SITE, designated SEQ ID:5779, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34307] Another function of GAM281 is therefore inhibition of LOC158228 (Accession XP_098903.4) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158228.

[34308] LOC158310 (Accession XP_098919.1) is another GAM281 target gene, herein designated TARGET GENE. LOC158310 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158310, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158310 BINDING SITE, designated SEQ ID:14859, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34309] Another function of GAM281 is therefore inhibition of LOC158310 (Accession XP_098919.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158310.

[34310] LOC158402 (Accession XP_098936.1) is another GAM281 target gene, herein designated TARGET GENE. LOC158402 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158402, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158402 BINDING SITE, designated SEQ ID:17964, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34311] Another function of GAM281 is therefore inhibition of LOC158402 (Accession XP_098936.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158402.

[34312] LOC158436 (Accession XP_098942.1) is another GAM281 target gene, herein designated TARGET GENE. LOC158436 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158436 BINDING SITE, designated SEQ ID:1263, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34313] Another function of GAM281 is therefore inhibition of LOC158436 (Accession XP_098942.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC158436.

[34314] LOC158476 (Accession XP_098955.1) is another GAM281 target gene, herein designated TARGET GENE. LOC158476 BINDING SITE1 and LOC158476 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC158476, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158476 BINDING SITE1 and LOC158476 BINDING SITE2, designated SEQ ID:17016 and SEQ ID:935 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34315] Another function of GAM281 is therefore inhibition of LOC158476 (Accession XP_098955.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158476.

[34316] LOC158563 (Accession XP_088606.1) is another GAM281 target gene, herein designated TARGET GENE. LOC158563 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158563, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158563 BINDING SITE, designated SEQ ID:3426, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34317] Another function of GAM281 is therefore inhibition of LOC158563 (Accession XP_088606.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158563.

[34318] LOC158572 (Accession XP_088608.1) is another GAM281 target gene, herein designated TARGET GENE. LOC158572 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158572, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158572 BINDING SITE, designated SEQ ID:12003, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34319] Another function of GAM281 is therefore inhibition of LOC158572 (Accession XP_088608.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158572.

[34320] LOC158668 (Accession XP_045161.1) is another GAM281 target gene, herein designated TARGET GENE. LOC158668 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158668, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158668 BINDING SITE, designated SEQ ID:16260, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34321] Another function of GAM281 is therefore inhibition of LOC158668 (Accession XP_045161.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158668.

[34322] LOC160897 (Accession XP_090573.3) is another GAM281 target gene, herein designated TARGET GENE. LOC160897 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC160897, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC160897 BINDING SITE, designated SEQ ID:17208, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34323] Another function of GAM281 is therefore inhibition of LOC160897 (Accession XP_090573.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160897.

[34324] LOC161247 (Accession XP_090783.3) is another GAM281 target gene, herein designated TARGET GENE. LOC161247 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC161247, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC161247 BINDING SITE, designated SEQ ID:16016, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34325] Another function of GAM281 is therefore inhibition of LOC161247 (Accession XP_090783.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC161247.

[34326] LOC162427 (Accession XP_091549.3) is another GAM281 target gene, herein designated TARGET GENE. LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC162427, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2, designated SEQ ID:12068 and SEQ ID:12068 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34327] Another function of GAM281 is therefore inhibition of LOC162427 (Accession XP_091549.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162427.

[34328] LOC162427 (Accession NP_835227.1) is another GAM281 target gene, herein designated TARGET GENE. LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2 are target binding sites found in untranslated regions of multiple

transcripts of mRNA encoded by LOC162427, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2, designated SEQ ID:8231 and SEQ ID:8231 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34329] Another function of GAM281 is therefore inhibition of LOC162427 (Accession NP_835227.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162427.

[34330] LOC162962 (Accession XP_091886.7) is another GAM281 target gene, herein designated TARGET GENE. LOC162962 BINDING SITE1 and LOC162962 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC162962, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162962 BINDING SITE1 and LOC162962 BINDING SITE2, designated SEQ ID:3249 and SEQ ID:13131 respectively, to the nucleotide se-

quence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34331] Another function of GAM281 is therefore inhibition of LOC162962 (Accession XP_091886.7) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162962.

[34332] LOC162967 (Accession XP_091890.6) is another GAM281 target gene, herein designated TARGET GENE. LOC162967 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC162967, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162967 BINDING SITE, designated SEQ ID:13831, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34333] Another function of GAM281 is therefore inhibition of LOC162967 (Accession XP_091890.6) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162967.

[34334] LOC163227 (Accession NP_775802.1) is another GAM281

target gene, herein designated TARGET GENE. LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC163227, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2, designated SEQ ID:11854 and SEQ ID:9147 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34335] Another function of GAM281 is therefore inhibition of LOC163227 (Accession NP_775802.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163227.

[34336] LOC164091 (Accession XP_089356.1) is another GAM281 target gene, herein designated TARGET GENE. LOC164091 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC164091, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC164091 BINDING SITE, designated SEQ ID:7989, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34337] Another function of GAM281 is therefore inhibition of LOC164091 (Accession XP_089356.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164091.

[34338] LOC168002 (Accession XP_094794.2) is another GAM281 target gene, herein designated TARGET GENE. LOC168002 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC168002, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC168002 BINDING SITE, designated SEQ ID:3971, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34339] Another function of GAM281 is therefore inhibition of LOC168002 (Accession XP_094794.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168002.

[34340] LOC168451 (Accession XP_095114.2) is another GAM281 target gene, herein designated TARGET GENE. LOC168451 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC168451, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC168451 BINDING SITE, designated SEQ ID:19786, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34341] Another function of GAM281 is therefore inhibition of LOC168451 (Accession XP_095114.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168451.

[34342] LOC170409 (Accession XP_096330.1) is another GAM281 target gene, herein designated TARGET GENE. LOC170409 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC170409, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC170409 BINDING SITE, designated SEQ ID:15561, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34343] Another function of GAM281 is therefore inhibition of LOC170409 (Accession XP_096330.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170409.

[34344] LOC196264 (Accession XP_113683.1) is another GAM281 target gene, herein designated TARGET GENE. LOC196264 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196264, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196264 BINDING SITE, designated SEQ ID:2452, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34345] Another function of GAM281 is therefore inhibition of LOC196264 (Accession XP_113683.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196264.

[34346] LOC197358 (Accession XP_113872.2) is another GAM281

target gene, herein designated TARGET GENE. LOC197358 BINDING SITE1 and LOC197358 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC197358, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC197358 BINDING SITE1 and LOC197358 BINDING SITE2, designated SEQ ID:6387 and SEQ ID:4625 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34347] Another function of GAM281 is therefore inhibition of LOC197358 (Accession XP_113872.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197358.

[34348] LOC199725 (Accession XP_117119.1) is another GAM281 target gene, herein designated TARGET GENE. LOC199725 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC199725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC199725 BINDING SITE, designated SEQ ID:10884, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34349] Another function of GAM281 is therefore inhibition of LOC199725 (Accession XP_117119.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199725.

[34350] LOC199899 (Accession XP_117153.1) is another GAM281 target gene, herein designated TARGET GENE. LOC199899 BINDING SITE1 and LOC199899 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC199899, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199899 BINDING SITE1 and LOC199899 BINDING SITE2, designated SEQ ID:5253 and SEQ ID:8292 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34351] Another function of GAM281 is therefore inhibition of LOC199899 (Accession XP_117153.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC199899.

[34352] LOC199906 (Accession XP_114052.1) is another GAM281 target gene, herein designated TARGET GENE. LOC199906 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC199906, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199906 BINDING SITE, designated SEQ ID:19756, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34353] Another function of GAM281 is therefore inhibition of LOC199906 (Accession XP_114052.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199906.

[34354] LOC200169 (Accession XP_117200.1) is another GAM281 target gene, herein designated TARGET GENE. LOC200169 BINDING SITE1 and LOC200169 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC200169, corresponding to target binding sites such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200169 BINDING SITE1 and LOC200169 BINDING SITE2, designated SEQ ID:6122 and SEQ ID:5066 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34355] Another function of GAM281 is therefore inhibition of LOC200169 (Accession XP_117200.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200169.

[34356] LOC200860 (Accession XP_117289.1) is another GAM281 target gene, herein designated TARGET GENE. LOC200860 BINDING SITE1 and LOC200860 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC200860, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200860 BINDING SITE1 and LOC200860 BINDING SITE2, designated SEQ ID:4175 and SEQ ID:12075 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34357] Another function of GAM281 is therefore inhibition of LOC200860 (Accession XP_117289.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200860.

[34358] LOC200895 (Accession NP_789785.1) is another GAM281 target gene, herein designated TARGET GENE. LOC200895 BINDING SITE1 and LOC200895 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC200895, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200895 BINDING SITE1 and LOC200895 BINDING SITE2, designated SEQ ID:17681 and SEQ ID:11863 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34359] Another function of GAM281 is therefore inhibition of LOC200895 (Accession NP_789785.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200895.

[34360] LOC200916 (Accession XP_114317.3) is another GAM281

target gene, herein designated TARGET GENE. LOC200916 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200916, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200916 BINDING SITE, designated SEQ ID:3465, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34361] Another function of GAM281 is therefore inhibition of LOC200916 (Accession XP_114317.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200916.

[34362] LOC201164 (Accession NP_849158.1) is another GAM281 target gene, herein designated TARGET GENE. LOC201164 BINDING SITE1 and LOC201164 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC201164, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201164 BINDING SITE1 and LOC201164 BINDING

SITE2, designated SEQ ID:16993 and SEQ ID:13384 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34363] Another function of GAM281 is therefore inhibition of LOC201164 (Accession NP_849158.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201164.

[34364] LOC201292 (Accession NP_775818.1) is another GAM281 target gene, herein designated TARGET GENE. LOC201292 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201292, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201292 BINDING SITE, designated SEQ ID:4556, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34365] Another function of GAM281 is therefore inhibition of LOC201292 (Accession NP_775818.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201292.

[34366] LOC201562 (Accession XP_114343.2) is another GAM281 target gene, herein designated TARGET GENE. LOC201562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201562 BINDING SITE, designated SEQ ID:15044, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34367] Another function of GAM281 is therefore inhibition of LOC201562 (Accession XP_114343.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201562.

[34368] LOC201725 (Accession XP_114370.1) is another GAM281 target gene, herein designated TARGET GENE. LOC201725 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201725 BINDING SITE, designated SEQ ID:5492, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34369] Another function of GAM281 is therefore inhibition of LOC201725 (Accession XP_114370.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201725.

[34370] LOC202400 (Accession XP_117397.1) is another GAM281 target gene, herein designated TARGET GENE. LOC202400 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC202400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202400 BINDING SITE, designated SEQ ID:9145, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34371] Another function of GAM281 is therefore inhibition of LOC202400 (Accession XP_117397.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202400.

[34372] LOC202404 (Accession XP_114481.4) is another GAM281

target gene, herein designated TARGET GENE. LOC202404 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC202404, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202404 BINDING SITE, designated SEQ ID:18628, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34373] Another function of GAM281 is therefore inhibition of LOC202404 (Accession XP_114481.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202404.

[34374] LOC202460 (Accession XP_114493.1) is another GAM281 target gene, herein designated TARGET GENE. LOC202460 BINDING SITE1 and LOC202460 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC202460, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202460 BINDING SITE1 and LOC202460 BINDING SITE2, designated SEQ ID:16450

and SEQ ID:11010 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34375] Another function of GAM281 is therefore inhibition of LOC202460 (Accession XP_114493.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202460.

[34376] LOC202934 (Accession XP_117486.2) is another GAM281 target gene, herein designated TARGET GENE. LOC202934 BINDING SITE1 and LOC202934 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC202934, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE1 and LOC202934 BINDING SITE2, designated SEQ ID:4820 and SEQ ID:1729 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34377] Another function of GAM281 is therefore inhibition of LOC202934 (Accession XP_117486.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC202934.

[34378] LOC203547 (Accession XP_114719.1) is another GAM281 target gene, herein designated TARGET GENE. LOC203547 BINDING SITE1 and LOC203547 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC203547, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC203547 BINDING SITE1 and LOC203547 BINDING SITE2, designated SEQ ID:9545 and SEQ ID:2351 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34379] Another function of GAM281 is therefore inhibition of LOC203547 (Accession XP_114719.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203547.

[34380] LOC204288 (Accession XP_115295.1) is another GAM281 target gene, herein designated TARGET GENE. LOC204288 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC204288, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC204288 BINDING SITE, designated SEQ ID:10724, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34381] Another function of GAM281 is therefore inhibition of LOC204288 (Accession XP_115295.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC204288.

[34382] LOC219293 (Accession XP_166599.2) is another GAM281 target gene, herein designated TARGET GENE. LOC219293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219293 BINDING SITE, designated SEQ ID:19361, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34383] Another function of GAM281 is therefore inhibition of LOC219293 (Accession XP_166599.2) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219293.

[34384] LOC219700 (Accession XP_167570.1) is another GAM281 target gene, herein designated TARGET GENE. LOC219700 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC219700, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219700 BINDING SITE, designated SEQ ID:2410, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34385] Another function of GAM281 is therefore inhibition of LOC219700 (Accession XP_167570.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219700.

[34386] LOC219731 (Accession XP_167596.1) is another GAM281 target gene, herein designated TARGET GENE. LOC219731 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC219731, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219731 BINDING SITE, designated SEQ ID:4678, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34387] Another function of GAM281 is therefore inhibition of LOC219731 (Accession XP_167596.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219731.

[34388] LOC219735 (Accession XP_167601.1) is another GAM281 target gene, herein designated TARGET GENE. LOC219735 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219735 BINDING SITE, designated SEQ ID:18913, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34389] Another function of GAM281 is therefore inhibition of LOC219735 (Accession XP_167601.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC219735.

[34390] LOC219894 (Accession XP_167782.1) is another GAM281 target gene, herein designated TARGET GENE. LOC219894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219894 BINDING SITE, designated SEQ ID:14588, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34391] Another function of GAM281 is therefore inhibition of LOC219894 (Accession XP_167782.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219894.

[34392] LOC220074 (Accession NP_660352.1) is another GAM281 target gene, herein designated TARGET GENE. LOC220074 BINDING SITE1 through LOC220074 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC220074, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220074 BINDING SITE1 through LOC220074 BINDING SITE3, designated SEQ ID:6497, SEQ ID:9147 and SEQ ID:16838 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34393] Another function of GAM281 is therefore inhibition of LOC220074 (Accession NP_660352.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220074.

[34394] LOC221663 (Accession XP_168131.1) is another GAM281 target gene, herein designated TARGET GENE. LOC221663 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221663 BINDING SITE, designated SEQ ID:1939, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34395] Another function of GAM281 is therefore inhibition of LOC221663 (Accession XP_168131.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221663.

[34396] LOC221889 (Accession XP_166513.1) is another GAM281 target gene, herein designated TARGET GENE. LOC221889 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221889, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221889 BINDING SITE, designated SEQ ID:3555, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34397] Another function of GAM281 is therefore inhibition of LOC221889 (Accession XP_166513.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221889.

[34398] LOC221946 (Accession XP_168340.1) is another GAM281 target gene, herein designated TARGET GENE. LOC221946 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221946, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221946 BINDING SITE, designated SEQ ID:15948, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34399] Another function of GAM281 is therefore inhibition of LOC221946 (Accession XP_168340.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221946.

[34400] LOC221960 (Accession XP_165859.1) is another GAM281 target gene, herein designated TARGET GENE. LOC221960 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221960, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221960 BINDING SITE, designated SEQ ID:14860, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34401] Another function of GAM281 is therefore inhibition of LOC221960 (Accession XP_165859.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC221960.

[34402] LOC221964 (Accession XP_168342.1) is another GAM281 target gene, herein designated TARGET GENE. LOC221964 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221964, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221964 BINDING SITE, designated SEQ ID:17029, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34403] Another function of GAM281 is therefore inhibition of LOC221964 (Accession XP_168342.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221964.

[34404] LOC222031 (Accession XP_168371.1) is another GAM281 target gene, herein designated TARGET GENE. LOC222031 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222031, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC222031 BINDING SITE, designated SEQ ID:7700, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34405] Another function of GAM281 is therefore inhibition of LOC222031 (Accession XP_168371.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222031.

[34406] LOC222057 (Accession XP_166594.2) is another GAM281 target gene, herein designated TARGET GENE. LOC222057 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222057, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222057 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34407] Another function of GAM281 is therefore inhibition of LOC222057 (Accession XP_166594.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC222057.

[34408] LOC222068 (Accession XP_166556.1) is another GAM281 target gene, herein designated TARGET GENE. LOC222068 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC222068, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222068 BINDING SITE, designated SEQ ID:3232, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34409] Another function of GAM281 is therefore inhibition of LOC222068 (Accession XP_166556.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222068.

[34410] LOC222159 (Accession XP_212100.1) is another GAM281 target gene, herein designated TARGET GENE. LOC222159 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC222159, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of LOC222159 BINDING SITE, designated SEQ ID:16228, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34411] Another function of GAM281 is therefore inhibition of LOC222159 (Accession XP_212100.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222159.

[34412] LOC253612 (Accession XP_172985.2) is another GAM281 target gene, herein designated TARGET GENE. LOC253612 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253612, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253612 BINDING SITE, designated SEQ ID:5487, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34413] Another function of GAM281 is therefore inhibition of LOC253612 (Accession XP_172985.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC253612.

[34414] LOC253805 (Accession XP_172854.1) is another GAM281 target gene, herein designated TARGET GENE. LOC253805 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC253805, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253805 BINDING SITE, designated SEQ ID:4532, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34415] Another function of GAM281 is therefore inhibition of LOC253805 (Accession XP_172854.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253805.

[34416] LOC253992 (Accession XP_172953.2) is another GAM281 target gene, herein designated TARGET GENE. LOC253992 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253992, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC253992 BINDING SITE, designated SEQ ID:3617, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34417] Another function of GAM281 is therefore inhibition of LOC253992 (Accession XP_172953.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253992.

[34418] LOC254875 (Accession XP_171170.1) is another GAM281 target gene, herein designated TARGET GENE. LOC254875 BINDING SITE1 and LOC254875 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC254875, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254875 BINDING SITE1 and LOC254875 BINDING SITE2, designated SEQ ID:14560 and SEQ ID:6188 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34419] Another function of GAM281 is therefore inhibition of LOC254875 (Accession XP_171170.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC254875.

[34420] LOC255031 (Accession XP_173187.1) is another GAM281 target gene, herein designated TARGET GENE. LOC255031 BINDING SITE1 and LOC255031 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC255031, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255031 BINDING SITE1 and LOC255031 BINDING SITE2, designated SEQ ID:13629 and SEQ ID:3261 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34421] Another function of GAM281 is therefore inhibition of LOC255031 (Accession XP_173187.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255031.

[34422] LOC255177 (Accession XP_172941.1) is another GAM281 target gene, herein designated TARGET GENE. LOC255177 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC255177, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255177 BINDING SITE, designated SEQ ID:6294, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34423] Another function of GAM281 is therefore inhibition of LOC255177 (Accession XP_172941.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255177.

[34424] LOC255458 (Accession XP_173150.1) is another GAM281 target gene, herein designated TARGET GENE. LOC255458 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255458, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255458 BINDING SITE, designated SEQ ID:6365, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34425] Another function of GAM281 is therefore inhibition of LOC255458 (Accession XP_173150.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255458.

[34426] LOC255488 (Accession XP_172581.2) is another GAM281 target gene, herein designated TARGET GENE. LOC255488 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC255488, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255488 BINDING SITE, designated SEQ ID:3150, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34427] Another function of GAM281 is therefore inhibition of LOC255488 (Accession XP_172581.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255488.

[34428] LOC255736 (Accession XP_170898.2) is another GAM281 target gene, herein designated TARGET GENE. LOC255736 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255736, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255736 BINDING SITE, designated SEQ ID:2873, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34429] Another function of GAM281 is therefore inhibition of LOC255736 (Accession XP_170898.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255736.

[34430] LOC255975 (Accession XP_171083.2) is another GAM281 target gene, herein designated TARGET GENE. LOC255975 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255975 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34431] Another function of GAM281 is therefore inhibition of LOC255975 (Accession XP_171083.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC255975.

[34432] LOC256614 (Accession XP_172864.1) is another GAM281 target gene, herein designated TARGET GENE. LOC256614 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC256614, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256614 BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34433] Another function of GAM281 is therefore inhibition of LOC256614 (Accession XP_172864.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256614.

[34434] LOC282905 (Accession XP_212606.1) is another GAM281 target gene, herein designated TARGET GENE. LOC282905 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282905, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC282905 BINDING SITE, designated SEQ ID:986, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34435] Another function of GAM281 is therefore inhibition of LOC282905 (Accession XP_212606.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282905.

[34436] LOC282943 (Accession XP_212647.1) is another GAM281 target gene, herein designated TARGET GENE. LOC282943 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282943, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282943 BINDING SITE, designated SEQ ID:986, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34437] Another function of GAM281 is therefore inhibition of LOC282943 (Accession XP_212647.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC282943.

[34438] LOC282963 (Accession XP_210834.1) is another GAM281 target gene, herein designated TARGET GENE. LOC282963 BINDING SITE1 and LOC282963 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC282963, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282963 BINDING SITE1 and LOC282963 BINDING SITE2, designated SEQ ID:814 and SEQ ID:2675 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34439] Another function of GAM281 is therefore inhibition of LOC282963 (Accession XP_210834.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282963.

[34440] LOC282972 (Accession XP_210837.1) is another GAM281 target gene, herein designated TARGET GENE. LOC282972 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282972, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282972 BINDING SITE, designated SEQ ID:18172, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34441] Another function of GAM281 is therefore inhibition of LOC282972 (Accession XP_210837.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282972.

[34442] LOC282987 (Accession XP_210845.1) is another GAM281 target gene, herein designated TARGET GENE. LOC282987 BINDING SITE1 and LOC282987 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC282987, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282987 BINDING SITE1 and LOC282987 BINDING SITE2, designated SEQ ID:16541 and SEQ ID:12068 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34443] Another function of GAM281 is therefore inhibition of

LOC282987 (Accession XP_210845.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282987.

[34444] LOC282997 (Accession XP_208473.1) is another GAM281 target gene, herein designated TARGET GENE. LOC282997 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282997, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282997 BINDING SITE, designated SEQ ID:11798, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34445] Another function of GAM281 is therefore inhibition of LOC282997 (Accession XP_208473.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282997.

[34446] LOC283031 (Accession XP_210859.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283031 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283031, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283031 BINDING SITE, designated SEQ ID:6384, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34447] Another function of GAM281 is therefore inhibition of LOC283031 (Accession XP_210859.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283031.

[34448] LOC283035 (Accession XP_208488.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283035 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283035, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283035 BINDING SITE, designated SEQ ID:1940, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34449] Another function of GAM281 is therefore inhibition of LOC283035 (Accession XP_208488.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283035.

[34450] LOC283047 (Accession XP_210870.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283047 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283047, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283047 BINDING SITE, designated SEQ ID:17587, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34451] Another function of GAM281 is therefore inhibition of LOC283047 (Accession XP_210870.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283047.

[34452] LOC283061 (Accession XP_210875.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283061, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283061 BINDING SITE, designated SEQ ID:7252, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34453] Another function of GAM281 is therefore inhibition of LOC283061 (Accession XP_210875.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283061.

[34454] LOC283087 (Accession XP_208509.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283087 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283087, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283087 BINDING SITE, designated SEQ ID:4176, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34455] Another function of GAM281 is therefore inhibition of LOC283087 (Accession XP_208509.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283087.

[34456] LOC283089 (Accession XP_210885.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283089 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283089, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283089 BINDING SITE, designated SEQ ID:2219, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34457] Another function of GAM281 is therefore inhibition of LOC283089 (Accession XP_210885.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283089.

[34458] LOC283119 (Accession XP_210895.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283119 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283119, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC283119 BINDING SITE, designated SEQ ID:16397, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34459] Another function of GAM281 is therefore inhibition of LOC283119 (Accession XP_210895.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283119.

[34460] LOC283130 (Accession XP_208525.3) is another GAM281 target gene, herein designated TARGET GENE. LOC283130 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283130, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283130 BINDING SITE, designated SEQ ID:5323, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34461] Another function of GAM281 is therefore inhibition of LOC283130 (Accession XP_208525.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283130.

[34462] LOC283140 (Accession XP_210911.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283140 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283140 BINDING SITE, designated SEQ ID:12544, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34463] Another function of GAM281 is therefore inhibition of LOC283140 (Accession XP_210911.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283140.

[34464] LOC283143 (Accession XP_210920.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC283143 BINDING SITE, designated SEQ ID:2650, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34465] Another function of GAM281 is therefore inhibition of LOC283143 (Accession XP_210920.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283143.

[34466] LOC283152 (Accession XP_210917.2) is another GAM281 target gene, herein designated TARGET GENE. LOC283152 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283152, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283152 BINDING SITE, designated SEQ ID:19812, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34467] Another function of GAM281 is therefore inhibition of LOC283152 (Accession XP_210917.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283152.

[34468] LOC283170 (Accession XP_208535.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283170 BINDING SITE, designated SEQ ID:4979, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34469] Another function of GAM281 is therefore inhibition of LOC283170 (Accession XP_208535.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283170.

[34470] LOC283177 (Accession XP_210903.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283177 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283177 BINDING SITE, designated SEQ ID:15574, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34471] Another function of GAM281 is therefore inhibition of LOC283177 (Accession XP_210903.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283177.

[34472] LOC283215 (Accession XP_208555.2) is another GAM281 target gene, herein designated TARGET GENE. LOC283215 BINDING SITE1 and LOC283215 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283215, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283215 BINDING SITE1 and LOC283215 BINDING SITE2, designated SEQ ID:10112 and SEQ ID:8144 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34473] Another function of GAM281 is therefore inhibition of LOC283215 (Accession XP_208555.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283215.

[34474] LOC283241 (Accession NP_787089.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283241 BINDING SITE, designated SEQ ID:9525, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34475] Another function of GAM281 is therefore inhibition of LOC283241 (Accession NP_787089.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283241.

[34476] LOC283262 (Accession XP_210952.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283262 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC283262 BINDING SITE, designated SEQ ID:8223, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34477] Another function of GAM281 is therefore inhibition of LOC283262 (Accession XP_210952.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283262.

[34478] LOC283278 (Accession XP_210961.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283278 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283278, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283278 BINDING SITE, designated SEQ ID:9036, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34479] Another function of GAM281 is therefore inhibition of LOC283278 (Accession XP_210961.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283278.

[34480] LOC283293 (Accession XP_210962.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283293 BINDING SITE, designated SEQ ID:17952, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34481] Another function of GAM281 is therefore inhibition of LOC283293 (Accession XP_210962.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283293.

[34482] LOC283299 (Accession XP_210965.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283299 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283299, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283299 BINDING SITE, designated SEQ ID:9585, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34483] Another function of GAM281 is therefore inhibition of LOC283299 (Accession XP_210965.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283299.

[34484] LOC283329 (Accession XP_210978.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283329 BINDING SITE1 and LOC283329 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283329, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283329 BINDING SITE1 and LOC283329 BINDING SITE2, designated SEQ ID:2201 and SEQ ID:12183 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34485] Another function of GAM281 is therefore inhibition of LOC283329 (Accession XP_210978.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283329.

[34486] LOC283335 (Accession XP_210981.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283335 BINDING SITE1 and LOC283335 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283335, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283335 BINDING SITE1 and LOC283335 BINDING SITE2, designated SEQ ID:16144 and SEQ ID:2143 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34487] Another function of GAM281 is therefore inhibition of LOC283335 (Accession XP_210981.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283335.

[34488] LOC283377 (Accession XP_208647.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283377 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283377, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283377 BINDING SITE, designated SEQ ID:8232, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34489] Another function of GAM281 is therefore inhibition of LOC283377 (Accession XP_208647.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283377.

[34490] LOC283387 (Accession XP_211007.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283387 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283387, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283387 BINDING SITE, designated SEQ ID:7265, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34491] Another function of GAM281 is therefore inhibition of LOC283387 (Accession XP_211007.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283387.

[34492] LOC283394 (Accession XP_211021.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283394 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283394, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283394 BINDING SITE, designated SEQ ID:1730, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34493] Another function of GAM281 is therefore inhibition of LOC283394 (Accession XP_211021.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283394.

[34494] LOC283395 (Accession XP_211020.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283395 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283395, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC283395 BINDING SITE, designated SEQ ID:9003, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34495] Another function of GAM281 is therefore inhibition of LOC283395 (Accession XP_211020.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283395.

[34496] LOC283400 (Accession XP_211024.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283400 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283400 BINDING SITE, designated SEQ ID:19206, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34497] Another function of GAM281 is therefore inhibition of LOC283400 (Accession XP_211024.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283400.

[34498] LOC283432 (Accession XP_211032.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283432 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283432, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283432 BINDING SITE, designated SEQ ID:16658, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34499] Another function of GAM281 is therefore inhibition of LOC283432 (Accession XP_211032.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283432.

[34500] LOC283434 (Accession XP_211034.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283434 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283434, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC283434 BINDING SITE, designated SEQ ID:16366, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34501] Another function of GAM281 is therefore inhibition of LOC283434 (Accession XP_211034.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283434.

[34502] LOC283441 (Accession XP_211043.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283441 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283441, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283441 BINDING SITE, designated SEQ ID:2220, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34503] Another function of GAM281 is therefore inhibition of LOC283441 (Accession XP_211043.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283441.

[34504] LOC283442 (Accession XP_211037.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283442 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283442 BINDING SITE, designated SEQ ID:10032, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34505] Another function of GAM281 is therefore inhibition of LOC283442 (Accession XP_211037.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283442.

[34506] LOC283445 (Accession XP_211044.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283445 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283445 BINDING SITE, designated SEQ ID:5683, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34507] Another function of GAM281 is therefore inhibition of LOC283445 (Accession XP_211044.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283445.

[34508] LOC283452 (Accession XP_208679.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283452 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283452 BINDING SITE, designated SEQ ID:7397, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34509] Another function of GAM281 is therefore inhibition of LOC283452 (Accession XP_208679.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283452.

[34510] LOC283454 (Accession XP_211049.1) is another GAM281

target gene, herein designated TARGET GENE. LOC283454 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283454, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283454 BINDING SITE, designated SEQ ID:14861, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34511] Another function of GAM281 is therefore inhibition of LOC283454 (Accession XP_211049.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283454.

[34512] LOC283467 (Accession XP_211050.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283467 BINDING SITE, designated SEQ ID:13967, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34513] Another function of GAM281 is therefore inhibition of LOC283467 (Accession XP_211050.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283467.

[34514] LOC283475 (Accession XP_211056.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283475 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283475 BINDING SITE, designated SEQ ID:9892, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34515] Another function of GAM281 is therefore inhibition of LOC283475 (Accession XP_211056.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283475.

[34516] LOC283484 (Accession XP_211053.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283484

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283484, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283484 BINDING SITE, designated SEQ ID:17710, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34517] Another function of GAM281 is therefore inhibition of LOC283484 (Accession XP_211053.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283484.

[34518] LOC283487 (Accession XP_211062.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283487 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC283487, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283487 BINDING SITE, designated SEQ ID:7371, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[34519] Another function of GAM281 is therefore inhibition of LOC283487 (Accession XP_211062.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283487.

[34520] LOC283507 (Accession XP_211075.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283507 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283507 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34521] Another function of GAM281 is therefore inhibition of LOC283507 (Accession XP_211075.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283507.

[34522] LOC283520 (Accession XP_211071.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283520

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283520, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283520 BINDING SITE, designated SEQ ID:2025, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34523] Another function of GAM281 is therefore inhibition of LOC283520 (Accession XP_211071.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283520.

[34524] LOC283534 (Accession XP_211083.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283534 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283534, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283534 BINDING SITE, designated SEQ ID:3199, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34525] Another function of GAM281 is therefore inhibition of LOC283534 (Accession XP_211083.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283534.

[34526] LOC283566 (Accession XP_211114.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283566 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283566, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283566 BINDING SITE, designated SEQ ID:15869, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34527] Another function of GAM281 is therefore inhibition of LOC283566 (Accession XP_211114.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283566.

[34528] LOC283570 (Accession XP_211118.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283570 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC283570, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283570 BINDING SITE, designated SEQ ID:13652, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34529] Another function of GAM281 is therefore inhibition of LOC283570 (Accession XP_211118.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283570.

[34530] LOC283575 (Accession XP_211095.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283575 BINDING SITE1 and LOC283575 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283575, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283575 BINDING SITE1 and LOC283575 BINDING SITE2, designated SEQ ID:10067 and SEQ ID:6183 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[34531] Another function of GAM281 is therefore inhibition of LOC283575 (Accession XP_211095.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283575.

[34532] LOC283585 (Accession XP_294741.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283585 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283585, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283585 BINDING SITE, designated SEQ ID:10466, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34533] Another function of GAM281 is therefore inhibition of LOC283585 (Accession XP_294741.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283585.

[34534] LOC283588 (Accession NP_787093.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283588

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283588, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283588 BINDING SITE, designated SEQ ID:10638, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34535] Another function of GAM281 is therefore inhibition of LOC283588 (Accession NP_787093.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283588.

[34536] LOC283624 (Accession XP_211126.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283624 BINDING SITE1 and LOC283624 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283624, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283624 BINDING SITE1 and LOC283624 BINDING SITE2, designated SEQ ID:4420 and SEQ ID:15245 respectively, to the nucleotide se-

quence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34537] Another function of GAM281 is therefore inhibition of LOC283624 (Accession XP_211126.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283624.

[34538] LOC283637 (Accession XP_211134.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283637 BINDING SITE1 and LOC283637 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283637, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283637 BINDING SITE1 and LOC283637 BINDING SITE2, designated SEQ ID:3581 and SEQ ID:14859 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34539] Another function of GAM281 is therefore inhibition of LOC283637 (Accession XP_211134.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283637.

[34540] LOC283641 (Accession XP_208764.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283641 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283641, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283641 BINDING SITE, designated SEQ ID:17964, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34541] Another function of GAM281 is therefore inhibition of LOC283641 (Accession XP_208764.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283641.

[34542] LOC283663 (Accession XP_211147.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283663 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC283663 BINDING SITE, designated SEQ ID:16674, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34543] Another function of GAM281 is therefore inhibition of LOC283663 (Accession XP_211147.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283663.

[34544] LOC283664 (Accession XP_208773.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283664 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283664, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283664 BINDING SITE, designated SEQ ID:8450, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34545] Another function of GAM281 is therefore inhibition of LOC283664 (Accession XP_208773.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283664.

[34546] LOC283672 (Accession XP_211152.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283672 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283672, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283672 BINDING SITE, designated SEQ ID:1730, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34547] Another function of GAM281 is therefore inhibition of LOC283672 (Accession XP_211152.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283672.

[34548] LOC283687 (Accession NP_787094.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283687 BINDING SITE, designated SEQ ID:11904, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34549] Another function of GAM281 is therefore inhibition of LOC283687 (Accession NP_787094.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283687.

[34550] LOC283689 (Accession XP_211165.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283689 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283689, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283689 BINDING SITE, designated SEQ ID:3654, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34551] Another function of GAM281 is therefore inhibition of LOC283689 (Accession XP_211165.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283689.

[34552] LOC283693 (Accession XP_208788.1) is another GAM281

target gene, herein designated TARGET GENE. LOC283693 BINDING SITE1 and LOC283693 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283693, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283693 BINDING SITE1 and LOC283693 BINDING SITE2, designated SEQ ID:5305 and SEQ ID:16069 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34553] Another function of GAM281 is therefore inhibition of LOC283693 (Accession XP_208788.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283693.

[34554] LOC283701 (Accession XP_211170.3) is another GAM281 target gene, herein designated TARGET GENE. LOC283701 BINDING SITE1 and LOC283701 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283701, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC283701 BINDING SITE1 and LOC283701 BINDING SITE2, designated SEQ ID:13716 and SEQ ID:14381 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34555] Another function of GAM281 is therefore inhibition of LOC283701 (Accession XP_211170.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283701.

[34556] LOC283706 (Accession XP_208804.3) is another GAM281 target gene, herein designated TARGET GENE. LOC283706 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283706, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283706 BINDING SITE, designated SEQ ID:5985, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34557] Another function of GAM281 is therefore inhibition of LOC283706 (Accession XP_208804.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283706.

[34558] LOC283715 (Accession XP_208800.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283715 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283715, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283715 BINDING SITE, designated SEQ ID:15912, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34559] Another function of GAM281 is therefore inhibition of LOC283715 (Accession XP_208800.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283715.

[34560] LOC283741 (Accession XP_208115.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283741 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283741, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC283741 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34561] Another function of GAM281 is therefore inhibition of LOC283741 (Accession XP_208115.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283741.

[34562] LOC283767 (Accession XP_208835.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283767 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283767, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283767 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34563] Another function of GAM281 is therefore inhibition of LOC283767 (Accession XP_208835.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283767.

[34564] LOC283778 (Accession XP_211199.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283778 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283778, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283778 BINDING SITE, designated SEQ ID:4370, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34565] Another function of GAM281 is therefore inhibition of LOC283778 (Accession XP_211199.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283778.

[34566] LOC283779 (Accession XP_211198.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283779 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283779, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC283779 BINDING SITE, designated SEQ ID:17644, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34567] Another function of GAM281 is therefore inhibition of LOC283779 (Accession XP_211198.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283779.

[34568] LOC283801 (Accession XP_208122.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283801 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283801, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283801 BINDING SITE, designated SEQ ID:6265, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34569] Another function of GAM281 is therefore inhibition of LOC283801 (Accession XP_208122.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283801.

[34570] LOC283802 (Accession XP_208850.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283802 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283802, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283802 BINDING SITE, designated SEQ ID:16700, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34571] Another function of GAM281 is therefore inhibition of LOC283802 (Accession XP_208850.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283802.

[34572] LOC283810 (Accession XP_208853.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283810 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283810, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283810 BINDING SITE, designated SEQ ID:9395, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34573] Another function of GAM281 is therefore inhibition of LOC283810 (Accession XP_208853.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283810.

[34574] LOC283818 (Accession XP_211218.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283818 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283818 BINDING SITE, designated SEQ ID:9546, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34575] Another function of GAM281 is therefore inhibition of LOC283818 (Accession XP_211218.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283818.

[34576] LOC283851 (Accession XP_211229.1) is another GAM281

target gene, herein designated TARGET GENE. LOC283851 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283851, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283851 BINDING SITE, designated SEQ ID:4974, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34577] Another function of GAM281 is therefore inhibition of LOC283851 (Accession XP_211229.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283851.

[34578] LOC283856 (Accession XP_211233.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283856 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283856 BINDING SITE, designated SEQ ID:6184, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34579] Another function of GAM281 is therefore inhibition of LOC283856 (Accession XP_211233.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283856.

[34580] LOC283857 (Accession XP_211236.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283857 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283857, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283857 BINDING SITE, designated SEQ ID:10167, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34581] Another function of GAM281 is therefore inhibition of LOC283857 (Accession XP_211236.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283857.

[34582] LOC283861 (Accession NP_787095.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283861

BINDING SITE1 through LOC283861 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC283861, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283861 BINDING SITE1 through LOC283861 BINDING SITE3, designated SEQ ID:1635, SEQ ID:1401 and SEQ ID:7476 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34583] Another function of GAM281 is therefore inhibition of LOC283861 (Accession NP_787095.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283861.

[34584] LOC283863 (Accession XP_208875.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283863 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283863, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283863 BINDING SITE, designated SEQ ID:13285, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34585] Another function of GAM281 is therefore inhibition of LOC283863 (Accession XP_208875.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283863.

[34586] LOC283887 (Accession XP_211248.2) is another GAM281 target gene, herein designated TARGET GENE. LOC283887 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283887, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283887 BINDING SITE, designated SEQ ID:18993, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34587] Another function of GAM281 is therefore inhibition of LOC283887 (Accession XP_211248.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283887.

[34588] LOC283888 (Accession XP_211249.1) is another GAM281

target gene, herein designated TARGET GENE. LOC283888 BINDING SITE1 and LOC283888 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283888, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283888 BINDING SITE1 and LOC283888 BINDING SITE2, designated SEQ ID:11072 and SEQ ID:14104 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34589] Another function of GAM281 is therefore inhibition of LOC283888 (Accession XP_211249.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283888.

[34590] LOC283889 (Accession XP_208899.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283889 BINDING SITE1 and LOC283889 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283889, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC283889 BINDING SITE1 and LOC283889 BINDING SITE2, designated SEQ ID:5525 and SEQ ID:3899 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34591] Another function of GAM281 is therefore inhibition of LOC283889 (Accession XP_208899.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283889.

[34592] LOC283894 (Accession XP_211250.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283894 BINDING SITE, designated SEQ ID:7156, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34593] Another function of GAM281 is therefore inhibition of LOC283894 (Accession XP_211250.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283894.

[34594] LOC283909 (Accession XP_211256.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283909 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283909, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283909 BINDING SITE, designated SEQ ID:7156, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34595] Another function of GAM281 is therefore inhibition of LOC283909 (Accession XP_211256.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283909.

[34596] LOC283928 (Accession XP_208909.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283928 BINDING SITE1 through LOC283928 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC283928, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283928 BINDING SITE1 through LOC283928 BINDING SITE3, designated SEQ ID:20101, SEQ ID:4703 and SEQ ID:11501 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34597] Another function of GAM281 is therefore inhibition of LOC283928 (Accession XP_208909.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283928.

[34598] LOC283929 (Accession XP_208905.2) is another GAM281 target gene, herein designated TARGET GENE. LOC283929 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283929, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283929 BINDING SITE, designated SEQ ID:15775, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34599] Another function of GAM281 is therefore inhibition of LOC283929 (Accession XP_208905.2) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283929.

[34600] LOC283954 (Accession XP_208931.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283954 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283954, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283954 BINDING SITE, designated SEQ ID:10461, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34601] Another function of GAM281 is therefore inhibition of LOC283954 (Accession XP_208931.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283954.

[34602] LOC283964 (Accession XP_208145.2) is another GAM281 target gene, herein designated TARGET GENE. LOC283964 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283964, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283964 BINDING SITE, designated SEQ ID:19569, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34603] Another function of GAM281 is therefore inhibition of LOC283964 (Accession XP_208145.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283964.

[34604] LOC283983 (Accession XP_211289.1) is another GAM281 target gene, herein designated TARGET GENE. LOC283983 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283983, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283983 BINDING SITE, designated SEQ ID:4650, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34605] Another function of GAM281 is therefore inhibition of LOC283983 (Accession XP_211289.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283983.

[34606] LOC284001 (Accession XP_208958.2) is another GAM281 target gene, herein designated TARGET GENE. LOC284001 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284001 BINDING SITE, designated SEQ ID:18161, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34607] Another function of GAM281 is therefore inhibition of LOC284001 (Accession XP_208958.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284001.

[34608] LOC284016 (Accession XP_211298.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284016 BINDING SITE1 and LOC284016 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284016, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284016 BINDING SITE1 and LOC284016 BINDING SITE2, designated SEQ ID:3244 and SEQ ID:17923 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34609] Another function of GAM281 is therefore inhibition of LOC284016 (Accession XP_211298.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284016.

[34610] LOC284017 (Accession XP_208961.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284017 BINDING SITE, designated SEQ ID:18610, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34611] Another function of GAM281 is therefore inhibition of LOC284017 (Accession XP_208961.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284017.

[34612] LOC284019 (Accession XP_211302.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284019 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284019, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284019 BINDING SITE, designated SEQ ID:10124, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34613] Another function of GAM281 is therefore inhibition of LOC284019 (Accession XP_211302.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284019.

[34614] LOC284023 (Accession XP_208983.3) is another GAM281 target gene, herein designated TARGET GENE. LOC284023 BINDING SITE1 and LOC284023 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284023, corresponding to target binding

sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284023 BINDING SITE1 and LOC284023 BINDING SITE2, designated SEQ ID:14597 and SEQ ID:17953 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34615] Another function of GAM281 is therefore inhibition of LOC284023 (Accession XP_208983.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284023.

[34616] LOC284048 (Accession XP_208152.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284048 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284048, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284048 BINDING SITE, designated SEQ ID:10847, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34617] Another function of GAM281 is therefore inhibition of

LOC284048 (Accession XP_208152.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284048.

[34618] LOC284063 (Accession XP_208992.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284063 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284063, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284063 BINDING SITE, designated SEQ ID:6213, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34619] Another function of GAM281 is therefore inhibition of LOC284063 (Accession XP_208992.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284063.

[34620] LOC284074 (Accession XP_211321.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284074 BINDING SITE1 and LOC284074 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by LOC284074, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284074 BINDING SITE1 and LOC284074 BINDING SITE2, designated SEQ ID:1596 and SEQ ID:15531 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34621] Another function of GAM281 is therefore inhibition of LOC284074 (Accession XP_211321.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284074.

[34622] LOC284082 (Accession XP_211323.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284082 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284082, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284082 BINDING SITE, designated SEQ ID:18527, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34623] Another function of GAM281 is therefore inhibition of LOC284082 (Accession XP_211323.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284082.

[34624] LOC284095 (Accession XP_211324.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284095 BINDING SITE1 through LOC284095 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284095, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284095 BINDING SITE1 through LOC284095 BINDING SITE3, designated SEQ ID:7333, SEQ ID:11799 and SEQ ID:15513 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34625] Another function of GAM281 is therefore inhibition of LOC284095 (Accession XP_211324.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284095.

[34626] LOC284098 (Accession XP_209008.3) is another GAM281

target gene, herein designated TARGET GENE. LOC284098 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284098, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284098 BINDING SITE, designated SEQ ID:8582, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34627] Another function of GAM281 is therefore inhibition of LOC284098 (Accession XP_209008.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284098.

[34628] LOC284100 (Accession XP_209015.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284100 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284100, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284100 BINDING SITE, designated SEQ ID:1777, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34629] Another function of GAM281 is therefore inhibition of LOC284100 (Accession XP_209015.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284100.

[34630] LOC284101 (Accession XP_209019.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284101 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284101 BINDING SITE, designated SEQ ID:19537, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34631] Another function of GAM281 is therefore inhibition of LOC284101 (Accession XP_209019.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284101.

[34632] LOC284102 (Accession XP_211327.3) is another GAM281 target gene, herein designated TARGET GENE. LOC284102

BINDING SITE1 through LOC284102 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284102, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284102 BINDING SITE1 through LOC284102 BINDING SITE3, designated SEQ ID:18149, SEQ ID:3233 and SEQ ID:7745 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34633] Another function of GAM281 is therefore inhibition of LOC284102 (Accession XP_211327.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284102.

[34634] LOC284117 (Accession XP_209024.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284117 BINDING SITE, designated SEQ ID:3725, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34635] Another function of GAM281 is therefore inhibition of LOC284117 (Accession XP_209024.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284117.

[34636] LOC284128 (Accession XP_211342.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284128 BINDING SITE1 and LOC284128 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284128, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284128 BINDING SITE1 and LOC284128 BINDING SITE2, designated SEQ ID:17271 and SEQ ID:1966 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34637] Another function of GAM281 is therefore inhibition of LOC284128 (Accession XP_211342.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284128.

[34638] LOC284135 (Accession XP_209032.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284135 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284135 BINDING SITE, designated SEQ ID:12779, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34639] Another function of GAM281 is therefore inhibition of LOC284135 (Accession XP_209032.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284135.

[34640] LOC284145 (Accession XP_211353.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284145 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284145, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC284145 BINDING SITE, designated SEQ ID:4102, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34641] Another function of GAM281 is therefore inhibition of LOC284145 (Accession XP_211353.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284145.

[34642] LOC284171 (Accession XP_209051.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284171 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284171, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284171 BINDING SITE, designated SEQ ID:11530, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34643] Another function of GAM281 is therefore inhibition of LOC284171 (Accession XP_209051.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284171.

[34644] LOC284183 (Accession XP_209059.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284183 BINDING SITE1 and LOC284183 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284183, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284183 BINDING SITE1 and LOC284183 BINDING SITE2, designated SEQ ID:1111 and SEQ ID:9456 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34645] Another function of GAM281 is therefore inhibition of LOC284183 (Accession XP_209059.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284183.

[34646] LOC284186 (Accession XP_209060.2) is another GAM281 target gene, herein designated TARGET GENE. LOC284186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC284186 BINDING SITE, designated SEQ ID:14861, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34647] Another function of GAM281 is therefore inhibition of LOC284186 (Accession XP_209060.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284186.

[34648] LOC284245 (Accession XP_211397.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284245 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284245, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284245 BINDING SITE, designated SEQ ID:8707, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34649] Another function of GAM281 is therefore inhibition of LOC284245 (Accession XP_211397.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284245.

[34650] LOC284267 (Accession XP_211411.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284267 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284267, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284267 BINDING SITE, designated SEQ ID:8494, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34651] Another function of GAM281 is therefore inhibition of LOC284267 (Accession XP_211411.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284267.

[34652] LOC284276 (Accession XP_211412.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284276 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284276, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC284276 BINDING SITE, designated SEQ ID:1026, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34653] Another function of GAM281 is therefore inhibition of LOC284276 (Accession XP_211412.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284276.

[34654] LOC284286 (Accession XP_211419.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284286 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284286, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284286 BINDING SITE, designated SEQ ID:19875, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34655] Another function of GAM281 is therefore inhibition of LOC284286 (Accession XP_211419.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284286.

[34656] LOC284289 (Accession XP_209105.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284289 BINDING SITE, designated SEQ ID:1885, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34657] Another function of GAM281 is therefore inhibition of LOC284289 (Accession XP_209105.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284289.

[34658] LOC284304 (Accession XP_211426.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284304 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284304, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284304 BINDING SITE, designated SEQ ID:4849, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34659] Another function of GAM281 is therefore inhibition of LOC284304 (Accession XP_211426.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284304.

[34660] LOC284305 (Accession XP_211425.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284305 BINDING SITE1 and LOC284305 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284305, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284305 BINDING SITE1 and LOC284305 BINDING SITE2, designated SEQ ID:2477 and SEQ ID:3802 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34661] Another function of GAM281 is therefore inhibition of LOC284305 (Accession XP_211425.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284305.

[34662] LOC284317 (Accession XP_209162.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284317 BINDING SITE1 and LOC284317 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284317, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284317 BINDING SITE1 and LOC284317 BINDING SITE2, designated SEQ ID:7077 and SEQ ID:3386 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34663] Another function of GAM281 is therefore inhibition of LOC284317 (Accession XP_209162.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284317.

[34664] LOC284321 (Accession XP_211432.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284321 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284321, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284321 BINDING SITE, designated SEQ ID:11129, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34665] Another function of GAM281 is therefore inhibition of LOC284321 (Accession XP_211432.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284321.

[34666] LOC284325 (Accession XP_209143.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284325 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284325, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284325 BINDING SITE, designated SEQ ID:1731, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34667] Another function of GAM281 is therefore inhibition of LOC284325 (Accession XP_209143.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284325.

[34668] LOC284356 (Accession XP_211437.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284356 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284356 BINDING SITE, designated SEQ ID:11986, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34669] Another function of GAM281 is therefore inhibition of LOC284356 (Accession XP_211437.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284356.

[34670] LOC284362 (Accession XP_211435.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284362 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC284362, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284362 BINDING SITE, designated SEQ ID:18898, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34671] Another function of GAM281 is therefore inhibition of LOC284362 (Accession XP_211435.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284362.

[34672] LOC284375 (Accession XP_209154.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284375 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284375, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284375 BINDING SITE, designated SEQ ID:16701, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34673] Another function of GAM281 is therefore inhibition of

LOC284375 (Accession XP_209154.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284375.

[34674] LOC284376 (Accession XP_209157.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284376 BINDING SITE1 and LOC284376 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284376, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284376 BINDING SITE1 and LOC284376 BINDING SITE2, designated SEQ ID:19718 and SEQ ID:981 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34675] Another function of GAM281 is therefore inhibition of LOC284376 (Accession XP_209157.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284376.

[34676] LOC284379 (Accession XP_209163.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284379

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284379, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284379 BINDING SITE, designated SEQ ID:9312, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34677] Another function of GAM281 is therefore inhibition of LOC284379 (Accession XP_209163.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284379.

[34678] LOC284396 (Accession XP_211452.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284396 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284396, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284396 BINDING SITE, designated SEQ ID:10399, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34679] Another function of GAM281 is therefore inhibition of LOC284396 (Accession XP_211452.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284396.

[34680] LOC284405 (Accession XP_209183.2) is another GAM281 target gene, herein designated TARGET GENE. LOC284405 BINDING SITE1 and LOC284405 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284405, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284405 BINDING SITE1 and LOC284405 BINDING SITE2, designated SEQ ID:2645 and SEQ ID:19462 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34681] Another function of GAM281 is therefore inhibition of LOC284405 (Accession XP_209183.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284405.

[34682] LOC284408 (Accession XP_211443.1) is another GAM281

target gene, herein designated TARGET GENE. LOC284408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284408 BINDING SITE, designated SEQ ID:14364, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34683] Another function of GAM281 is therefore inhibition of LOC284408 (Accession XP_211443.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284408.

[34684] LOC284410 (Accession XP_211449.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284410 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284410, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284410 BINDING SITE, designated SEQ ID:17304, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34685] Another function of GAM281 is therefore inhibition of LOC284410 (Accession XP_211449.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284410.

[34686] LOC284421 (Accession XP_209200.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284421 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284421, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284421 BINDING SITE, designated SEQ ID:4533, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34687] Another function of GAM281 is therefore inhibition of LOC284421 (Accession XP_209200.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284421.

[34688] LOC284426 (Accession XP_209198.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284426

BINDING SITE1 and LOC284426 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284426, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284426 BINDING SITE1 and LOC284426 BINDING SITE2, designated SEQ ID:4975 and SEQ ID:5357 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34689] Another function of GAM281 is therefore inhibition of LOC284426 (Accession XP_209198.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284426.

[34690] LOC284436 (Accession XP_290862.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284436 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284436 BINDING SITE, designated SEQ ID:16193, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34691] Another function of GAM281 is therefore inhibition of LOC284436 (Accession XP_290862.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284436.

[34692] LOC284439 (Accession XP_209204.2) is another GAM281 target gene, herein designated TARGET GENE. LOC284439 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284439, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284439 BINDING SITE, designated SEQ ID:3825, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34693] Another function of GAM281 is therefore inhibition of LOC284439 (Accession XP_209204.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284439.

[34694] LOC284440 (Accession XP_209210.1) is another GAM281

target gene, herein designated TARGET GENE. LOC284440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284440 BINDING SITE, designated SEQ ID:8752, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34695] Another function of GAM281 is therefore inhibition of LOC284440 (Accession XP_209210.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284440.

[34696] LOC284454 (Accession XP_209216.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284454 BINDING SITE1 through LOC284454 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284454, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284454 BINDING SITE1 through LOC284454 BINDING SITE3, des-

ignated SEQ ID:16031, SEQ ID:17976 and SEQ ID:3999 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34697] Another function of GAM281 is therefore inhibition of LOC284454 (Accession XP_209216.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284454.

[34698] LOC284456 (Accession XP_211470.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284456 BINDING SITE1 and LOC284456 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284456, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284456 BINDING SITE1 and LOC284456 BINDING SITE2, designated SEQ ID:10621 and SEQ ID:18777 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34699] Another function of GAM281 is therefore inhibition of LOC284456 (Accession XP_211470.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284456.

[34700] LOC284459 (Accession XP_290826.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284459 BINDING SITE, designated SEQ ID:10211, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34701] Another function of GAM281 is therefore inhibition of LOC284459 (Accession XP_290826.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284459.

[34702] LOC284471 (Accession XP_209225.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284471 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284471, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC284471 BINDING SITE, designated SEQ ID:19286, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34703] Another function of GAM281 is therefore inhibition of LOC284471 (Accession XP_209225.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284471.

[34704] LOC284495 (Accession XP_302752.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284495 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284495, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284495 BINDING SITE, designated SEQ ID:12538, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34705] Another function of GAM281 is therefore inhibition of LOC284495 (Accession XP_302752.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284495.

[34706] LOC284512 (Accession XP_211500.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284512 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284512, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284512 BINDING SITE, designated SEQ ID:14119, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34707] Another function of GAM281 is therefore inhibition of LOC284512 (Accession XP_211500.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284512.

[34708] LOC284513 (Accession XP_211502.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284513 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284513, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC284513 BINDING SITE, designated SEQ ID:18865, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34709] Another function of GAM281 is therefore inhibition of LOC284513 (Accession XP_211502.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284513.

[34710] LOC284514 (Accession XP_209244.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284514 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284514, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284514 BINDING SITE, designated SEQ ID:4125, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34711] Another function of GAM281 is therefore inhibition of LOC284514 (Accession XP_209244.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284514.

[34712] LOC284549 (Accession XP_211514.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284549 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284549, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284549 BINDING SITE, designated SEQ ID:19112, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34713] Another function of GAM281 is therefore inhibition of LOC284549 (Accession XP_211514.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284549.

[34714] LOC284551 (Accession XP_211515.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284551 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284551, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284551 BINDING SITE, designated SEQ ID:9493, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34715] Another function of GAM281 is therefore inhibition of LOC284551 (Accession XP_211515.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284551.

[34716] LOC284568 (Accession XP_209263.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284568 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284568, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284568 BINDING SITE, designated SEQ ID:3996, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34717] Another function of GAM281 is therefore inhibition of LOC284568 (Accession XP_209263.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284568.

[34718] LOC284577 (Accession XP_211522.1) is another GAM281

target gene, herein designated TARGET GENE. LOC284577 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284577, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284577 BINDING SITE, designated SEQ ID:19533, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34719] Another function of GAM281 is therefore inhibition of LOC284577 (Accession XP_211522.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284577.

[34720] LOC284587 (Accession XP_209278.3) is another GAM281 target gene, herein designated TARGET GENE. LOC284587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284587 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34721] Another function of GAM281 is therefore inhibition of LOC284587 (Accession XP_209278.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284587.

[34722] LOC284606 (Accession XP_211543.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284606 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284606, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284606 BINDING SITE, designated SEQ ID:2771, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34723] Another function of GAM281 is therefore inhibition of LOC284606 (Accession XP_211543.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284606.

[34724] LOC284611 (Accession XP_211552.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284611

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284611, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284611 BINDING SITE, designated SEQ ID:12497, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34725] Another function of GAM281 is therefore inhibition of LOC284611 (Accession XP_211552.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284611.

[34726] LOC284628 (Accession XP_211561.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284628 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284628, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284628 BINDING SITE, designated SEQ ID:18882, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34727] Another function of GAM281 is therefore inhibition of LOC284628 (Accession XP_211561.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284628.

[34728] LOC284630 (Accession XP_211562.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284630 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284630, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284630 BINDING SITE, designated SEQ ID:8272, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34729] Another function of GAM281 is therefore inhibition of LOC284630 (Accession XP_211562.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284630.

[34730] LOC284663 (Accession XP_209310.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284663 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC284663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284663 BINDING SITE, designated SEQ ID:5249, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34731] Another function of GAM281 is therefore inhibition of LOC284663 (Accession XP_209310.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284663.

[34732] LOC284675 (Accession XP_209319.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284675 BINDING SITE1 through LOC284675 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284675, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284675 BINDING SITE1 through LOC284675 BINDING SITE3, designated SEQ ID:5250, SEQ ID:2389 and SEQ ID:501 respectively, to the nucleotide sequence of GAM281 RNA,

herein designated GAM RNA, also designated SEQ ID:278.

[34733] Another function of GAM281 is therefore inhibition of LOC284675 (Accession XP_209319.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284675.

[34734] LOC284701 (Accession XP_294994.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284701 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284701, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284701 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34735] Another function of GAM281 is therefore inhibition of LOC284701 (Accession XP_294994.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284701.

[34736] LOC284708 (Accession XP_209332.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284708

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284708 BINDING SITE, designated SEQ ID:5153, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34737] Another function of GAM281 is therefore inhibition of LOC284708 (Accession XP_209332.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284708.

[34738] LOC284723 (Accession XP_211602.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284723 BINDING SITE1 and LOC284723 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284723, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284723 BINDING SITE1 and LOC284723 BINDING SITE2, designated SEQ ID:6498 and SEQ ID:3182 respectively, to the nucleotide sequence

of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34739] Another function of GAM281 is therefore inhibition of LOC284723 (Accession XP_211602.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284723.

[34740] LOC284754 (Accession XP_211627.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284754 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284754, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284754 BINDING SITE, designated SEQ ID:10930, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34741] Another function of GAM281 is therefore inhibition of LOC284754 (Accession XP_211627.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284754.

[34742] LOC284805 (Accession XP_209371.1) is another GAM281

target gene, herein designated TARGET GENE. LOC284805 BINDING SITE1 through LOC284805 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284805, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284805 BINDING SITE1 through LOC284805 BINDING SITE3, designated SEQ ID:1544, SEQ ID:8046 and SEQ ID:853 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34743] Another function of GAM281 is therefore inhibition of LOC284805 (Accession XP_209371.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284805.

[34744] LOC284839 (Accession XP_211661.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284839 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284839, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC284839 BINDING SITE, designated SEQ ID:19401, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34745] Another function of GAM281 is therefore inhibition of LOC284839 (Accession XP_211661.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284839.

[34746] LOC284853 (Accession XP_209383.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284853 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284853, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284853 BINDING SITE, designated SEQ ID:3582, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34747] Another function of GAM281 is therefore inhibition of LOC284853 (Accession XP_209383.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284853.

[34748] LOC284856 (Accession XP_211668.2) is another GAM281 target gene, herein designated TARGET GENE. LOC284856 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC284856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284856 BINDING SITE, designated SEQ ID:12736, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34749] Another function of GAM281 is therefore inhibition of LOC284856 (Accession XP_211668.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284856.

[34750] LOC284856 (Accession XP_302835.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284856 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC284856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of LOC284856 BINDING SITE, designated SEQ ID:12736, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34751] Another function of GAM281 is therefore inhibition of LOC284856 (Accession XP_302835.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284856.

[34752] LOC284865 (Accession XP_211672.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284865 BINDING SITE, designated SEQ ID:1645, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34753] Another function of GAM281 is therefore inhibition of LOC284865 (Accession XP_211672.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284865.

[34754] LOC284874 (Accession XP_209394.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284874 BINDING SITE1 and LOC284874 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284874, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284874 BINDING SITE1 and LOC284874 BINDING SITE2, designated SEQ ID:16244 and SEQ ID:3846 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34755] Another function of GAM281 is therefore inhibition of LOC284874 (Accession XP_209394.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284874.

[34756] LOC284934 (Accession XP_211696.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284934 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284934, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284934 BINDING SITE, designated SEQ ID:14894, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34757] Another function of GAM281 is therefore inhibition of LOC284934 (Accession XP_211696.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284934.

[34758] LOC284950 (Accession XP_211703.1) is another GAM281 target gene, herein designated TARGET GENE. LOC284950 BINDING SITE1 and LOC284950 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284950, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284950 BINDING SITE1 and LOC284950 BINDING SITE2, designated SEQ ID:4025 and SEQ ID:17553 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34759] Another function of GAM281 is therefore inhibition of

LOC284950 (Accession XP_211703.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284950.

[34760] LOC285002 (Accession XP_211731.2) is another GAM281 target gene, herein designated TARGET GENE. LOC285002 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285002, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285002 BINDING SITE, designated SEQ ID:3500, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34761] Another function of GAM281 is therefore inhibition of LOC285002 (Accession XP_211731.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285002.

[34762] LOC285026 (Accession XP_209440.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285026 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285026, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285026 BINDING SITE, designated SEQ ID:17523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34763] Another function of GAM281 is therefore inhibition of LOC285026 (Accession XP_209440.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285026.

[34764] LOC285036 (Accession XP_210798.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285036 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285036, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285036 BINDING SITE, designated SEQ ID:13688, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34765] Another function of GAM281 is therefore inhibition of LOC285036 (Accession XP_210798.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285036.

[34766] LOC285052 (Accession XP_211751.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285052 BINDING SITE, designated SEQ ID:2174, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34767] Another function of GAM281 is therefore inhibition of LOC285052 (Accession XP_211751.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285052.

[34768] LOC285058 (Accession XP_211753.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285058 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285058, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285058 BINDING SITE, designated SEQ ID:20023, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34769] Another function of GAM281 is therefore inhibition of LOC285058 (Accession XP_211753.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285058.

[34770] LOC285083 (Accession XP_209464.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285083 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285083, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285083 BINDING SITE, designated SEQ ID:5667, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34771] Another function of GAM281 is therefore inhibition of LOC285083 (Accession XP_209464.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285083.

[34772] LOC285088 (Accession XP_209465.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285088 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285088, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285088 BINDING SITE, designated SEQ ID:6092, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34773] Another function of GAM281 is therefore inhibition of LOC285088 (Accession XP_209465.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285088.

[34774] LOC285123 (Accession XP_211773.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285123 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC285123 BINDING SITE, designated SEQ ID:17113, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34775] Another function of GAM281 is therefore inhibition of LOC285123 (Accession XP_211773.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285123.

[34776] LOC285127 (Accession XP_211771.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285127 BINDING SITE1 and LOC285127 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285127, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285127 BINDING SITE1 and LOC285127 BINDING SITE2, designated SEQ ID:5921 and SEQ ID:11528 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34777] Another function of GAM281 is therefore inhibition of LOC285127 (Accession XP_211771.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285127.

[34778] LOC285166 (Accession XP_211791.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285166 BINDING SITE1 and LOC285166 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285166, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285166 BINDING SITE1 and LOC285166 BINDING SITE2, designated SEQ ID:4283 and SEQ ID:19378 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34779] Another function of GAM281 is therefore inhibition of LOC285166 (Accession XP_211791.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285166.

[34780] LOC285176 (Accession XP_209500.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285176 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC285176, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285176 BINDING SITE, designated SEQ ID:7860, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34781] Another function of GAM281 is therefore inhibition of LOC285176 (Accession XP_209500.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285176.

[34782] LOC285193 (Accession XP_209509.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285193, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285193 BINDING SITE, designated SEQ ID:1745, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34783] Another function of GAM281 is therefore inhibition of

LOC285193 (Accession XP_209509.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285193.

[34784] LOC285221 (Accession XP_209521.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285221 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285221, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285221 BINDING SITE, designated SEQ ID:13597, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34785] Another function of GAM281 is therefore inhibition of LOC285221 (Accession XP_209521.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285221.

[34786] LOC285231 (Accession XP_211813.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285231 BINDING SITE1 and LOC285231 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by LOC285231, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285231 BINDING SITE1 and LOC285231 BINDING SITE2, designated SEQ ID:8001 and SEQ ID:15366 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34787] Another function of GAM281 is therefore inhibition of LOC285231 (Accession XP_211813.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285231.

[34788] LOC285231 (Accession XP_211813.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285231 BINDING SITE1 and LOC285231 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285231, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285231 BINDING SITE1 and LOC285231 BINDING SITE2, designated SEQ ID:8001 and SEQ ID:5012 respectively, to the nucleotide sequence

of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34789] Another function of GAM281 is therefore inhibition of LOC285231 (Accession XP_211813.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285231.

[34790] LOC285281 (Accession XP_211829.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285281 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285281, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285281 BINDING SITE, designated SEQ ID:15575, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34791] Another function of GAM281 is therefore inhibition of LOC285281 (Accession XP_211829.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285281.

[34792] LOC285299 (Accession XP_209554.1) is another GAM281

target gene, herein designated TARGET GENE. LOC285299 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285299, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285299 BINDING SITE, designated SEQ ID:9374, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34793] Another function of GAM281 is therefore inhibition of LOC285299 (Accession XP_209554.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285299.

[34794] LOC285334 (Accession XP_211844.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285334 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285334 BINDING SITE, designated SEQ ID:1027, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34795] Another function of GAM281 is therefore inhibition of LOC285334 (Accession XP_211844.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285334.

[34796] LOC285345 (Accession XP_211854.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285345 BINDING SITE1 and LOC285345 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285345, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285345 BINDING SITE1 and LOC285345 BINDING SITE2, designated SEQ ID:18883 and SEQ ID:556 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34797] Another function of GAM281 is therefore inhibition of LOC285345 (Accession XP_211854.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285345.

[34798] LOC285366 (Accession XP_209581.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285366 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285366, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285366 BINDING SITE, designated SEQ ID:6117, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34799] Another function of GAM281 is therefore inhibition of LOC285366 (Accession XP_209581.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285366.

[34800] LOC285369 (Accession XP_211861.3) is another GAM281 target gene, herein designated TARGET GENE. LOC285369 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285369, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285369 BINDING SITE, designated SEQ ID:10352, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34801] Another function of GAM281 is therefore inhibition of LOC285369 (Accession XP_211861.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285369.

[34802] LOC285389 (Accession XP_211873.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285389 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285389, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285389 BINDING SITE, designated SEQ ID:19692, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34803] Another function of GAM281 is therefore inhibition of LOC285389 (Accession XP_211873.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285389.

[34804] LOC285392 (Accession XP_211879.1) is another GAM281

target gene, herein designated TARGET GENE. LOC285392 BINDING SITE1 and LOC285392 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285392, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285392 BINDING SITE1 and LOC285392 BINDING SITE2, designated SEQ ID:9688 and SEQ ID:17969 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34805] Another function of GAM281 is therefore inhibition of LOC285392 (Accession XP_211879.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285392.

[34806] LOC285398 (Accession XP_209593.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285398 BINDING SITE1 and LOC285398 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285398, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC285398 BINDING SITE1 and LOC285398 BINDING SITE2, designated SEQ ID:13286 and SEQ ID:4655 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34807] Another function of GAM281 is therefore inhibition of LOC285398 (Accession XP_209593.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285398.

[34808] LOC285429 (Accession XP_209607.3) is another GAM281 target gene, herein designated TARGET GENE. LOC285429 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285429, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285429 BINDING SITE, designated SEQ ID:4171, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34809] Another function of GAM281 is therefore inhibition of LOC285429 (Accession XP_209607.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285429.

[34810] LOC285488 (Accession XP_211914.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285488 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285488, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285488 BINDING SITE, designated SEQ ID:13804, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34811] Another function of GAM281 is therefore inhibition of LOC285488 (Accession XP_211914.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285488.

[34812] LOC285491 (Accession XP_211917.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285491 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285491, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC285491 BINDING SITE, designated SEQ ID:11239, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34813] Another function of GAM281 is therefore inhibition of LOC285491 (Accession XP_211917.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285491.

[34814] LOC285509 (Accession XP_211923.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285509 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285509, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285509 BINDING SITE, designated SEQ ID:3519, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34815] Another function of GAM281 is therefore inhibition of LOC285509 (Accession XP_211923.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285509.

[34816] LOC285540 (Accession XP_209654.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285540 BINDING SITE1 and LOC285540 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285540, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285540 BINDING SITE1 and LOC285540 BINDING SITE2, designated SEQ ID:9543 and SEQ ID:6961 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34817] Another function of GAM281 is therefore inhibition of LOC285540 (Accession XP_209654.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285540.

[34818] LOC285560 (Accession XP_209660.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285560 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285560, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285560 BINDING SITE, designated SEQ ID:8718, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34819] Another function of GAM281 is therefore inhibition of LOC285560 (Accession XP_209660.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285560.

[34820] LOC285577 (Accession XP_211941.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285577 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285577, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285577 BINDING SITE, designated SEQ ID:4455, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34821] Another function of GAM281 is therefore inhibition of LOC285577 (Accession XP_211941.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285577.

[34822] LOC285589 (Accession XP_209671.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285589 BINDING SITE1 and LOC285589 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285589, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285589 BINDING SITE1 and LOC285589 BINDING SITE2, designated SEQ ID:12804 and SEQ ID:17087 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34823] Another function of GAM281 is therefore inhibition of LOC285589 (Accession XP_209671.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285589.

[34824] LOC285626 (Accession XP_211959.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285626 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285626, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285626 BINDING SITE, designated SEQ ID:13843, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34825] Another function of GAM281 is therefore inhibition of LOC285626 (Accession XP_211959.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285626.

[34826] LOC285633 (Accession XP_211965.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285633 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285633, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285633 BINDING SITE, designated SEQ ID:12452, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34827] Another function of GAM281 is therefore inhibition of LOC285633 (Accession XP_211965.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285633.

[34828] LOC285638 (Accession XP_209693.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285638 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285638, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285638 BINDING SITE, designated SEQ ID:4949, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34829] Another function of GAM281 is therefore inhibition of LOC285638 (Accession XP_209693.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285638.

[34830] LOC285679 (Accession XP_209719.2) is another GAM281 target gene, herein designated TARGET GENE. LOC285679 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285679, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285679 BINDING SITE, designated SEQ ID:19299, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34831] Another function of GAM281 is therefore inhibition of LOC285679 (Accession XP_209719.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285679.

[34832] LOC285683 (Accession XP_211980.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285683 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285683, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285683 BINDING SITE, designated SEQ ID:959, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34833] Another function of GAM281 is therefore inhibition of LOC285683 (Accession XP_211980.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285683.

[34834] LOC285689 (Accession XP_209724.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285689 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285689, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285689 BINDING SITE, designated SEQ ID:17726, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34835] Another function of GAM281 is therefore inhibition of LOC285689 (Accession XP_209724.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285689.

[34836] LOC285693 (Accession XP_211981.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285693 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285693, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC285693 BINDING SITE, designated SEQ ID:16940, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34837] Another function of GAM281 is therefore inhibition of LOC285693 (Accession XP_211981.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285693.

[34838] LOC285713 (Accession XP_211992.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285713 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285713, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285713 BINDING SITE, designated SEQ ID:3414, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34839] Another function of GAM281 is therefore inhibition of LOC285713 (Accession XP_211992.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285713.

[34840] LOC285722 (Accession XP_211997.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285722 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285722, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285722 BINDING SITE, designated SEQ ID:18012, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34841] Another function of GAM281 is therefore inhibition of LOC285722 (Accession XP_211997.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285722.

[34842] LOC285744 (Accession XP_209743.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285744 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285744, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC285744 BINDING SITE, designated SEQ ID:11141, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34843] Another function of GAM281 is therefore inhibition of LOC285744 (Accession XP_209743.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285744.

[34844] LOC285747 (Accession XP_209742.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285747 BINDING SITE1 and LOC285747 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285747, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285747 BINDING SITE1 and LOC285747 BINDING SITE2, designated SEQ ID:11528 and SEQ ID:7537 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34845] Another function of GAM281 is therefore inhibition of LOC285747 (Accession XP_209742.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285747.

[34846] LOC285760 (Accession XP_209750.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285760 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285760, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285760 BINDING SITE, designated SEQ ID:13412, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34847] Another function of GAM281 is therefore inhibition of LOC285760 (Accession XP_209750.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285760.

[34848] LOC285766 (Accession XP_295177.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285766 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285766, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC285766 BINDING SITE, designated SEQ ID:1304, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34849] Another function of GAM281 is therefore inhibition of LOC285766 (Accession XP_295177.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285766.

[34850] LOC285777 (Accession XP_212013.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285777 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285777, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285777 BINDING SITE, designated SEQ ID:16810, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34851] Another function of GAM281 is therefore inhibition of LOC285777 (Accession XP_212013.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285777.

[34852] LOC285812 (Accession XP_212055.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285812 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285812 BINDING SITE, designated SEQ ID:559, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34853] Another function of GAM281 is therefore inhibition of LOC285812 (Accession XP_212055.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285812.

[34854] LOC285813 (Accession XP_212036.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285813 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC285813 BINDING SITE, designated SEQ ID:12389, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34855] Another function of GAM281 is therefore inhibition of LOC285813 (Accession XP_212036.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285813.

[34856] LOC285822 (Accession XP_209777.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285822 BINDING SITE1 and LOC285822 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285822, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285822 BINDING SITE1 and LOC285822 BINDING SITE2, designated SEQ ID:1847 and SEQ ID:9753 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34857] Another function of GAM281 is therefore inhibition of LOC285822 (Accession XP_209777.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285822.

[34858] LOC285830 (Accession XP_212043.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285830 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285830, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285830 BINDING SITE, designated SEQ ID:986, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34859] Another function of GAM281 is therefore inhibition of LOC285830 (Accession XP_212043.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285830.

[34860] LOC285843 (Accession XP_212034.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285843 BINDING SITE1 through LOC285843 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC285843, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285843 BINDING SITE1 through LOC285843 BINDING SITE3, designated SEQ ID:14125, SEQ ID:4368 and SEQ ID:17964 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34861] Another function of GAM281 is therefore inhibition of LOC285843 (Accession XP_212034.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285843.

[34862] LOC285847 (Accession XP_212045.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285847 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285847, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285847 BINDING SITE, designated SEQ ID:18945, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34863] Another function of GAM281 is therefore inhibition of LOC285847 (Accession XP_212045.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285847.

[34864] LOC285872 (Accession XP_212061.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285872 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285872, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285872 BINDING SITE, designated SEQ ID:10885, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34865] Another function of GAM281 is therefore inhibition of LOC285872 (Accession XP_212061.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285872.

[34866] LOC285896 (Accession XP_209806.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285896 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285896, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285896 BINDING SITE, designated SEQ ID:15236, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34867] Another function of GAM281 is therefore inhibition of LOC285896 (Accession XP_209806.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285896.

[34868] LOC285914 (Accession XP_209810.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285914 BINDING SITE1 and LOC285914 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285914, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285914 BINDING SITE1 and LOC285914 BINDING SITE2, designated SEQ ID:14560 and SEQ ID:6188 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34869] Another function of GAM281 is therefore inhibition of

LOC285914 (Accession XP_209810.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285914.

[34870] LOC285922 (Accession XP_209822.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285922 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285922 BINDING SITE, designated SEQ ID:12799, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34871] Another function of GAM281 is therefore inhibition of LOC285922 (Accession XP_209822.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285922.

[34872] LOC285923 (Accession XP_212104.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285923 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285923, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285923 BINDING SITE, designated SEQ ID:19536, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34873] Another function of GAM281 is therefore inhibition of LOC285923 (Accession XP_212104.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285923.

[34874] LOC285930 (Accession XP_209818.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285930 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285930, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285930 BINDING SITE, designated SEQ ID:1867, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34875] Another function of GAM281 is therefore inhibition of LOC285930 (Accession XP_209818.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285930.

[34876] LOC285945 (Accession XP_212092.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285945 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285945, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285945 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34877] Another function of GAM281 is therefore inhibition of LOC285945 (Accession XP_212092.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285945.

[34878] LOC285946 (Accession XP_212103.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285946 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285946, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285946 BINDING SITE, designated SEQ ID:11558, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34879] Another function of GAM281 is therefore inhibition of LOC285946 (Accession XP_212103.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285946.

[34880] LOC285952 (Accession XP_209821.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285952 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285952, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285952 BINDING SITE, designated SEQ ID:15323, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34881] Another function of GAM281 is therefore inhibition of LOC285952 (Accession XP_209821.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285952.

[34882] LOC285961 (Accession XP_209833.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285961 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285961, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285961 BINDING SITE, designated SEQ ID:2604, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34883] Another function of GAM281 is therefore inhibition of LOC285961 (Accession XP_209833.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285961.

[34884] LOC285968 (Accession XP_212107.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285968 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285968, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC285968 BINDING SITE, designated SEQ ID:10956, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34885] Another function of GAM281 is therefore inhibition of LOC285968 (Accession XP_212107.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285968.

[34886] LOC285972 (Accession XP_212105.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285972 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285972 BINDING SITE, designated SEQ ID:5318, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34887] Another function of GAM281 is therefore inhibition of LOC285972 (Accession XP_212105.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285972.

[34888] LOC285979 (Accession XP_212117.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285979 BINDING SITE1 and LOC285979 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285979, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285979 BINDING SITE1 and LOC285979 BINDING SITE2, designated SEQ ID:1397 and SEQ ID:6388 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34889] Another function of GAM281 is therefore inhibition of LOC285979 (Accession XP_212117.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285979.

[34890] LOC285989 (Accession XP_212111.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285989 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285989, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285989 BINDING SITE, designated SEQ ID:11742, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34891] Another function of GAM281 is therefore inhibition of LOC285989 (Accession XP_212111.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285989.

[34892] LOC285999 (Accession XP_212120.1) is another GAM281 target gene, herein designated TARGET GENE. LOC285999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285999 BINDING SITE, designated SEQ ID:17306, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34893] Another function of GAM281 is therefore inhibition of LOC285999 (Accession XP_212120.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285999.

[34894] LOC286029 (Accession XP_209866.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286029 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286029, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286029 BINDING SITE, designated SEQ ID:15231, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34895] Another function of GAM281 is therefore inhibition of LOC286029 (Accession XP_209866.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286029.

[34896] LOC286030 (Accession XP_209868.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286030 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286030, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC286030 BINDING SITE, designated SEQ ID:2244, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34897] Another function of GAM281 is therefore inhibition of LOC286030 (Accession XP_209868.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286030.

[34898] LOC286032 (Accession XP_209867.2) is another GAM281 target gene, herein designated TARGET GENE. LOC286032 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286032, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286032 BINDING SITE, designated SEQ ID:7792, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34899] Another function of GAM281 is therefore inhibition of LOC286032 (Accession XP_209867.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC286032.

[34900] LOC286039 (Accession XP_209873.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286039 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286039, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286039 BINDING SITE, designated SEQ ID:11035, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34901] Another function of GAM281 is therefore inhibition of LOC286039 (Accession XP_209873.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286039.

[34902] LOC286052 (Accession XP_212152.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC286052 BINDING SITE, designated SEQ ID:9367, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34903] Another function of GAM281 is therefore inhibition of LOC286052 (Accession XP_212152.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286052.

[34904] LOC286058 (Accession XP_212158.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286058 BINDING SITE, designated SEQ ID:9186, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34905] Another function of GAM281 is therefore inhibition of LOC286058 (Accession XP_212158.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286058.

[34906] LOC286075 (Accession NP_776192.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286075 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286075, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286075 BINDING SITE, designated SEQ ID:17965, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34907] Another function of GAM281 is therefore inhibition of LOC286075 (Accession NP_776192.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286075.

[34908] LOC286078 (Accession XP_212163.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286078 BINDING SITE1 through LOC286078 BINDING SITE5 are target binding sites found in untranslated regions of mRNA encoded by LOC286078, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286078

BINDING SITE1 through LOC286078 BINDING SITE5, designated SEQ ID:16716, SEQ ID:15083, SEQ ID:3810, SEQ ID:15589 and SEQ ID:13100 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34909] Another function of GAM281 is therefore inhibition of LOC286078 (Accession XP_212163.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286078.

[34910] LOC286090 (Accession XP_212166.3) is another GAM281 target gene, herein designated TARGET GENE. LOC286090 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286090, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286090 BINDING SITE, designated SEQ ID:16409, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34911] Another function of GAM281 is therefore inhibition of LOC286090 (Accession XP_212166.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC286090.

[34912] LOC286103 (Accession XP_209897.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286103 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC286103, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286103 BINDING SITE, designated SEQ ID:11672, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34913] Another function of GAM281 is therefore inhibition of LOC286103 (Accession XP_209897.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286103.

[34914] LOC286103 (Accession NP_848630.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286103 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC286103, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286103 BINDING SITE, designated SEQ ID:11672, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34915] Another function of GAM281 is therefore inhibition of LOC286103 (Accession NP_848630.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286103.

[34916] LOC286126 (Accession XP_212185.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286126 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286126, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286126 BINDING SITE, designated SEQ ID:7847, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34917] Another function of GAM281 is therefore inhibition of LOC286126 (Accession XP_212185.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286126.

[34918] LOC286132 (Accession XP_212194.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286132 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286132 BINDING SITE, designated SEQ ID:7113, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34919] Another function of GAM281 is therefore inhibition of LOC286132 (Accession XP_212194.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286132.

[34920] LOC286166 (Accession XP_209925.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286166 BINDING SITE1 and LOC286166 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC286166, corresponding to target binding

sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286166 BINDING SITE1 and LOC286166 BINDING SITE2, designated SEQ ID:3927 and SEQ ID:12946 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34921] Another function of GAM281 is therefore inhibition of LOC286166 (Accession XP_209925.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286166.

[34922] LOC286170 (Accession XP_212211.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286170 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286170 BINDING SITE, designated SEQ ID:8426, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34923] Another function of GAM281 is therefore inhibition of

LOC286170 (Accession XP_212211.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286170.

[34924] LOC286184 (Accession XP_212216.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286184 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286184, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286184 BINDING SITE, designated SEQ ID:12053, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34925] Another function of GAM281 is therefore inhibition of LOC286184 (Accession XP_212216.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286184.

[34926] LOC286186 (Accession XP_212219.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286186 BINDING SITE1 and LOC286186 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by LOC286186, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286186 BINDING SITE1 and LOC286186 BINDING SITE2, designated SEQ ID:3430 and SEQ ID:18020 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34927] Another function of GAM281 is therefore inhibition of LOC286186 (Accession XP_212219.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286186.

[34928] LOC286206 (Accession XP_209953.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286206 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286206, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286206 BINDING SITE, designated SEQ ID:2600, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34929] Another function of GAM281 is therefore inhibition of LOC286206 (Accession XP_209953.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286206.

[34930] LOC286207 (Accession XP_209941.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286207 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286207, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286207 BINDING SITE, designated SEQ ID:19893, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34931] Another function of GAM281 is therefore inhibition of LOC286207 (Accession XP_209941.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286207.

[34932] LOC286208 (Accession XP_212230.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286208 BINDING SITE1 through LOC286208 BINDING SITE3 are

target binding sites found in untranslated regions of mRNA encoded by LOC286208, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286208 BINDING SITE1 through LOC286208 BINDING SITE3, designated SEQ ID:9724, SEQ ID:4372 and SEQ ID:2849 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34933] Another function of GAM281 is therefore inhibition of LOC286208 (Accession XP_212230.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286208.

[34934] LOC286215 (Accession XP_212228.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286215 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286215, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286215 BINDING SITE, designated SEQ ID:19240, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34935] Another function of GAM281 is therefore inhibition of LOC286215 (Accession XP_212228.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286215.

[34936] LOC286218 (Accession XP_212235.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286218 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286218, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286218 BINDING SITE, designated SEQ ID:6316, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34937] Another function of GAM281 is therefore inhibition of LOC286218 (Accession XP_212235.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286218.

[34938] LOC286221 (Accession XP_212233.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286221

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286221, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286221 BINDING SITE, designated SEQ ID:7774, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34939] Another function of GAM281 is therefore inhibition of LOC286221 (Accession XP_212233.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286221.

[34940] LOC286245 (Accession XP_212244.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286245 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286245, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286245 BINDING SITE, designated SEQ ID:6868, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34941] Another function of GAM281 is therefore inhibition of LOC286245 (Accession XP_212244.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286245.

[34942] LOC286258 (Accession XP_209972.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286258 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286258, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286258 BINDING SITE, designated SEQ ID:11262, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34943] Another function of GAM281 is therefore inhibition of LOC286258 (Accession XP_209972.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286258.

[34944] LOC286337 (Accession XP_212274.3) is another GAM281 target gene, herein designated TARGET GENE. LOC286337 BINDING SITE1 and LOC286337 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by LOC286337, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286337 BINDING SITE1 and LOC286337 BINDING SITE2, designated SEQ ID:14911 and SEQ ID:7808 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34945] Another function of GAM281 is therefore inhibition of LOC286337 (Accession XP_212274.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286337.

[34946] LOC286341 (Accession XP_212278.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286341 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286341, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286341 BINDING SITE, designated SEQ ID:15975, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34947] Another function of GAM281 is therefore inhibition of LOC286341 (Accession XP_212278.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286341.

[34948] LOC286354 (Accession XP_212286.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286354 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286354, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286354 BINDING SITE, designated SEQ ID:15730, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34949] Another function of GAM281 is therefore inhibition of LOC286354 (Accession XP_212286.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286354.

[34950] LOC286356 (Accession XP_212290.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286356

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286356 BINDING SITE, designated SEQ ID:7385, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34951] Another function of GAM281 is therefore inhibition of LOC286356 (Accession XP_212290.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286356.

[34952] LOC286357 (Accession XP_212285.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286357 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286357, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286357 BINDING SITE, designated SEQ ID:14974, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34953] Another function of GAM281 is therefore inhibition of LOC286357 (Accession XP_212285.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286357.

[34954] LOC286371 (Accession XP_212291.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286371 BINDING SITE, designated SEQ ID:3785, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34955] Another function of GAM281 is therefore inhibition of LOC286371 (Accession XP_212291.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286371.

[34956] LOC286395 (Accession XP_212308.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286395 BINDING SITE1 through LOC286395 BINDING SITE4 are

target binding sites found in untranslated regions of mRNA encoded by LOC286395, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286395 BINDING SITE1 through LOC286395 BINDING SITE4, designated SEQ ID:2180, SEQ ID:2722, SEQ ID:5359 and SEQ ID:16177 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34957] Another function of GAM281 is therefore inhibition of LOC286395 (Accession XP_212308.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286395.

[34958] LOC286401 (Accession XP_212310.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286401 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286401, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286401 BINDING SITE, designated SEQ ID:1038, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34959] Another function of GAM281 is therefore inhibition of LOC286401 (Accession XP_212310.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286401.

[34960] LOC286441 (Accession XP_212319.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286441 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286441, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286441 BINDING SITE, designated SEQ ID:2754, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34961] Another function of GAM281 is therefore inhibition of LOC286441 (Accession XP_212319.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286441.

[34962] LOC286467 (Accession XP_210063.1) is another GAM281

target gene, herein designated TARGET GENE. LOC286467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286467 BINDING SITE, designated SEQ ID:9580, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34963] Another function of GAM281 is therefore inhibition of LOC286467 (Accession XP_210063.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286467.

[34964] LOC286553 (Accession XP_212340.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286553 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286553, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286553 BINDING SITE, designated SEQ ID:3183, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34965] Another function of GAM281 is therefore inhibition of LOC286553 (Accession XP_212340.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286553.

[34966] LOC286558 (Accession XP_210106.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286558 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286558, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286558 BINDING SITE, designated SEQ ID:9264, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34967] Another function of GAM281 is therefore inhibition of LOC286558 (Accession XP_210106.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286558.

[34968] LOC286564 (Accession XP_210108.1) is another GAM281 target gene, herein designated TARGET GENE. LOC286564

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286564, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286564 BINDING SITE, designated SEQ ID:9264, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34969] Another function of GAM281 is therefore inhibition of LOC286564 (Accession XP_210108.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286564.

[34970] LOC338562 (Accession XP_294654.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338562 BINDING SITE, designated SEQ ID:13760, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34971] Another function of GAM281 is therefore inhibition of LOC338562 (Accession XP_294654.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338562.

[34972] LOC338565 (Accession XP_294653.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338565 BINDING SITE1 and LOC338565 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC338565, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338565 BINDING SITE1 and LOC338565 BINDING SITE2, designated SEQ ID:12867 and SEQ ID:7596 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34973] Another function of GAM281 is therefore inhibition of LOC338565 (Accession XP_294653.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338565.

[34974] LOC338579 (Accession XP_290472.1) is another GAM281

target gene, herein designated TARGET GENE. LOC338579 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338579, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338579 BINDING SITE, designated SEQ ID:4528, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34975] Another function of GAM281 is therefore inhibition of LOC338579 (Accession XP_290472.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338579.

[34976] LOC338585 (Accession XP_294658.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338585 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338585, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338585 BINDING SITE, designated SEQ ID:7523, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34977] Another function of GAM281 is therefore inhibition of LOC338585 (Accession XP_294658.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338585.

[34978] LOC338609 (Accession XP_294664.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338609 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338609, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338609 BINDING SITE, designated SEQ ID:18810, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34979] Another function of GAM281 is therefore inhibition of LOC338609 (Accession XP_294664.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338609.

[34980] LOC338645 (Accession XP_290494.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338645

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338645, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338645 BINDING SITE, designated SEQ ID:6626, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34981] Another function of GAM281 is therefore inhibition of LOC338645 (Accession XP_290494.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338645.

[34982] LOC338709 (Accession XP_211595.2) is another GAM281 target gene, herein designated TARGET GENE. LOC338709 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338709, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338709 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34983] Another function of GAM281 is therefore inhibition of LOC338709 (Accession XP_211595.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338709.

[34984] LOC338739 (Accession XP_294690.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338739 BINDING SITE1 and LOC338739 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC338739, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338739 BINDING SITE1 and LOC338739 BINDING SITE2, designated SEQ ID:15044 and SEQ ID:14732 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34985] Another function of GAM281 is therefore inhibition of LOC338739 (Accession XP_294690.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338739.

[34986] LOC338773 (Accession XP_290570.1) is another GAM281

target gene, herein designated TARGET GENE. LOC338773 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338773, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338773 BINDING SITE, designated SEQ ID:16493, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34987] Another function of GAM281 is therefore inhibition of LOC338773 (Accession XP_290570.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338773.

[34988] LOC338819 (Accession XP_290216.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338819 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338819, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338819 BINDING SITE, designated SEQ ID:11507, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[34989] Another function of GAM281 is therefore inhibition of LOC338819 (Accession XP_290216.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338819.

[34990] LOC338899 (Accession XP_294740.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338899 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338899 BINDING SITE, designated SEQ ID:12341, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34991] Another function of GAM281 is therefore inhibition of LOC338899 (Accession XP_294740.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338899.

[34992] LOC338923 (Accession XP_294742.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338923

BINDING SITE1 and LOC338923 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC338923, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338923 BINDING SITE1 and LOC338923 BINDING SITE2, designated SEQ ID:4298 and SEQ ID:8559 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34993] Another function of GAM281 is therefore inhibition of LOC338923 (Accession XP_294742.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338923.

[34994] LOC338963 (Accession XP_294757.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338963 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338963, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338963 BINDING SITE, designated SEQ ID:3348, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34995] Another function of GAM281 is therefore inhibition of LOC338963 (Accession XP_294757.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338963.

[34996] LOC338991 (Accession XP_290663.1) is another GAM281 target gene, herein designated TARGET GENE. LOC338991 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338991, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338991 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34997] Another function of GAM281 is therefore inhibition of LOC338991 (Accession XP_290663.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338991.

[34998] LOC338999 (Accession XP_290659.1) is another GAM281

target gene, herein designated TARGET GENE. LOC338999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338999 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[34999] Another function of GAM281 is therefore inhibition of LOC338999 (Accession XP_290659.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338999.

[35000] LOC339077 (Accession XP_294802.2) is another GAM281 target gene, herein designated TARGET GENE. LOC339077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339077 BINDING SITE, designated SEQ ID:17484, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[35001] Another function of GAM281 is therefore inhibition of LOC339077 (Accession XP_294802.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339077.

[35002] LOC339078 (Accession XP_290692.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339078 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339078 BINDING SITE, designated SEQ ID:9543, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35003] Another function of GAM281 is therefore inhibition of LOC339078 (Accession XP_290692.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339078.

[35004] LOC339108 (Accession XP_290711.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339108

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339108, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339108 BINDING SITE, designated SEQ ID:14266, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35005] Another function of GAM281 is therefore inhibition of LOC339108 (Accession XP_290711.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339108.

[35006] LOC339146 (Accession XP_294825.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339146 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339146 BINDING SITE, designated SEQ ID:15614, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35007] Another function of GAM281 is therefore inhibition of LOC339146 (Accession XP_294825.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339146.

[35008] LOC339153 (Accession XP_294827.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339153 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339153, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339153 BINDING SITE, designated SEQ ID:13344, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35009] Another function of GAM281 is therefore inhibition of LOC339153 (Accession XP_294827.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339153.

[35010] LOC339154 (Accession XP_294832.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339154 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC339154, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339154 BINDING SITE, designated SEQ ID:4196, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35011] Another function of GAM281 is therefore inhibition of LOC339154 (Accession XP_294832.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339154.

[35012] LOC339178 (Accession XP_290742.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339178 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339178, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339178 BINDING SITE, designated SEQ ID:16261, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35013] Another function of GAM281 is therefore inhibition of

LOC339178 (Accession XP_290742.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339178.

[35014] LOC339201 (Accession XP_290756.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339201 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339201 BINDING SITE, designated SEQ ID:4056, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35015] Another function of GAM281 is therefore inhibition of LOC339201 (Accession XP_290756.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339201.

[35016] LOC339216 (Accession XP_290762.2) is another GAM281 target gene, herein designated TARGET GENE. LOC339216 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339216, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339216 BINDING SITE, designated SEQ ID:19537, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35017] Another function of GAM281 is therefore inhibition of LOC339216 (Accession XP_290762.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339216.

[35018] LOC339282 (Accession XP_294900.2) is another GAM281 target gene, herein designated TARGET GENE. LOC339282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339282 BINDING SITE, designated SEQ ID:19537, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35019] Another function of GAM281 is therefore inhibition of LOC339282 (Accession XP_294900.2) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339282.

[35020] LOC339283 (Accession XP_294899.2) is another GAM281 target gene, herein designated TARGET GENE. LOC339283 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339283, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339283 BINDING SITE, designated SEQ ID:11314, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35021] Another function of GAM281 is therefore inhibition of LOC339283 (Accession XP_294899.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339283.

[35022] LOC339298 (Accession XP_294903.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339298 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339298, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339298 BINDING SITE, designated SEQ ID:12349, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35023] Another function of GAM281 is therefore inhibition of LOC339298 (Accession XP_294903.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339298.

[35024] LOC339321 (Accession XP_290831.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339321 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339321, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339321 BINDING SITE, designated SEQ ID:2039, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35025] Another function of GAM281 is therefore inhibition of LOC339321 (Accession XP_290831.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC339321.

[35026] LOC339324 (Accession XP_290838.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339324 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339324, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339324 BINDING SITE, designated SEQ ID:9544, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35027] Another function of GAM281 is therefore inhibition of LOC339324 (Accession XP_290838.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339324.

[35028] LOC339325 (Accession XP_290830.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339325 BINDING SITE1 and LOC339325 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339325, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339325 BINDING SITE1 and LOC339325 BINDING SITE2, designated SEQ ID:17114 and SEQ ID:16940 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35029] Another function of GAM281 is therefore inhibition of LOC339325 (Accession XP_290830.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339325.

[35030] LOC339400 (Accession XP_294926.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339400 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339400 BINDING SITE, designated SEQ ID:14072, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35031] Another function of GAM281 is therefore inhibition of LOC339400 (Accession XP_294926.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339400.

[35032] LOC339417 (Accession XP_294944.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339417 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339417, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339417 BINDING SITE, designated SEQ ID:2027, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35033] Another function of GAM281 is therefore inhibition of LOC339417 (Accession XP_294944.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339417.

[35034] LOC339448 (Accession XP_290902.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339448 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339448, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339448 BINDING SITE, designated SEQ ID:10679, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35035] Another function of GAM281 is therefore inhibition of LOC339448 (Accession XP_290902.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339448.

[35036] LOC339458 (Accession XP_290911.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339458 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339458, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339458 BINDING SITE, designated SEQ ID:5488, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35037] Another function of GAM281 is therefore inhibition of LOC339458 (Accession XP_290911.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC339458.

[35038] LOC339459 (Accession XP_290907.2) is another GAM281 target gene, herein designated TARGET GENE. LOC339459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339459 BINDING SITE, designated SEQ ID:13513, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35039] Another function of GAM281 is therefore inhibition of LOC339459 (Accession XP_290907.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339459.

[35040] LOC339492 (Accession XP_290919.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339492 BINDING SITE1 and LOC339492 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339492, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339492 BINDING SITE1 and LOC339492 BINDING SITE2, designated SEQ ID:8590 and SEQ ID:7386 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35041] Another function of GAM281 is therefore inhibition of LOC339492 (Accession XP_290919.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339492.

[35042] LOC339577 (Accession XP_295005.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339577 BINDING SITE1 and LOC339577 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339577, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339577 BINDING SITE1 and LOC339577 BINDING SITE2, designated SEQ ID:14733 and SEQ ID:12075 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35043] Another function of GAM281 is therefore inhibition of LOC339577 (Accession XP_295005.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339577.

[35044] LOC339600 (Accession XP_295014.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339600 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339600, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339600 BINDING SITE, designated SEQ ID:15295, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35045] Another function of GAM281 is therefore inhibition of LOC339600 (Accession XP_295014.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339600.

[35046] LOC339659 (Accession XP_290981.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339659 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC339659, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339659 BINDING SITE, designated SEQ ID:17076, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35047] Another function of GAM281 is therefore inhibition of LOC339659 (Accession XP_290981.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339659.

[35048] LOC339685 (Accession XP_295032.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339685 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339685, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339685 BINDING SITE, designated SEQ ID:1982, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35049] Another function of GAM281 is therefore inhibition of

LOC339685 (Accession XP_295032.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339685.

[35050] LOC339694 (Accession XP_295035.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339694 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339694, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339694 BINDING SITE, designated SEQ ID:15954, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35051] Another function of GAM281 is therefore inhibition of LOC339694 (Accession XP_295035.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339694.

[35052] LOC339711 (Accession XP_295038.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339711 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339711, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339711 BINDING SITE, designated SEQ ID:11528, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35053] Another function of GAM281 is therefore inhibition of LOC339711 (Accession XP_295038.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339711.

[35054] LOC339720 (Accession XP_295041.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339720 BINDING SITE1 and LOC339720 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339720, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339720 BINDING SITE1 and LOC339720 BINDING SITE2, designated SEQ ID:16942 and SEQ ID:18414 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35055] Another function of GAM281 is therefore inhibition of LOC339720 (Accession XP_295041.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339720.

[35056] LOC339803 (Accession XP_295072.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339803 BINDING SITE, designated SEQ ID:13337, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35057] Another function of GAM281 is therefore inhibition of LOC339803 (Accession XP_295072.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339803.

[35058] LOC339809 (Accession XP_291020.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339809 BINDING SITE1 and LOC339809 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by LOC339809, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339809 BINDING SITE1 and LOC339809 BINDING SITE2, designated SEQ ID:1744 and SEQ ID:17750 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35059] Another function of GAM281 is therefore inhibition of LOC339809 (Accession XP_291020.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339809.

[35060] LOC339833 (Accession XP_291031.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339833 BINDING SITE1 and LOC339833 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339833, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339833 BINDING SITE1 and LOC339833 BINDING SITE2, designated SEQ ID:10421

and SEQ ID:7633 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35061] Another function of GAM281 is therefore inhibition of LOC339833 (Accession XP_291031.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339833.

[35062] LOC339834 (Accession NP_835467.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339834 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC339834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339834 BINDING SITE, designated SEQ ID:14645, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35063] Another function of GAM281 is therefore inhibition of LOC339834 (Accession NP_835467.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC339834.

[35064] LOC339834 (Accession XP_291033.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339834 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC339834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339834 BINDING SITE, designated SEQ ID:14645, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35065] Another function of GAM281 is therefore inhibition of LOC339834 (Accession XP_291033.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339834.

[35066] LOC339872 (Accession XP_291050.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339872 BINDING SITE1 through LOC339872 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC339872, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339872 BINDING SITE1 through LOC339872 BINDING SITE3, designated SEQ ID:5858, SEQ ID:9299 and SEQ ID:4026 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35067] Another function of GAM281 is therefore inhibition of LOC339872 (Accession XP_291050.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339872.

[35068] LOC339894 (Accession XP_295095.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339894 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339894 BINDING SITE, designated SEQ ID:1081, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35069] Another function of GAM281 is therefore inhibition of LOC339894 (Accession XP_295095.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339894.

[35070] LOC339907 (Accession XP_291065.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339907 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339907, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339907 BINDING SITE, designated SEQ ID:3425, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35071] Another function of GAM281 is therefore inhibition of LOC339907 (Accession XP_291065.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339907.

[35072] LOC339909 (Accession XP_291069.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339909 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339909, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339909 BINDING SITE, designated SEQ ID:10709, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35073] Another function of GAM281 is therefore inhibition of LOC339909 (Accession XP_291069.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339909.

[35074] LOC339914 (Accession XP_295099.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339914 BINDING SITE1 and LOC339914 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339914, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339914 BINDING SITE1 and LOC339914 BINDING SITE2, designated SEQ ID:714 and SEQ ID:18305 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35075] Another function of GAM281 is therefore inhibition of

LOC339914 (Accession XP_295099.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339914.

[35076] LOC339970 (Accession XP_291095.1) is another GAM281 target gene, herein designated TARGET GENE. LOC339970 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339970, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339970 BINDING SITE, designated SEQ ID:16942, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35077] Another function of GAM281 is therefore inhibition of LOC339970 (Accession XP_291095.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339970.

[35078] LOC340012 (Accession XP_291113.2) is another GAM281 target gene, herein designated TARGET GENE. LOC340012 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340012, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340012 BINDING SITE, designated SEQ ID:3454, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35079] Another function of GAM281 is therefore inhibition of LOC340012 (Accession XP_291113.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340012.

[35080] LOC340037 (Accession XP_295137.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340037 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340037, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340037 BINDING SITE, designated SEQ ID:12244, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35081] Another function of GAM281 is therefore inhibition of LOC340037 (Accession XP_295137.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340037.

[35082] LOC340125 (Accession XP_291150.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340125 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340125, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340125 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35083] Another function of GAM281 is therefore inhibition of LOC340125 (Accession XP_291150.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340125.

[35084] LOC340133 (Accession XP_291151.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340133 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340133, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340133 BINDING SITE, designated SEQ ID:10105, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35085] Another function of GAM281 is therefore inhibition of LOC340133 (Accession XP_291151.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340133.

[35086] LOC340138 (Accession XP_291153.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340138 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340138 BINDING SITE, designated SEQ ID:11753, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35087] Another function of GAM281 is therefore inhibition of LOC340138 (Accession XP_291153.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC340138.

[35088] LOC340156 (Accession XP_291158.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340156 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340156, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340156 BINDING SITE, designated SEQ ID:10096, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35089] Another function of GAM281 is therefore inhibition of LOC340156 (Accession XP_291158.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340156.

[35090] LOC340227 (Accession XP_291203.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340227 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340227, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC340227 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35091] Another function of GAM281 is therefore inhibition of LOC340227 (Accession XP_291203.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340227.

[35092] LOC340238 (Accession XP_295188.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340238 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340238, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340238 BINDING SITE, designated SEQ ID:2179, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35093] Another function of GAM281 is therefore inhibition of LOC340238 (Accession XP_295188.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC340238.

[35094] LOC340249 (Accession XP_291211.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340249 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340249, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340249 BINDING SITE, designated SEQ ID:7647, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35095] Another function of GAM281 is therefore inhibition of LOC340249 (Accession XP_291211.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340249.

[35096] LOC340259 (Accession XP_295190.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340259 BINDING SITE1 and LOC340259 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC340259, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of LOC340259 BINDING SITE1 and LOC340259 BINDING SITE2, designated SEQ ID:18147 and SEQ ID:11519 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35097] Another function of GAM281 is therefore inhibition of LOC340259 (Accession XP_295190.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340259.

[35098] LOC340290 (Accession XP_291214.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340290 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340290, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340290 BINDING SITE, designated SEQ ID:15740, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35099] Another function of GAM281 is therefore inhibition of LOC340290 (Accession XP_291214.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC340290.

[35100] LOC340390 (Accession XP_291269.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340390 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340390, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340390 BINDING SITE, designated SEQ ID:18868, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35101] Another function of GAM281 is therefore inhibition of LOC340390 (Accession XP_291269.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340390.

[35102] LOC340408 (Accession XP_291274.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC340408 BINDING SITE, designated SEQ ID:1309, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35103] Another function of GAM281 is therefore inhibition of LOC340408 (Accession XP_291274.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340408.

[35104] LOC340414 (Accession XP_295240.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340414 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340414, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340414 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35105] Another function of GAM281 is therefore inhibition of LOC340414 (Accession XP_295240.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC340414.

[35106] LOC340450 (Accession XP_295252.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340450 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340450, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340450 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35107] Another function of GAM281 is therefore inhibition of LOC340450 (Accession XP_295252.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340450.

[35108] LOC340815 (Accession XP_295776.1) is another GAM281 target gene, herein designated TARGET GENE. LOC340815 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340815, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC340815 BINDING SITE, designated SEQ ID:6038, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35109] Another function of GAM281 is therefore inhibition of LOC340815 (Accession XP_295776.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340815.

[35110] LOC342663 (Accession XP_297028.1) is another GAM281 target gene, herein designated TARGET GENE. LOC342663 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC342663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC342663 BINDING SITE, designated SEQ ID:12875, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35111] Another function of GAM281 is therefore inhibition of LOC342663 (Accession XP_297028.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC342663.

[35112] LOC342926 (Accession XP_292790.2) is another GAM281 target gene, herein designated TARGET GENE. LOC342926 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC342926, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC342926 BINDING SITE, designated SEQ ID:13464, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35113] Another function of GAM281 is therefore inhibition of LOC342926 (Accession XP_292790.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC342926.

[35114] LOC345119 (Accession XP_298539.1) is another GAM281 target gene, herein designated TARGET GENE. LOC345119 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC345119, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC345119 BINDING SITE, designated SEQ ID:17910, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35115] Another function of GAM281 is therefore inhibition of LOC345119 (Accession XP_298539.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC345119.

[35116] LOC345275 (Accession NP_835236.1) is another GAM281 target gene, herein designated TARGET GENE. LOC345275 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC345275, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC345275 BINDING SITE, designated SEQ ID:523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35117] Another function of GAM281 is therefore inhibition of LOC345275 (Accession NP_835236.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC345275.

[35118] LOC345878 (Accession XP_293993.2) is another GAM281 target gene, herein designated TARGET GENE. LOC345878 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC345878, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC345878 BINDING SITE, designated SEQ ID:12611, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35119] Another function of GAM281 is therefore inhibition of LOC345878 (Accession XP_293993.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC345878.

[35120] LOC346546 (Accession XP_294264.2) is another GAM281 target gene, herein designated TARGET GENE. LOC346546 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC346546, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC346546 BINDING SITE, designated SEQ ID:18735, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35121] Another function of GAM281 is therefore inhibition of LOC346546 (Accession XP_294264.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC346546.

[35122] LOC346653 (Accession XP_294357.2) is another GAM281 target gene, herein designated TARGET GENE. LOC346653 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC346653, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC346653 BINDING SITE, designated SEQ ID:17927, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35123] Another function of GAM281 is therefore inhibition of LOC346653 (Accession XP_294357.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC346653.

[35124] LOC347648 (Accession XP_300226.1) is another GAM281

target gene, herein designated TARGET GENE. LOC347648 BINDING SITE1 and LOC347648 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC347648, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347648 BINDING SITE1 and LOC347648 BINDING SITE2, designated SEQ ID:19153 and SEQ ID:9837 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35125] Another function of GAM281 is therefore inhibition of LOC347648 (Accession XP_300226.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347648.

[35126] LOC347918 (Accession XP_300565.1) is another GAM281 target gene, herein designated TARGET GENE. LOC347918 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347918, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC347918 BINDING SITE, designated SEQ ID:17689, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35127] Another function of GAM281 is therefore inhibition of LOC347918 (Accession XP_300565.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347918.

[35128] LOC348071 (Accession XP_300620.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348071 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348071, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348071 BINDING SITE, designated SEQ ID:5985, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35129] Another function of GAM281 is therefore inhibition of LOC348071 (Accession XP_300620.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348071.

[35130] LOC348075 (Accession XP_302653.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348075 BINDING SITE1 and LOC348075 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348075, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348075 BINDING SITE1 and LOC348075 BINDING SITE2, designated SEQ ID:14381 and SEQ ID:13716 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35131] Another function of GAM281 is therefore inhibition of LOC348075 (Accession XP_302653.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348075.

[35132] LOC348094 (Accession XP_300615.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348094 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348094, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC348094 BINDING SITE, designated SEQ ID:16473, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35133] Another function of GAM281 is therefore inhibition of LOC348094 (Accession XP_300615.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348094.

[35134] LOC348113 (Accession XP_300623.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348113 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35135] Another function of GAM281 is therefore inhibition of LOC348113 (Accession XP_300623.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC348113.

[35136] LOC348115 (Accession XP_300626.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348115 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348115, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348115 BINDING SITE, designated SEQ ID:13705, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35137] Another function of GAM281 is therefore inhibition of LOC348115 (Accession XP_300626.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348115.

[35138] LOC348125 (Accession XP_302665.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348125 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348125, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC348125 BINDING SITE, designated SEQ ID:4673, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35139] Another function of GAM281 is therefore inhibition of LOC348125 (Accession XP_302665.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348125.

[35140] LOC348137 (Accession XP_300635.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348137 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35141] Another function of GAM281 is therefore inhibition of LOC348137 (Accession XP_300635.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348137.

[35142] LOC348142 (Accession XP_300636.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348142 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348142 BINDING SITE, designated SEQ ID:12479, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35143] Another function of GAM281 is therefore inhibition of LOC348142 (Accession XP_300636.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348142.

[35144] LOC348212 (Accession XP_302685.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348212 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348212, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348212 BINDING SITE, designated SEQ ID:15020, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35145] Another function of GAM281 is therefore inhibition of LOC348212 (Accession XP_302685.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348212.

[35146] LOC348235 (Accession XP_300670.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348235 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348235 BINDING SITE, designated SEQ ID:15852, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35147] Another function of GAM281 is therefore inhibition of LOC348235 (Accession XP_300670.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348235.

[35148] LOC348261 (Accession XP_302704.1) is another GAM281

target gene, herein designated TARGET GENE. LOC348261 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348261, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348261 BINDING SITE, designated SEQ ID:10989, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35149] Another function of GAM281 is therefore inhibition of LOC348261 (Accession XP_302704.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348261.

[35150] LOC348262 (Accession XP_300683.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348262 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348262 BINDING SITE, designated SEQ ID:7306, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[35151] Another function of GAM281 is therefore inhibition of LOC348262 (Accession XP_300683.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348262.

[35152] LOC348314 (Accession XP_302716.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348314 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348314, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348314 BINDING SITE, designated SEQ ID:16669, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35153] Another function of GAM281 is therefore inhibition of LOC348314 (Accession XP_302716.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348314.

[35154] LOC348326 (Accession XP_300696.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348326

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348326, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348326 BINDING SITE, designated SEQ ID:19778, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35155] Another function of GAM281 is therefore inhibition of LOC348326 (Accession XP_300696.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348326.

[35156] LOC348327 (Accession XP_030209.2) is another GAM281 target gene, herein designated TARGET GENE. LOC348327 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348327, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348327 BINDING SITE, designated SEQ ID:8820, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35157] Another function of GAM281 is therefore inhibition of LOC348327 (Accession XP_030209.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348327.

[35158] LOC348369 (Accession XP_302732.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348369 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348369, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348369 BINDING SITE, designated SEQ ID:2235, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35159] Another function of GAM281 is therefore inhibition of LOC348369 (Accession XP_302732.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348369.

[35160] LOC348393 (Accession XP_302741.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348393 BINDING SITE1 and LOC348393 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by LOC348393, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348393 BINDING SITE1 and LOC348393 BINDING SITE2, designated SEQ ID:11192 and SEQ ID:872 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35161] Another function of GAM281 is therefore inhibition of LOC348393 (Accession XP_302741.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348393.

[35162] LOC348396 (Accession XP_300729.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348396 BINDING SITE1 through LOC348396 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC348396, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348396 BINDING SITE1 through LOC348396 BINDING SITE4, des-

ignated SEQ ID:1569, SEQ ID:9545, SEQ ID:10270 and SEQ ID:4081 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35163] Another function of GAM281 is therefore inhibition of LOC348396 (Accession XP_300729.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348396.

[35164] LOC348402 (Accession XP_300730.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348402 BINDING SITE1 and LOC348402 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348402, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348402 BINDING SITE1 and LOC348402 BINDING SITE2, designated SEQ ID:8590 and SEQ ID:7386 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35165] Another function of GAM281 is therefore inhibition of LOC348402 (Accession XP_300730.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348402.

[35166] LOC348445 (Accession XP_300738.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348445 BINDING SITE, designated SEQ ID:19778, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35167] Another function of GAM281 is therefore inhibition of LOC348445 (Accession XP_300738.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348445.

[35168] LOC348455 (Accession XP_302760.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348455 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348455, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348455 BINDING SITE, designated SEQ ID:15049, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35169] Another function of GAM281 is therefore inhibition of LOC348455 (Accession XP_302760.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348455.

[35170] LOC348460 (Accession XP_300743.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348460 BINDING SITE1 and LOC348460 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348460, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348460 BINDING SITE1 and LOC348460 BINDING SITE2, designated SEQ ID:13465 and SEQ ID:4143 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35171] Another function of GAM281 is therefore inhibition of

LOC348460 (Accession XP_300743.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348460.

[35172] LOC348474 (Accession XP_209299.2) is another GAM281 target gene, herein designated TARGET GENE. LOC348474 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348474, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348474 BINDING SITE, designated SEQ ID:17206, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35173] Another function of GAM281 is therefore inhibition of LOC348474 (Accession XP_209299.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348474.

[35174] LOC348494 (Accession XP_302789.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348494 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348494, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348494 BINDING SITE, designated SEQ ID:6119, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35175] Another function of GAM281 is therefore inhibition of LOC348494 (Accession XP_302789.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348494.

[35176] LOC348499 (Accession XP_302799.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348499 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348499, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348499 BINDING SITE, designated SEQ ID:2771, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35177] Another function of GAM281 is therefore inhibition of LOC348499 (Accession XP_302799.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348499.

[35178] LOC348503 (Accession XP_300762.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348503 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348503, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348503 BINDING SITE, designated SEQ ID:19361, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35179] Another function of GAM281 is therefore inhibition of LOC348503 (Accession XP_300762.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348503.

[35180] LOC348508 (Accession XP_302806.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348508 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348508, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348508 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35181] Another function of GAM281 is therefore inhibition of LOC348508 (Accession XP_302806.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348508.

[35182] LOC348525 (Accession XP_300778.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348525 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348525, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348525 BINDING SITE, designated SEQ ID:5488, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35183] Another function of GAM281 is therefore inhibition of LOC348525 (Accession XP_300778.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348525.

[35184] LOC348532 (Accession XP_302818.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348532 BINDING SITE1 and LOC348532 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348532, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348532 BINDING SITE1 and LOC348532 BINDING SITE2, designated SEQ ID:872 and SEQ ID:11192 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35185] Another function of GAM281 is therefore inhibition of LOC348532 (Accession XP_302818.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348532.

[35186] LOC348581 (Accession XP_302830.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348581 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348581, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348581 BINDING SITE, designated SEQ ID:1998, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35187] Another function of GAM281 is therefore inhibition of LOC348581 (Accession XP_302830.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348581.

[35188] LOC348699 (Accession XP_300816.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348699 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348699, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348699 BINDING SITE, designated SEQ ID:10599, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35189] Another function of GAM281 is therefore inhibition of LOC348699 (Accession XP_300816.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348699.

[35190] LOC348702 (Accession XP_300808.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348702 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348702, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348702 BINDING SITE, designated SEQ ID:7387, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35191] Another function of GAM281 is therefore inhibition of LOC348702 (Accession XP_300808.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348702.

[35192] LOC348738 (Accession XP_300826.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348738 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348738, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348738 BINDING SITE, designated SEQ ID:2286, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35193] Another function of GAM281 is therefore inhibition of LOC348738 (Accession XP_300826.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348738.

[35194] LOC348790 (Accession XP_300843.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348790 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348790, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348790 BINDING SITE, designated SEQ ID:810, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35195] Another function of GAM281 is therefore inhibition of LOC348790 (Accession XP_300843.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348790.

[35196] LOC348797 (Accession XP_302888.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348797 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348797, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348797 BINDING SITE, designated SEQ ID:7741, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35197] Another function of GAM281 is therefore inhibition of LOC348797 (Accession XP_302888.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348797.

[35198] LOC348798 (Accession XP_300845.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348798 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348798, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC348798 BINDING SITE, designated SEQ ID:19402, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35199] Another function of GAM281 is therefore inhibition of LOC348798 (Accession XP_300845.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348798.

[35200] LOC348825 (Accession XP_300853.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348825 BINDING SITE1 and LOC348825 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348825, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348825 BINDING SITE1 and LOC348825 BINDING SITE2, designated SEQ ID:15126 and SEQ ID:11688 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35201] Another function of GAM281 is therefore inhibition of LOC348825 (Accession XP_300853.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348825.

[35202] LOC348842 (Accession XP_300861.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348842 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348842 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35203] Another function of GAM281 is therefore inhibition of LOC348842 (Accession XP_300861.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348842.

[35204] LOC348899 (Accession XP_302914.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348899 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348899, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348899 BINDING SITE, designated SEQ ID:3454, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35205] Another function of GAM281 is therefore inhibition of LOC348899 (Accession XP_302914.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348899.

[35206] LOC348928 (Accession XP_209688.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348928 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348928, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348928 BINDING SITE, designated SEQ ID:1305, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35207] Another function of GAM281 is therefore inhibition of LOC348928 (Accession XP_209688.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348928.

[35208] LOC348995 (Accession XP_300434.1) is another GAM281 target gene, herein designated TARGET GENE. LOC348995 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348995, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348995 BINDING SITE, designated SEQ ID:1900, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35209] Another function of GAM281 is therefore inhibition of LOC348995 (Accession XP_300434.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348995.

[35210] LOC349024 (Accession XP_300250.1) is another GAM281 target gene, herein designated TARGET GENE. LOC349024 BINDING SITE1 and LOC349024 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC349024, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349024 BINDING SITE1 and LOC349024 BINDING SITE2, designated SEQ ID:1746 and SEQ ID:4617 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35211] Another function of GAM281 is therefore inhibition of LOC349024 (Accession XP_300250.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349024.

[35212] LOC349075 (Accession XP_300932.1) is another GAM281 target gene, herein designated TARGET GENE. LOC349075 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349075, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349075 BINDING SITE, designated SEQ ID:16022, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35213] Another function of GAM281 is therefore inhibition of LOC349075 (Accession XP_300932.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349075.

[35214] LOC349096 (Accession XP_300937.1) is another GAM281 target gene, herein designated TARGET GENE. LOC349096 BINDING SITE1 and LOC349096 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC349096, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349096 BINDING SITE1 and LOC349096 BINDING SITE2, designated SEQ ID:14560 and SEQ ID:6188 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35215] Another function of GAM281 is therefore inhibition of LOC349096 (Accession XP_300937.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349096.

[35216] LOC349114 (Accession XP_302960.1) is another GAM281 target gene, herein designated TARGET GENE. LOC349114 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC349114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349114 BINDING SITE, designated SEQ ID:12803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35217] Another function of GAM281 is therefore inhibition of LOC349114 (Accession XP_302960.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349114.

[35218] LOC349136 (Accession XP_300958.1) is another GAM281 target gene, herein designated TARGET GENE. LOC349136 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349136 BINDING SITE, designated SEQ ID:6676, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35219] Another function of GAM281 is therefore inhibition of

LOC349136 (Accession XP_300958.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349136.

[35220] LOC349170 (Accession XP_300969.1) is another GAM281 target gene, herein designated TARGET GENE. LOC349170 BINDING SITE1 through LOC349170 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC349170, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349170 BINDING SITE1 through LOC349170 BINDING SITE4, designated SEQ ID:3349, SEQ ID:9545, SEQ ID:18074 and SEQ ID:11508 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35221] Another function of GAM281 is therefore inhibition of LOC349170 (Accession XP_300969.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349170.

[35222] LOC349251 (Accession XP_300251.1) is another GAM281

target gene, herein designated TARGET GENE. LOC349251 BINDING SITE1 and LOC349251 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC349251, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349251 BINDING SITE1 and LOC349251 BINDING SITE2, designated SEQ ID:2323 and SEQ ID:4454 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35223] Another function of GAM281 is therefore inhibition of LOC349251 (Accession XP_300251.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349251.

[35224] LOC349360 (Accession XP_088528.1) is another GAM281 target gene, herein designated TARGET GENE. LOC349360 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349360, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC349360 BINDING SITE, designated SEQ ID:10639, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35225] Another function of GAM281 is therefore inhibition of LOC349360 (Accession XP_088528.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349360.

[35226] LOC349408 (Accession XP_303044.1) is another GAM281 target gene, herein designated TARGET GENE. LOC349408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349408 BINDING SITE, designated SEQ ID:13466, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35227] Another function of GAM281 is therefore inhibition of LOC349408 (Accession XP_303044.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349408.

[35228] LOC349440 (Accession XP_300513.1) is another GAM281 target gene, herein designated TARGET GENE. LOC349440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349440 BINDING SITE, designated SEQ ID:4112, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35229] Another function of GAM281 is therefore inhibition of LOC349440 (Accession XP_300513.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349440.

[35230] LOC350106 (Accession XP_303810.1) is another GAM281 target gene, herein designated TARGET GENE. LOC350106 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC350106, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC350106 BINDING SITE, designated SEQ ID:18715, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35231] Another function of GAM281 is therefore inhibition of LOC350106 (Accession XP_303810.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC350106.

[35232] LOC350395 (Accession XP_304054.1) is another GAM281 target gene, herein designated TARGET GENE. LOC350395 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC350395, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC350395 BINDING SITE, designated SEQ ID:8276, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35233] Another function of GAM281 is therefore inhibition of LOC350395 (Accession XP_304054.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC350395.

[35234] LOC51058 (Accession NP_056995.1) is another GAM281

target gene, herein designated TARGET GENE. LOC51058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51058 BINDING SITE, designated SEQ ID:5678, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35235] Another function of GAM281 is therefore inhibition of LOC51058 (Accession NP_056995.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51058.

[35236] LOC51122 (Accession NP_057178.1) is another GAM281 target gene, herein designated TARGET GENE. LOC51122 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51122, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51122 BINDING SITE, designated SEQ ID:1167, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[35237] Another function of GAM281 is therefore inhibition of LOC51122 (Accession NP_057178.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51122.

[35238] LOC51193 (Accession NP_057415.1) is another GAM281 target gene, herein designated TARGET GENE. LOC51193 BINDING SITE1 and LOC51193 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC51193, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51193 BINDING SITE1 and LOC51193 BINDING SITE2, designated SEQ ID:3111 and SEQ ID:14721 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35239] Another function of GAM281 is therefore inhibition of LOC51193 (Accession NP_057415.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51193.

[35240] LOC51257 (Accession NP_057580.2) is another GAM281 target gene, herein designated TARGET GENE. LOC51257 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC51257, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51257 BINDING SITE, designated SEQ ID:14855, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35241] Another function of GAM281 is therefore inhibition of LOC51257 (Accession NP_057580.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51257.

[35242] LOC51334 (Accession NP_057728.1) is another GAM281 target gene, herein designated TARGET GENE. LOC51334 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC51334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51334 BINDING SITE, designated SEQ ID:8243, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35243] Another function of GAM281 is therefore inhibition of LOC51334 (Accession NP_057728.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51334.

[35244] LOC51336 (Accession NP_057730.1) is another GAM281 target gene, herein designated TARGET GENE. LOC51336 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51336 BINDING SITE, designated SEQ ID:18703, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35245] Another function of GAM281 is therefore inhibition of LOC51336 (Accession NP_057730.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51336.

[35246] LOC55954 (Accession NP_061976.1) is another GAM281

target gene, herein designated TARGET GENE. LOC55954 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC55954, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC55954 BINDING SITE, designated SEQ ID:17853, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35247] Another function of GAM281 is therefore inhibition of LOC55954 (Accession NP_061976.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC55954.

[35248] LOC56902 (Accession NP_064528.1) is another GAM281 target gene, herein designated TARGET GENE. LOC56902 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC56902, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC56902 BINDING SITE, designated SEQ ID:5945, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[35249] Another function of GAM281 is therefore inhibition of LOC56902 (Accession NP_064528.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56902.

[35250] LOC57107 (Accession NP_065114.2) is another GAM281 target gene, herein designated TARGET GENE. LOC57107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC57107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC57107 BINDING SITE, designated SEQ ID:16916, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35251] Another function of GAM281 is therefore inhibition of LOC57107 (Accession NP_065114.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57107.

[35252] LOC57146 (Accession NP_065155.2) is another GAM281 target gene, herein designated TARGET GENE. LOC57146

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC57146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC57146 BINDING SITE, designated SEQ ID:11036, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35253] Another function of GAM281 is therefore inhibition of LOC57146 (Accession NP_065155.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57146.

[35254] LOC57209 (Accession XP_290488.1) is another GAM281 target gene, herein designated TARGET GENE. LOC57209 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC57209, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC57209 BINDING SITE, designated SEQ ID:2349, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35255] Another function of GAM281 is therefore inhibition of LOC57209 (Accession XP_290488.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57209.

[35256] LOC90110 (Accession XP_029046.1) is another GAM281 target gene, herein designated TARGET GENE. LOC90110 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90110, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90110 BINDING SITE, designated SEQ ID:10533, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35257] Another function of GAM281 is therefore inhibition of LOC90110 (Accession XP_029046.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90110.

[35258] LOC90408 (Accession XP_031517.1) is another GAM281 target gene, herein designated TARGET GENE. LOC90408 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC90408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90408 BINDING SITE, designated SEQ ID:7704, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35259] Another function of GAM281 is therefore inhibition of LOC90408 (Accession XP_031517.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90408.

[35260] LOC90485 (Accession XP_032059.1) is another GAM281 target gene, herein designated TARGET GENE. LOC90485 BINDING SITE1 and LOC90485 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC90485, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90485 BINDING SITE1 and LOC90485 BINDING SITE2, designated SEQ ID:6896 and SEQ ID:18698 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[35261] Another function of GAM281 is therefore inhibition of LOC90485 (Accession XP_032059.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90485.

[35262] LOC90999 (Accession XP_035410.1) is another GAM281 target gene, herein designated TARGET GENE. LOC90999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90999 BINDING SITE, designated SEQ ID:15038, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35263] Another function of GAM281 is therefore inhibition of LOC90999 (Accession XP_035410.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90999.

[35264] LOC91056 (Accession NP_612377.1) is another GAM281 target gene, herein designated TARGET GENE. LOC91056

BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC91056, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91056 BINDING SITE, designated SEQ ID:14660, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35265] Another function of GAM281 is therefore inhibition of LOC91056 (Accession NP_612377.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91056.

[35266] LOC91115 (Accession XP_036218.1) is another GAM281 target gene, herein designated TARGET GENE. LOC91115 BINDING SITE1 through LOC91115 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC91115, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91115 BINDING SITE1 through LOC91115 BINDING SITE3, designated SEQ

ID:19989, SEQ ID:17831 and SEQ ID:12591 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35267] Another function of GAM281 is therefore inhibition of LOC91115 (Accession XP_036218.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91115.

[35268] LOC91170 (Accession XP_036612.1) is another GAM281 target gene, herein designated TARGET GENE. LOC91170 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91170 BINDING SITE, designated SEQ ID:16178, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35269] Another function of GAM281 is therefore inhibition of LOC91170 (Accession XP_036612.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91170.

[35270] LOC91250 (Accession XP_037135.1) is another GAM281 target gene, herein designated TARGET GENE. LOC91250 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91250, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91250 BINDING SITE, designated SEQ ID:8577, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35271] Another function of GAM281 is therefore inhibition of LOC91250 (Accession XP_037135.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91250.

[35272] LOC91266 (Accession XP_037268.1) is another GAM281 target gene, herein designated TARGET GENE. LOC91266 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91266, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91266 BINDING SITE, designated SEQ ID:18355, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35273] Another function of GAM281 is therefore inhibition of LOC91266 (Accession XP_037268.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91266.

[35274] LOC91373 (Accession XP_038063.5) is another GAM281 target gene, herein designated TARGET GENE. LOC91373 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91373, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91373 BINDING SITE, designated SEQ ID:9077, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35275] Another function of GAM281 is therefore inhibition of LOC91373 (Accession XP_038063.5) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91373.

[35276] LOC91549 (Accession XP_039115.1) is another GAM281

target gene, herein designated TARGET GENE. LOC91549 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91549, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91549 BINDING SITE, designated SEQ ID:17238, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35277] Another function of GAM281 is therefore inhibition of LOC91549 (Accession XP_039115.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91549.

[35278] LOC91661 (Accession NP_612381.1) is another GAM281 target gene, herein designated TARGET GENE. LOC91661 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91661, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91661 BINDING SITE, designated SEQ ID:8303, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[35279] Another function of GAM281 is therefore inhibition of LOC91661 (Accession NP_612381.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91661.

[35280] LOC91663 (Accession NP_612382.1) is another GAM281 target gene, herein designated TARGET GENE. LOC91663 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91663 BINDING SITE, designated SEQ ID:8075, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35281] Another function of GAM281 is therefore inhibition of LOC91663 (Accession NP_612382.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91663.

[35282] LOC91893 (Accession XP_041340.1) is another GAM281 target gene, herein designated TARGET GENE. LOC91893

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91893, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91893 BINDING SITE, designated SEQ ID:14589, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35283] Another function of GAM281 is therefore inhibition of LOC91893 (Accession XP_041340.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91893.

[35284] LOC92017 (Accession XP_042234.2) is another GAM281 target gene, herein designated TARGET GENE. LOC92017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92017 BINDING SITE, designated SEQ ID:9327, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35285] Another function of GAM281 is therefore inhibition of LOC92017 (Accession XP_042234.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92017.

[35286] LOC92148 (Accession XP_043160.1) is another GAM281 target gene, herein designated TARGET GENE. LOC92148 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC92148, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92148 BINDING SITE, designated SEQ ID:4097, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35287] Another function of GAM281 is therefore inhibition of LOC92148 (Accession XP_043160.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92148.

[35288] LOC92360 (Accession XP_044589.1) is another GAM281 target gene, herein designated TARGET GENE. LOC92360 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC92360, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92360 BINDING SITE, designated SEQ ID:1082, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35289] Another function of GAM281 is therefore inhibition of LOC92360 (Accession XP_044589.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92360.

[35290] LOC92597 (Accession NP_775739.1) is another GAM281 target gene, herein designated TARGET GENE. LOC92597 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92597, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92597 BINDING SITE, designated SEQ ID:19339, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35291] Another function of GAM281 is therefore inhibition of

LOC92597 (Accession NP_775739.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92597.

[35292] LOC92659 (Accession XP_046434.3) is another GAM281 target gene, herein designated TARGET GENE. LOC92659 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92659, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92659 BINDING SITE, designated SEQ ID:10989, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35293] Another function of GAM281 is therefore inhibition of LOC92659 (Accession XP_046434.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92659.

[35294] LOC93132 (Accession XP_049396.1) is another GAM281 target gene, herein designated TARGET GENE. LOC93132 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC93132, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC93132 BINDING SITE, designated SEQ ID:9953, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35295] Another function of GAM281 is therefore inhibition of LOC93132 (Accession XP_049396.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93132.

[35296] LOC94431 (Accession NP_660280.1) is another GAM281 target gene, herein designated TARGET GENE. LOC94431 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC94431, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC94431 BINDING SITE, designated SEQ ID:18633, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35297] Another function of GAM281 is therefore inhibition of LOC94431 (Accession NP_660280.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC94431.

[35298] Lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS, Accession NP_002331.2) is another GAM281 target gene, herein designated TARGET GENE. LSS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LSS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LSS BINDING SITE, designated SEQ ID:6091, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35299] Another function of GAM281 is therefore inhibition of Lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS, Accession NP_002331.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LSS.

[35300] Leukotriene b4 receptor (LTB4R, Accession NP_000743.1) is another GAM281 target gene, herein designated TARGET GENE. LTB4R BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LTB4R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LTB4R BINDING SITE, designated SEQ ID:1022, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35301] Another function of GAM281 is therefore inhibition of Leukotriene b4 receptor (LTB4R, Accession NP_000743.1), a gene which may be the cardiac p2y receptor involved in the regulation of cardiac muscle contraction through modulation of l- type calcium currents. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LTB4R.

[35302] The function of LTB4R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Lymphocyte antigen 75 (LY75, Accession NP_002340.1) is another GAM281 target gene, herein designated TARGET GENE. LY75 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LY75, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LY75 BINDING SITE, designated SEQ ID:17724, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35303] Another function of GAM281 is therefore inhibition of Lymphocyte antigen 75 (LY75, Accession NP_002340.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LY75.

[35304] Lysozyme (renal amyloidosis) (LYZ, Accession NP_000230.1) is another GAM281 target gene, herein designated TARGET GENE. LYZ BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LYZ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LYZ BINDING SITE, designated SEQ ID:7382, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35305] Another function of GAM281 is therefore inhibition of Lysozyme (renal amyloidosis) (LYZ, Accession NP_000230.1), a gene which a bacteriolytic enzyme. and

therefore may be associated with Renal amyloidosis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Renal amyloidosis, and of other diseases and clinical conditions associated with LYZ.

[35306] The function of LYZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Leucine zipper, putative tumor suppressor 1 (LZTS1, Accession NP_066300.1) is another GAM281 target gene, herein designated TARGET GENE. LZTS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LZTS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LZTS1 BINDING SITE, designated SEQ ID:4518, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35307] Another function of GAM281 is therefore inhibition of Leucine zipper, putative tumor suppressor 1 (LZTS1, Accession NP_066300.1), a gene which is an essential component of the nucleoskeleton. potential role in crosslinking filaments or anchoring other molecules. it is essential

for growth. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTS1.

[35308] The function of LZTS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.MAC30 (Accession XP_031536.2) is another GAM281 target gene, herein designated TARGET GENE. MAC30 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAC30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAC30 BINDING SITE, designated SEQ ID:5069, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35309] Another function of GAM281 is therefore inhibition of MAC30 (Accession XP_031536.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAC30.

[35310] Map-kinase activating death domain (MADD, Accession NP_569832.1) is another GAM281 target gene, herein designated TARGET GENE. MADD BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MADD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MADD BINDING SITE, designated SEQ ID:3262, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35311] Another function of GAM281 is therefore inhibition of Map-kinase activating death domain (MADD, Accession NP_569832.1), a gene which may regulate two different pathways for neural activities.interacts with the type- 1 tumor necrosis factor receptor (TNFR1); death domain-containing protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADD.

[35312] The function of MADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.2.Map-kinase activating death domain (MADD, Accession NP_569828.1) is another GAM281 target gene, herein designated TARGET GENE. MADD BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by MADD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MADD BINDING SITE, designated SEQ ID:3262, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35313] Another function of GAM281 is therefore inhibition of Map-kinase activating death domain (MADD, Accession NP_569828.1), a gene which may regulate two different pathways for neural activities.interacts with the type- 1 tumor necrosis factor receptor (TNFR1); death domain-containing protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADD.

[35314] The function of MADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.2.Map-kinase activating death domain (MADD, Accession NP_003673.2) is another GAM281 target gene, herein designated TARGET GENE. MADD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MADD, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MADD BINDING SITE, designated SEQ ID:3262, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35315] Another function of GAM281 is therefore inhibition of Map-kinase activating death domain (MADD, Accession NP_003673.2), a gene which may regulate two different pathways for neural activities.interacts with the type- 1 tumor necrosis factor receptor (TNFR1); death domain-containing protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADD.

[35316] The function of MADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.2.Map-kinase activating death domain (MADD, Accession NP_569829.1) is another GAM281 target gene, herein designated TARGET GENE. MADD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MADD, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MADD BINDING SITE, designated SEQ ID:3262, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35317] Another function of GAM281 is therefore inhibition of Map-kinase activating death domain (MADD, Accession NP_569829.1), a gene which may regulate two different pathways for neural activities.interacts with the type- 1 tumor necrosis factor receptor (TNFR1); death domain-containing protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADD.

[35318] The function of MADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.2.Map-kinase activating death domain (MADD, Accession NP_569830.1) is another GAM281 target gene, herein designated TARGET GENE. MADD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MADD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MADD BINDING SITE, designated SEQ ID:3262, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35319] Another function of GAM281 is therefore inhibition of Map-kinase activating death domain (MADD, Accession NP_569830.1), a gene which may regulate two different pathways for neural activities.interacts with the type- 1 tumor necrosis factor receptor (TNFR1); death domain-containing protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADD.

[35320] The function of MADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.2.Map-kinase activating death domain (MADD, Accession NP_569826.1) is another GAM281 target gene, herein designated TARGET GENE. MADD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MADD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MADD BINDING SITE, designated SEQ ID:3262, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35321] Another function of GAM281 is therefore inhibition of Map-kinase activating death domain (MADD, Accession NP_569826.1), a gene which may regulate two different pathways for neural activities.interacts with the type- 1 tumor necrosis factor receptor (TNFR1); death domain-containing protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADD.

[35322] The function of MADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.2.Map-kinase activating death domain (MADD, Accession NP_569831.1) is another GAM281 target gene, herein designated TARGET GENE. MADD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MADD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MADD BINDING SITE, designated SEQ ID:3262, to the nu-

cleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35323] Another function of GAM281 is therefore inhibition of Map-kinase activating death domain (MADD, Accession NP_569831.1), a gene which may regulate two different pathways for neural activities.interacts with the type- 1 tumor necrosis factor receptor (TNFR1); death domain-containing protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADD.

[35324] The function of MADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.2.Map-kinase activating death domain (MADD, Accession NP_569827.1) is another GAM281 target gene, herein designated TARGET GENE. MADD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MADD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MADD BINDING SITE, designated SEQ ID:3262, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[35325] Another function of GAM281 is therefore inhibition of Map-kinase activating death domain (MADD, Accession NP_569827.1), a gene which may regulate two different pathways for neural activities.interacts with the type- 1 tumor necrosis factor receptor (TNFR1); death domain-containing protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADD.

[35326] The function of MADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.2.MAIL (Accession NP_113607.1) is another GAM281 target gene, herein designated TARGET GENE. MAIL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAIL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAIL BINDING SITE, designated SEQ ID:2338, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35327] Another function of GAM281 is therefore inhibition of

MAIL (Accession NP_113607.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAIL.

[35328] Male germ cell-associated kinase (MAK, Accession NP_005897.1) is another GAM281 target gene, herein designated TARGET GENE. MAK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAK BINDING SITE, designated SEQ ID:1989, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35329] Another function of GAM281 is therefore inhibition of Male germ cell-associated kinase (MAK, Accession NP_005897.1), a gene which plays an important role in spermatogenesis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAK.

[35330] The function of MAK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Mitogen-activated protein kinase kinase 1

(MAP2K1, Accession NP_002746.1) is another GAM281 target gene, herein designated TARGET GENE. MAP2K1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAP2K1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAP2K1 BINDING SITE, designated SEQ ID:5154, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35331] Another function of GAM281 is therefore inhibition of Mitogen-activated protein kinase kinase 1 (MAP2K1, Accession NP_002746.1), a gene which is a signaling intermediate, may take part in cell transformation and therefore may be associated with Colon cancer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Colon cancer, and of other diseases and clinical conditions associated with MAP2K1.

[35332] The function of MAP2K1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.1.MAPA (Accession NP_660299.1) is another GAM281 target gene, herein designated TARGET GENE.

MAPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPA BINDING SITE, designated SEQ ID:5231, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35333] Another function of GAM281 is therefore inhibition of MAPA (Accession NP_660299.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPA.

[35334] Mitogen-activated protein kinase 8 interacting protein 3 (MAPK8IP3, Accession NP_203750.1) is another GAM281 target gene, herein designated TARGET GENE. MAPK8IP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK8IP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPK8IP3 BINDING SITE, designated SEQ ID:14298, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ

ID:278.

[35335] Another function of GAM281 is therefore inhibition of Mitogen-activated protein kinase 8 interacting protein 3 (MAPK8IP3, Accession NP_203750.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK8IP3.

[35336] Microtubule-associated protein, rp/eb family, member 1 (MAPRE1, Accession NP_036457.1) is another GAM281 target gene, herein designated TARGET GENE. MAPRE1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAPRE1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPRE1 BINDING SITE, designated SEQ ID:20000, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35337] Another function of GAM281 is therefore inhibition of Microtubule-associated protein, rp/eb family, member 1 (MAPRE1, Accession NP_036457.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MAPRE1.

[35338] MCLC (Accession NP_055942.1) is another GAM281 target gene, herein designated TARGET GENE. MCLC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MCLC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCLC BINDING SITE, designated SEQ ID:7270, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35339] Another function of GAM281 is therefore inhibition of MCLC (Accession NP_055942.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCLC.

[35340] Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006869.1) is another GAM281 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35341] Another function of GAM281 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006869.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[35342] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006871.1) is another GAM281 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35343] Another function of GAM281 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006871.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[35344] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession

NP_006873.1) is another GAM281 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35345] Another function of GAM281 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006873.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[35346] The function of MDM2 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006870.1) is another GAM281 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35347] Another function of GAM281 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006870.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical condi-

tions associated with MDM2.

[35348] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006872.1) is another GAM281 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35349] Another function of GAM281 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006872.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[35350] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_002383.1) is another GAM281 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6671, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35351] Another function of GAM281 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_002383.1), a gene which binds to and downmodulates p53 (TP53) and

retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[35352] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm4, transformed 3t3 cell double minute 4, p53 binding protein (mouse) (MDM4, Accession NP_002384.1) is another GAM281 target gene, herein designated TARGET GENE. MDM4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MDM4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM4 BINDING SITE, designated SEQ ID:7078, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35353] Another function of GAM281 is therefore inhibition of Mdm4, transformed 3t3 cell double minute 4, p53 binding

protein (mouse) (MDM4, Accession NP_002384.1), a gene which Strongly similar to murine Mdm4; may interact with p53. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDM4.

[35354] The function of MDM4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.MDS009 (Accession NP_064619.1) is another GAM281 target gene, herein designated TARGET GENE. MDS009 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MDS009, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDS009 BINDING SITE, designated SEQ ID:835, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35355] Another function of GAM281 is therefore inhibition of MDS009 (Accession NP_064619.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDS009.

[35356] Mediterranean fever (MEFV, Accession NP_000234.1) is another GAM281 target gene, herein designated TARGET GENE. MEFV BINDING SITE1 and MEFV BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MEFV, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MEFV BINDING SITE1 and MEFV BINDING SITE2, designated SEQ ID:19829 and SEQ ID:5443 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35357] Another function of GAM281 is therefore inhibition of Mediterranean fever (MEFV, Accession NP_000234.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEFV.

[35358] Mesoderm development candidate 2 (MESDC2, Accession XP_051854.1) is another GAM281 target gene, herein designated TARGET GENE. MESDC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MESDC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MESDC2 BINDING SITE, designated SEQ ID:6523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35359] Another function of GAM281 is therefore inhibition of Mesoderm development candidate 2 (MESDC2, Accession XP_051854.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MESDC2.

[35360] Microfibrillar-associated protein 4 (MFAP4, Accession NP_002395.1) is another GAM281 target gene, herein designated TARGET GENE. MFAP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MFAP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MFAP4 BINDING SITE, designated SEQ ID:9082, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35361] Another function of GAM281 is therefore inhibition of Microfibrillar-associated protein 4 (MFAP4, Accession NP_002395.1) . Accordingly, utilities of GAM281 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with MFAP4.

[35362] MFTC (Accession NP_110407.2) is another GAM281 target gene, herein designated TARGET GENE. MFTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MFTC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MFTC BINDING SITE, designated SEQ ID:16545, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35363] Another function of GAM281 is therefore inhibition of MFTC (Accession NP_110407.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MFTC.

[35364] Mannosyl (alpha-1,6-)-glycoprotein beta-1,2-n-acetylglucosaminyltransferase (MGAT2, Accession NP_079374.1) is another GAM281 target gene, herein designated TARGET GENE. MGAT2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MGAT2, corresponding to a target binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGAT2 BINDING SITE, designated SEQ ID:9699, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35365] Another function of GAM281 is therefore inhibition of Mannosyl (alpha-1,6-)-glycoprotein beta-1,2-n-acetylglucosaminyltransferase (MGAT2, Accession NP_079374.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAT2.

[35366] MGC10200 (Accession NP_659497.1) is another GAM281 target gene, herein designated TARGET GENE. MGC10200 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10200, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10200 BINDING SITE, designated SEQ ID:5781, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35367] Another function of GAM281 is therefore inhibition of MGC10200 (Accession NP_659497.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10200.

[35368] MGC10772 (Accession NP_085044.2) is another GAM281 target gene, herein designated TARGET GENE. MGC10772 BINDING SITE1 and MGC10772 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC10772, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10772 BINDING SITE1 and MGC10772 BINDING SITE2, designated SEQ ID:6519 and SEQ ID:5386 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35369] Another function of GAM281 is therefore inhibition of MGC10772 (Accession NP_085044.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10772.

[35370] MGC10818 (Accession NP_085045.2) is another GAM281 target gene, herein designated TARGET GENE. MGC10818 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC10818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10818 BINDING SITE, designated SEQ ID:2199, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35371] Another function of GAM281 is therefore inhibition of MGC10818 (Accession NP_085045.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10818.

[35372] MGC11102 (Accession NP_115701.2) is another GAM281 target gene, herein designated TARGET GENE. MGC11102 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC11102, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC11102 BINDING SITE, designated SEQ ID:17609, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35373] Another function of GAM281 is therefore inhibition of

MGC11102 (Accession NP_115701.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11102.

[35374] MGC12262 (Accession NP_116085.1) is another GAM281 target gene, herein designated TARGET GENE. MGC12262 BINDING SITE1 and MGC12262 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC12262, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC12262 BINDING SITE1 and MGC12262 BINDING SITE2, designated SEQ ID:4245 and SEQ ID:12220 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35375] Another function of GAM281 is therefore inhibition of MGC12262 (Accession NP_116085.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12262.

[35376] MGC12518 (Accession NP_291026.1) is another GAM281 target gene, herein designated TARGET GENE. MGC12518

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC12518, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC12518 BINDING SITE, designated SEQ ID:18251, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35377] Another function of GAM281 is therefore inhibition of MGC12518 (Accession NP_291026.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12518.

[35378] MGC12760 (Accession NP_116112.1) is another GAM281 target gene, herein designated TARGET GENE. MGC12760 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC12760, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC12760 BINDING SITE, designated SEQ ID:10178, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35379] Another function of GAM281 is therefore inhibition of MGC12760 (Accession NP_116112.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12760.

[35380] MGC13017 (Accession NP_542387.1) is another GAM281 target gene, herein designated TARGET GENE. MGC13017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13017 BINDING SITE, designated SEQ ID:11562, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35381] Another function of GAM281 is therefore inhibition of MGC13017 (Accession NP_542387.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13017.

[35382] MGC13024 (Accession NP_689501.1) is another GAM281 target gene, herein designated TARGET GENE. MGC13024 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC13024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13024 BINDING SITE, designated SEQ ID:13564, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35383] Another function of GAM281 is therefore inhibition of MGC13024 (Accession NP_689501.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13024.

[35384] MGC13138 (Accession NP_219363.1) is another GAM281 target gene, herein designated TARGET GENE. MGC13138 BINDING SITE1 and MGC13138 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC13138, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13138 BINDING SITE1 and MGC13138 BINDING SITE2, designated SEQ ID:6646 and SEQ ID:9543 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[35385] Another function of GAM281 is therefore inhibition of MGC13138 (Accession NP_219363.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13138.

[35386] MGC13170 (Accession NP_116101.1) is another GAM281 target gene, herein designated TARGET GENE. MGC13170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13170 BINDING SITE, designated SEQ ID:20116, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35387] Another function of GAM281 is therefore inhibition of MGC13170 (Accession NP_116101.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13170.

[35388] MGC13204 (Accession NP_113653.1) is another GAM281 target gene, herein designated TARGET GENE. MGC13204

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13204, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13204 BINDING SITE, designated SEQ ID:9494, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35389] Another function of GAM281 is therefore inhibition of MGC13204 (Accession NP_113653.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13204.

[35390] MGC14289 (Accession NP_542391.1) is another GAM281 target gene, herein designated TARGET GENE. MGC14289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14289 BINDING SITE, designated SEQ ID:3677, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35391] Another function of GAM281 is therefore inhibition of MGC14289 (Accession NP_542391.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14289.

[35392] MGC14436 (Accession NP_116286.1) is another GAM281 target gene, herein designated TARGET GENE. MGC14436 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC14436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14436 BINDING SITE, designated SEQ ID:17347, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35393] Another function of GAM281 is therefore inhibition of MGC14436 (Accession NP_116286.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14436.

[35394] MGC14836 (Accession NP_219480.1) is another GAM281 target gene, herein designated TARGET GENE. MGC14836 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC14836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14836 BINDING SITE, designated SEQ ID:15044, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35395] Another function of GAM281 is therefore inhibition of MGC14836 (Accession NP_219480.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14836.

[35396] MGC15606 (Accession NP_659474.1) is another GAM281 target gene, herein designated TARGET GENE. MGC15606 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC15606, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15606 BINDING SITE, designated SEQ ID:10968, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35397] Another function of GAM281 is therefore inhibition of

MGC15606 (Accession NP_659474.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15606.

[35398] MGC15668 (Accession NP_116145.1) is another GAM281 target gene, herein designated TARGET GENE. MGC15668 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC15668, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15668 BINDING SITE, designated SEQ ID:3620, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35399] Another function of GAM281 is therefore inhibition of MGC15668 (Accession NP_116145.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15668.

[35400] MGC15873 (Accession NP_116309.1) is another GAM281 target gene, herein designated TARGET GENE. MGC15873 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC15873, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15873 BINDING SITE, designated SEQ ID:2894, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35401] Another function of GAM281 is therefore inhibition of MGC15873 (Accession NP_116309.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15873.

[35402] MGC16179 (Accession NP_116155.1) is another GAM281 target gene, herein designated TARGET GENE. MGC16179 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC16179, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC16179 BINDING SITE, designated SEQ ID:15168, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35403] Another function of GAM281 is therefore inhibition of MGC16179 (Accession NP_116155.1) . Accordingly, utili-

ties of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16179.

[35404] MGC1842 (Accession XP_037797.2) is another GAM281 target gene, herein designated TARGET GENE. MGC1842 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC1842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC1842 BINDING SITE, designated SEQ ID:15046, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35405] Another function of GAM281 is therefore inhibition of MGC1842 (Accession XP_037797.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC1842.

[35406] MGC21675 (Accession NP_443093.1) is another GAM281 target gene, herein designated TARGET GENE. MGC21675 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC21675, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC21675 BINDING SITE, designated SEQ ID:16916, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35407] Another function of GAM281 is therefore inhibition of MGC21675 (Accession NP_443093.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21675.

[35408] MGC2306 (Accession NP_002041.2) is another GAM281 target gene, herein designated TARGET GENE. MGC2306 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2306, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2306 BINDING SITE, designated SEQ ID:7160, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35409] Another function of GAM281 is therefore inhibition of MGC2306 (Accession NP_002041.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MGC2306.

[35410] MGC2474 (Accession NP_076420.1) is another GAM281 target gene, herein designated TARGET GENE. MGC2474 BINDING SITE1 and MGC2474 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC2474, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2474 BINDING SITE1 and MGC2474 BINDING SITE2, designated SEQ ID:7797 and SEQ ID:18665 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35411] Another function of GAM281 is therefore inhibition of MGC2474 (Accession NP_076420.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2474.

[35412] MGC2477 (Accession NP_077004.1) is another GAM281 target gene, herein designated TARGET GENE. MGC2477 BINDING SITE1 through MGC2477 BINDING SITE3 are target binding sites found in untranslated regions of mRNA

encoded by MGC2477, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2477 BINDING SITE1 through MGC2477 BINDING SITE3, designated SEQ ID:5609, SEQ ID:19729 and SEQ ID:8610 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35413] Another function of GAM281 is therefore inhibition of MGC2477 (Accession NP_077004.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2477.

[35414] MGC2603 (Accession NP_076942.1) is another GAM281 target gene, herein designated TARGET GENE. MGC2603 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2603 BINDING SITE, designated SEQ ID:5845, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35415] Another function of GAM281 is therefore inhibition of MGC2603 (Accession NP_076942.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2603.

[35416] MGC26914 (Accession NP_659413.1) is another GAM281 target gene, herein designated TARGET GENE. MGC26914 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC26914, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC26914 BINDING SITE, designated SEQ ID:15104, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35417] Another function of GAM281 is therefore inhibition of MGC26914 (Accession NP_659413.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC26914.

[35418] MGC2718 (Accession NP_076972.2) is another GAM281 target gene, herein designated TARGET GENE. MGC2718 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC2718, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2718 BINDING SITE, designated SEQ ID:3976, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35419] Another function of GAM281 is therefore inhibition of MGC2718 (Accession NP_076972.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2718.

[35420] MGC27345 (Accession XP_300964.1) is another GAM281 target gene, herein designated TARGET GENE. MGC27345 BINDING SITE1 and MGC27345 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MGC27345, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC27345 BINDING SITE1 and MGC27345 BINDING SITE2, designated SEQ ID:18352 and SEQ ID:19385 respectively, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[35421] Another function of GAM281 is therefore inhibition of MGC27345 (Accession XP_300964.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC27345.

[35422] MGC29891 (Accession NP_653219.1) is another GAM281 target gene, herein designated TARGET GENE. MGC29891 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC29891, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC29891 BINDING SITE, designated SEQ ID:14858, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35423] Another function of GAM281 is therefore inhibition of MGC29891 (Accession NP_653219.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29891.

[35424] MGC29898 (Accession NP_659485.1) is another GAM281 target gene, herein designated TARGET GENE. MGC29898

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC29898, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC29898 BINDING SITE, designated SEQ ID:16672, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35425] Another function of GAM281 is therefore inhibition of MGC29898 (Accession NP_659485.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29898.

[35426] MGC3113 (Accession NP_076940.1) is another GAM281 target gene, herein designated TARGET GENE. MGC3113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3113 BINDING SITE, designated SEQ ID:10136, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35427] Another function of GAM281 is therefore inhibition of MGC3113 (Accession NP_076940.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3113.

[35428] MGC3207 (Accession NP_115661.1) is another GAM281 target gene, herein designated TARGET GENE. MGC3207 BINDING SITE1 and MGC3207 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC3207, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3207 BINDING SITE1 and MGC3207 BINDING SITE2, designated SEQ ID:5157 and SEQ ID:13812 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35429] Another function of GAM281 is therefore inhibition of MGC3207 (Accession NP_115661.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3207.

[35430] MGC3329 (Accession NP_076991.2) is another GAM281

target gene, herein designated TARGET GENE. MGC3329 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3329 BINDING SITE, designated SEQ ID:4477, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35431] Another function of GAM281 is therefore inhibition of MGC3329 (Accession NP_076991.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3329.

[35432] MGC33486 (Accession NP_694998.1) is another GAM281 target gene, herein designated TARGET GENE. MGC33486 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC33486, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC33486 BINDING SITE, designated SEQ ID:11585, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[35433] Another function of GAM281 is therefore inhibition of MGC33486 (Accession NP_694998.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33486.

[35434] MGC33637 (Accession NP_689809.1) is another GAM281 target gene, herein designated TARGET GENE. MGC33637 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC33637, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC33637 BINDING SITE, designated SEQ ID:12069, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35435] Another function of GAM281 is therefore inhibition of MGC33637 (Accession NP_689809.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33637.

[35436] MGC33887 (Accession NP_659473.1) is another GAM281 target gene, herein designated TARGET GENE. MGC33887

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC33887, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC33887 BINDING SITE, designated SEQ ID:8724, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35437] Another function of GAM281 is therefore inhibition of MGC33887 (Accession NP_659473.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33887.

[35438] MGC34034 (Accession NP_694956.1) is another GAM281 target gene, herein designated TARGET GENE. MGC34034 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC34034, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34034 BINDING SITE, designated SEQ ID:9529, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35439] Another function of GAM281 is therefore inhibition of MGC34034 (Accession NP_694956.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34034.

[35440] MGC34079 (Accession NP_689688.1) is another GAM281 target gene, herein designated TARGET GENE. MGC34079 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC34079, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34079 BINDING SITE, designated SEQ ID:19817, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35441] Another function of GAM281 is therefore inhibition of MGC34079 (Accession NP_689688.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34079.

[35442] MGC34132 (Accession XP_291029.1) is another GAM281 target gene, herein designated TARGET GENE. MGC34132 BINDING SITE1 and MGC34132 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by MGC34132, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34132 BINDING SITE1 and MGC34132 BINDING SITE2, designated SEQ ID:9087 and SEQ ID:8232 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35443] Another function of GAM281 is therefore inhibition of MGC34132 (Accession XP_291029.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34132.

[35444] MGC35136 (Accession NP_689640.1) is another GAM281 target gene, herein designated TARGET GENE. MGC35136 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC35136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35136 BINDING SITE, designated SEQ ID:8535, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[35445] Another function of GAM281 is therefore inhibition of MGC35136 (Accession NP_689640.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35136.

[35446] MGC35440 (Accession NP_694952.1) is another GAM281 target gene, herein designated TARGET GENE. MGC35440 BINDING SITE1 and MGC35440 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC35440, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35440 BINDING SITE1 and MGC35440 BINDING SITE2, designated SEQ ID:7378 and SEQ ID:6886 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35447] Another function of GAM281 is therefore inhibition of MGC35440 (Accession NP_694952.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35440.

[35448] MGC35468 (Accession NP_694976.1) is another GAM281 target gene, herein designated TARGET GENE. MGC35468 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35468, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35468 BINDING SITE, designated SEQ ID:7484, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35449] Another function of GAM281 is therefore inhibition of MGC35468 (Accession NP_694976.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35468.

[35450] MGC3771 (Accession NP_112232.1) is another GAM281 target gene, herein designated TARGET GENE. MGC3771 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC3771, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3771 BINDING SITE, designated SEQ ID:3231, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35451] Another function of GAM281 is therefore inhibition of MGC3771 (Accession NP_112232.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3771.

[35452] MGC39320 (Accession NP_689642.2) is another GAM281 target gene, herein designated TARGET GENE. MGC39320 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC39320, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC39320 BINDING SITE, designated SEQ ID:13428, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35453] Another function of GAM281 is therefore inhibition of MGC39320 (Accession NP_689642.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC39320.

[35454] MGC40157 (Accession NP_689563.1) is another GAM281

target gene, herein designated TARGET GENE. MGC40157 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC40157, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40157 BINDING SITE, designated SEQ ID:10743, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35455] Another function of GAM281 is therefore inhibition of MGC40157 (Accession NP_689563.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40157.

[35456] MGC40168 (Accession NP_714920.1) is another GAM281 target gene, herein designated TARGET GENE. MGC40168 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC40168, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40168 BINDING SITE, designated SEQ ID:7220, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[35457] Another function of GAM281 is therefore inhibition of MGC40168 (Accession NP_714920.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40168.

[35458] MGC40579 (Accession NP_689989.1) is another GAM281 target gene, herein designated TARGET GENE. MGC40579 BINDING SITE1 and MGC40579 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC40579, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40579 BINDING SITE1 and MGC40579 BINDING SITE2, designated SEQ ID:16218 and SEQ ID:19220 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35459] Another function of GAM281 is therefore inhibition of MGC40579 (Accession NP_689989.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40579.

[35460] MGC4171 (Accession NP_077283.1) is another GAM281 target gene, herein designated TARGET GENE. MGC4171 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC4171, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4171 BINDING SITE, designated SEQ ID:10555, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35461] Another function of GAM281 is therefore inhibition of MGC4171 (Accession NP_077283.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4171.

[35462] MGC4248 (Accession NP_115709.2) is another GAM281 target gene, herein designated TARGET GENE. MGC4248 BINDING SITE1 and MGC4248 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC4248, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4248 BINDING SITE1 and

MGC4248 BINDING SITE2, designated SEQ ID:3338 and SEQ ID:8539 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35463] Another function of GAM281 is therefore inhibition of MGC4248 (Accession NP_115709.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4248.

[35464] MGC43122 (Accession NP_775784.1) is another GAM281 target gene, herein designated TARGET GENE. MGC43122 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC43122, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC43122 BINDING SITE, designated SEQ ID:12783, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35465] Another function of GAM281 is therefore inhibition of MGC43122 (Accession NP_775784.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC43122.

[35466] MGC4606 (Accession NP_078792.1) is another GAM281 target gene, herein designated TARGET GENE. MGC4606 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC4606, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4606 BINDING SITE, designated SEQ ID:11069, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35467] Another function of GAM281 is therefore inhibition of MGC4606 (Accession NP_078792.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4606.

[35468] MGC50452 (Accession NP_775733.1) is another GAM281 target gene, herein designated TARGET GENE. MGC50452 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC50452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC50452 BINDING SITE, designated SEQ ID:16867, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35469] Another function of GAM281 is therefore inhibition of MGC50452 (Accession NP_775733.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC50452.

[35470] MGC50559 (Accession NP_776163.1) is another GAM281 target gene, herein designated TARGET GENE. MGC50559 BINDING SITE1 and MGC50559 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC50559, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC50559 BINDING SITE1 and MGC50559 BINDING SITE2, designated SEQ ID:15151 and SEQ ID:11296 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35471] Another function of GAM281 is therefore inhibition of MGC50559 (Accession NP_776163.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC50559.

[35472] MGC5149 (Accession XP_051200.2) is another GAM281 target gene, herein designated TARGET GENE. MGC5149 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC5149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC5149 BINDING SITE, designated SEQ ID:13759, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35473] Another function of GAM281 is therefore inhibition of MGC5149 (Accession XP_051200.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5149.

[35474] MGC9912 (Accession NP_542395.1) is another GAM281 target gene, herein designated TARGET GENE. MGC9912 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC9912, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC9912 BINDING SITE, designated SEQ ID:12221, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35475] Another function of GAM281 is therefore inhibition of MGC9912 (Accession NP_542395.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC9912.

[35476] MGRN1 (Accession XP_048119.4) is another GAM281 target gene, herein designated TARGET GENE. MGRN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGRN1 BINDING SITE, designated SEQ ID:16616, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35477] Another function of GAM281 is therefore inhibition of MGRN1 (Accession XP_048119.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGRN1.

[35478] Mhc class ii transactivator (MHC2TA, Accession NP_000237.1) is another GAM281 target gene, herein designated TARGET GENE. MHC2TA BINDING SITE1 through MHC2TA BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by MHC2TA, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MHC2TA BINDING SITE1 through MHC2TA BINDING SITE3, designated SEQ ID:783, SEQ ID:2053 and SEQ ID:922 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35479] Another function of GAM281 is therefore inhibition of Mhc class ii transactivator (MHC2TA, Accession NP_000237.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MHC2TA.

[35480] MIRAB13 (Accession XP_039236.6) is another GAM281 target gene, herein designated TARGET GENE. MIRAB13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MIRAB13, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIRAB13 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35481] Another function of GAM281 is therefore inhibition of MIRAB13 (Accession XP_039236.6) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIRAB13.

[35482] MIRAB13 (Accession NP_203744.1) is another GAM281 target gene, herein designated TARGET GENE. MIRAB13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MIRAB13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIRAB13 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35483] Another function of GAM281 is therefore inhibition of

MIRAB13 (Accession NP_203744.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIRAB13.

[35484] Makorin, ring finger protein, 4 (MKRN4, Accession NP_110384.1) is another GAM281 target gene, herein designated TARGET GENE. MKRN4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MKRN4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MKRN4 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35485] Another function of GAM281 is therefore inhibition of Makorin, ring finger protein, 4 (MKRN4, Accession NP_110384.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKRN4.

[35486] Melan-a (MLANA, Accession NP_005502.1) is another GAM281 target gene, herein designated TARGET GENE. MLANA BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by MLANA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLANA BINDING SITE, designated SEQ ID:13029, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35487] Another function of GAM281 is therefore inhibition of Melan-a (MLANA, Accession NP_005502.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLANA.

[35488] Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_055981.1) is another GAM281 target gene, herein designated TARGET GENE. MLC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MLC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLC1 BINDING SITE, designated SEQ ID:19859, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ

ID:278.

[35489] Another function of GAM281 is therefore inhibition of Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_055981.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLC1.

[35490] Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_055981.1) is another GAM281 target gene, herein designated TARGET GENE. MLC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MLC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLC1 BINDING SITE, designated SEQ ID:19859, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35491] Another function of GAM281 is therefore inhibition of Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_055981.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with MLC1.

[35492] Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_631941.1) is another GAM281 target gene, herein designated TARGET GENE. MLC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MLC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLC1 BINDING SITE, designated SEQ ID:19859, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35493] Another function of GAM281 is therefore inhibition of Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_631941.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLC1.

[35494] Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_631941.1) is another GAM281 target gene, herein designated TARGET GENE.

MLC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MLC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLC1 BINDING SITE, designated SEQ ID:19859, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35495] Another function of GAM281 is therefore inhibition of Megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1, Accession NP_631941.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLC1.

[35496] Melanoma-derived leucine zipper, extra-nuclear factor (MLZE, Accession NP_113603.1) is another GAM281 target gene, herein designated TARGET GENE. MLZE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MLZE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLZE BIND-

ING SITE, designated SEQ ID:9728, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35497] Another function of GAM281 is therefore inhibition of Melanoma-derived leucine zipper, extra-nuclear factor (MLZE, Accession NP_113603.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLZE.

[35498] Matrix metalloproteinase-like 1 (MMPL1, Accession NP_004133.1) is another GAM281 target gene, herein designated TARGET GENE. MMPL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MMPL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MMPL1 BINDING SITE, designated SEQ ID:4374, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35499] Another function of GAM281 is therefore inhibition of Matrix metalloproteinase-like 1 (MMPL1, Accession NP_004133.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMPL1.

[35500] MO25 (Accession NP_057373.1) is another GAM281 target gene, herein designated TARGET GENE. MO25 BINDING SITE1 and MO25 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MO25, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MO25 BINDING SITE1 and MO25 BINDING SITE2, designated SEQ ID:7980 and SEQ ID:2695 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35501] Another function of GAM281 is therefore inhibition of MO25 (Accession NP_057373.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MO25.

[35502] Modulator of apoptosis 1 (MOAP1, Accession NP_071434.2) is another GAM281 target gene, herein designated TARGET GENE. MOAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MOAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MOAP1 BINDING SITE, designated

SEQ ID:1744, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35503] Another function of GAM281 is therefore inhibition of Modulator of apoptosis 1 (MOAP1, Accession NP_071434.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOAP1.

[35504] moblak (Accession NP_570719.1) is another GAM281 target gene, herein designated TARGET GENE. moblak BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by moblak, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of moblak BINDING SITE, designated SEQ ID:19657, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35505] Another function of GAM281 is therefore inhibition of moblak (Accession NP_570719.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with moblak.

[35506] Molybdenum cofactor synthesis 3 (MOCS3, Accession NP_055299.1) is another GAM281 target gene, herein

designated TARGET GENE. MOCS3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MOCS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MOCS3 BINDING SITE, designated SEQ ID:12064, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35507] Another function of GAM281 is therefore inhibition of Molybdenum cofactor synthesis 3 (MOCS3, Accession NP_055299.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOCS3.

[35508] Myeloproliferative leukemia virus oncogene (MPL, Accession NP_005364.1) is another GAM281 target gene, herein designated TARGET GENE. MPL BINDING SITE1 and MPL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MPL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPL BINDING SITE1 and MPL BINDING SITE2, designated SEQ ID:16608

and SEQ ID:11185 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35509] Another function of GAM281 is therefore inhibition of Myeloproliferative leukemia virus oncogene (MPL, Accession NP_005364.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPL.

[35510] Mitochondrial ribosomal protein l10 (MRPL10, Accession NP_683685.1) is another GAM281 target gene, herein designated TARGET GENE. MRPL10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MRPL10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL10 BINDING SITE, designated SEQ ID:13874, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35511] Another function of GAM281 is therefore inhibition of Mitochondrial ribosomal protein l10 (MRPL10, Accession NP_683685.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with MRPL10.

[35512] Mitochondrial ribosomal protein l35 (MRPL35, Accession NP_057706.2) is another GAM281 target gene, herein designated TARGET GENE. MRPL35 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL35, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL35 BINDING SITE, designated SEQ ID:9545, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35513] Another function of GAM281 is therefore inhibition of Mitochondrial ribosomal protein l35 (MRPL35, Accession NP_057706.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL35.

[35514] Mitochondrial ribosomal protein l44 (MRPL44, Accession NP_075066.1) is another GAM281 target gene, herein designated TARGET GENE. MRPL44 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPL44, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL44 BINDING SITE, designated SEQ ID:14596, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35515] Another function of GAM281 is therefore inhibition of Mitochondrial ribosomal protein l44 (MRPL44, Accession NP_075066.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL44.

[35516] Mitochondrial ribosomal protein l49 (MRPL49, Accession NP_004918.1) is another GAM281 target gene, herein designated TARGET GENE. MRPL49 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPL49, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL49 BINDING SITE, designated SEQ ID:5438, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35517] Another function of GAM281 is therefore inhibition of Mitochondrial ribosomal protein l49 (MRPL49, Accession

NP_004918.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL49.

[35518] Mitochondrial ribosomal protein s27 (MRPS27, Accession NP_055899.1) is another GAM281 target gene, herein designated TARGET GENE. MRPS27 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPS27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPS27 BINDING SITE, designated SEQ ID:4179, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35519] Another function of GAM281 is therefore inhibition of Mitochondrial ribosomal protein s27 (MRPS27, Accession NP_055899.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS27.

[35520] MSTP028 (Accession NP_114160.1) is another GAM281 target gene, herein designated TARGET GENE. MSTP028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MSTP028, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MSTP028 BINDING SITE, designated SEQ ID:12951, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35521] Another function of GAM281 is therefore inhibition of MSTP028 (Accession NP_114160.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSTP028.

[35522] MtFMT (Accession NP_640335.1) is another GAM281 target gene, herein designated TARGET GENE. MtFMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MtFMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MtFMT BINDING SITE, designated SEQ ID:12918, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35523] Another function of GAM281 is therefore inhibition of MtFMT (Accession NP_640335.1) . Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MtFMT.

[35524] MTH2 (Accession NP_060753.1) is another GAM281 target gene, herein designated TARGET GENE. MTH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTH2 BINDING SITE, designated SEQ ID:15874, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35525] Another function of GAM281 is therefore inhibition of MTH2 (Accession NP_060753.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTH2.

[35526] 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR, Accession NP_000245.1) is another GAM281 target gene, herein designated TARGET GENE. MTR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of MTR BINDING SITE, designated SEQ ID:2028, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35527] Another function of GAM281 is therefore inhibition of 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR, Accession NP_000245.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTR.

[35528] MU (Accession NP_071368.1) is another GAM281 target gene, herein designated TARGET GENE. MU BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MU BINDING SITE, designated SEQ ID:2453, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35529] Another function of GAM281 is therefore inhibition of MU (Accession NP_071368.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with MU.

[35530] V-myc myelocytomatosis viral oncogene homolog 2 (avian) (MYCL2, Accession NP_005368.1) is another GAM281 target gene, herein designated TARGET GENE. MYCL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYCL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYCL2 BINDING SITE, designated SEQ ID:16868, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35531] Another function of GAM281 is therefore inhibition of V-myc myelocytomatosis viral oncogene homolog 2 (avian) (MYCL2, Accession NP_005368.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYCL2.

[35532] MYLC2PL (Accession NP_612412.1) is another GAM281 target gene, herein designated TARGET GENE. MYLC2PL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MYLC2PL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MYLC2PL BINDING SITE, designated SEQ ID:3580, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35533] Another function of GAM281 is therefore inhibition of MYLC2PL (Accession NP_612412.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLC2PL.

[35534] Myosin 5c (MYO5C, Accession NP_061198.1) is another GAM281 target gene, herein designated TARGET GENE. MYO5C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYO5C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYO5C BINDING SITE, designated SEQ ID:4306, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35535] Another function of GAM281 is therefore inhibition of Myosin 5c (MYO5C, Accession NP_061198.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with MYO5C.

[35536] NACT (Accession NP_808218.1) is another GAM281 target gene, herein designated TARGET GENE. NACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NACT BINDING SITE, designated SEQ ID:19968, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35537] Another function of GAM281 is therefore inhibition of NACT (Accession NP_808218.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NACT.

[35538] NALP12 (Accession NP_150639.1) is another GAM281 target gene, herein designated TARGET GENE. NALP12 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NALP12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NALP12 BINDING SITE, designated

SEQ ID:3395, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35539] Another function of GAM281 is therefore inhibition of NALP12 (Accession NP_150639.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NALP12.

[35540] Nanog (Accession NP_079141.1) is another GAM281 target gene, herein designated TARGET GENE. Nanog BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Nanog, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Nanog BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35541] Another function of GAM281 is therefore inhibition of Nanog (Accession NP_079141.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Nanog.

[35542] NCAG1 (Accession NP_115536.1) is another GAM281 target gene, herein designated TARGET GENE. NCAG1 BIND-

ING SITE1 and NCAG1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCAG1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCAG1 BINDING SITE1 and NCAG1 BINDING SITE2, designated SEQ ID:3933 and SEQ ID:3766 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35543] Another function of GAM281 is therefore inhibition of NCAG1 (Accession NP_115536.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCAG1.

[35544] Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1) is another GAM281 target gene, herein designated TARGET GENE. NCOA6 BINDING SITE1 and NCOA6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCOA6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE1 and NCOA6 BINDING SITE2, designated SEQ ID:12826 and SEQ ID:19446 respectively, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35545] Another function of GAM281 is therefore inhibition of Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1), a gene which activates gene transcription through ligand- dependent association with coactivators. and therefore may be associated with Breast cancer. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Breast cancer., and of other diseases and clinical conditions associated with NCOA6.

[35546] The function of NCOA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NP_079107.5) is another GAM281 target gene, herein designated TARGET GENE. NCOA6IP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCOA6IP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6IP BINDING SITE, designated SEQ ID:8841, to the nucleotide sequence of GAM281 RNA,

herein designated GAM RNA, also designated SEQ ID:278.

[35547] Another function of GAM281 is therefore inhibition of Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NP_079107.5) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6IP.

[35548] NDP52 (Accession NP_005822.1) is another GAM281 target gene, herein designated TARGET GENE. NDP52 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDP52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDP52 BINDING SITE, designated SEQ ID:15337, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35549] Another function of GAM281 is therefore inhibition of NDP52 (Accession NP_005822.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDP52.

[35550] Ndrg family member 3 (NDRG3, Accession NP_114402.1) is another GAM281 target gene, herein designated TARGET GENE. NDRG3 BINDING SITE is a target binding site

found in the 3` untranslated region of multiple transcripts of mRNA encoded by NDRG3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDRG3 BINDING SITE, designated SEQ ID:15102, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35551] Another function of GAM281 is therefore inhibition of Ndrg family member 3 (NDRG3, Accession NP_114402.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG3.

[35552] Ndrg family member 4 (NDRG4, Accession NP_075061.1) is another GAM281 target gene, herein designated TARGET GENE. NDRG4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NDRG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDRG4 BINDING SITE, designated SEQ ID:6180, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[35553] Another function of GAM281 is therefore inhibition of Ndrg family member 4 (NDRG4, Accession NP_075061.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG4.

[35554] Ndrg family member 4 (NDRG4, Accession NP_065198.1) is another GAM281 target gene, herein designated TARGET GENE. NDRG4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NDRG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDRG4 BINDING SITE, designated SEQ ID:6180, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35555] Another function of GAM281 is therefore inhibition of Ndrg family member 4 (NDRG4, Accession NP_065198.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG4.

[35556] Nadh dehydrogenase (ubiquinone) 1, subcomplex un-

known, 2, 14.5kda (NDUFC2, Accession NP_004540.1) is another GAM281 target gene, herein designated TARGET GENE. NDUFC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDUFC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDUFC2 BINDING SITE, designated SEQ ID:10192, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35557] Another function of GAM281 is therefore inhibition of Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDUFC2.

[35558] Nadh dehydrogenase (ubiquinone) fe-s protein 1, 75kda (nadh-coenzyme q reductase) (NDUFS1, Accession NP_004997.3) is another GAM281 target gene, herein designated TARGET GENE. NDUFS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDUFS1, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDUFS1 BINDING SITE, designated SEQ ID:20168, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35559] Another function of GAM281 is therefore inhibition of Nadh dehydrogenase (ubiquinone) fe-s protein 1, 75kda (nadh-coenzyme q reductase) (NDUFS1, Accession NP_004997.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDUFS1.

[35560] Sialidase 3 (membrane sialidase) (NEU3, Accession NP_006647.2) is another GAM281 target gene, herein designated TARGET GENE. NEU3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NEU3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEU3 BINDING SITE, designated SEQ ID:12075, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35561] Another function of GAM281 is therefore inhibition of Sialidase 3 (membrane sialidase) (NEU3, Accession NP_006647.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEU3.

[35562] Neurofibromin 2 (bilateral acoustic neuroma) (NF2, Accession NP_057502.1) is another GAM281 target gene, herein designated TARGET GENE. NF2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NF2 BINDING SITE, designated SEQ ID:9169, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35563] Another function of GAM281 is therefore inhibition of Neurofibromin 2 (bilateral acoustic neuroma) (NF2, Accession NP_057502.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NF2.

[35564] Non-pou domain containing, octamer-binding (NONO, Accession NP_031389.2) is another GAM281 target gene,

herein designated TARGET GENE. NONO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NONO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NONO BINDING SITE, designated SEQ ID:17960, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35565] Another function of GAM281 is therefore inhibition of Non-pou domain containing, octamer-binding (NONO, Accession NP_031389.2), a gene which is a nuclear protein which contains RNA recognition motifs. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NONO.

[35566] The function of NONO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.NOSIP (Accession NP_057037.1) is another GAM281 target gene, herein designated TARGET GENE. NOSIP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NOSIP, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOSIP BINDING SITE, designated SEQ ID:7311, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35567] Another function of GAM281 is therefore inhibition of NOSIP (Accession NP_057037.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOSIP.

[35568] Notch homolog 2 (drosophila) (NOTCH2, Accession NP_077719.2) is another GAM281 target gene, herein designated TARGET GENE. NOTCH2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NOTCH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOTCH2 BINDING SITE, designated SEQ ID:18893, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35569] Another function of GAM281 is therefore inhibition of Notch homolog 2 (drosophila) (NOTCH2, Accession

NP_077719.2), a gene which is moderately similar to a region of murine Notch1 and contains an ankyrin repeat. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOTCH2.

[35570] The function of NOTCH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Nucleoside phosphorylase (NP, Accession NP_000261.1) is another GAM281 target gene, herein designated TARGET GENE. NP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NP BINDING SITE, designated SEQ ID:13473, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35571] Another function of GAM281 is therefore inhibition of Nucleoside phosphorylase (NP, Accession NP_000261.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NP.

[35572] NPCR (Accession NP_660361.1) is another GAM281 target gene, herein designated TARGET GENE. NPCR BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NPCR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPCR BINDING SITE, designated SEQ ID:5959, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35573] Another function of GAM281 is therefore inhibition of NPCR (Accession NP_660361.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPCR.

[35574] Neuronal pentraxin receptor (NPTXR, Accession NP_055108.2) is another GAM281 target gene, herein designated TARGET GENE. NPTXR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NPTXR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE, designated SEQ ID:5189, to the nu-

cleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35575] Another function of GAM281 is therefore inhibition of Neuronal pentraxin receptor (NPTXR, Accession NP_055108.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR.

[35576] Neuronal pentraxin receptor (NPTXR, Accession NP_478058.1) is another GAM281 target gene, herein designated TARGET GENE. NPTXR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NPTXR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE, designated SEQ ID:5189, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35577] Another function of GAM281 is therefore inhibition of Neuronal pentraxin receptor (NPTXR, Accession NP_478058.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR.

[35578] Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1) is another GAM281 target gene, herein designated TARGET GENE. NQO1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NQO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NQO1 BINDING SITE, designated SEQ ID:14855, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35579] Another function of GAM281 is therefore inhibition of Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1), a gene which is cytochrome b5 reductase which reduces redox dyes and quinones. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NQO1.

[35580] The function of NQO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Nuclear receptor subfamily 2, group e, member 1 (NR2E1, Accession NP_003260.1) is another

GAM281 target gene, herein designated TARGET GENE. NR2E1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NR2E1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NR2E1 BINDING SITE, designated SEQ ID:13178, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35581] Another function of GAM281 is therefore inhibition of Nuclear receptor subfamily 2, group e, member 1 (NR2E1, Accession NP_003260.1), a gene which may be required for brain development and be involved in the regulation of retinal development . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR2E1.

[35582] The function of NR2E1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.NRLN1 (Accession NP_660277.1) is another GAM281 target gene, herein designated TARGET GENE. NRLN1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NRLN1, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRLN1 BINDING SITE, designated SEQ ID:15825, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35583] Another function of GAM281 is therefore inhibition of NRLN1 (Accession NP_660277.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRLN1.

[35584] 5'-nucleotidase, cytosolic ii (NT5C2, Accession NP_036361.1) is another GAM281 target gene, herein designated TARGET GENE. NT5C2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NT5C2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NT5C2 BINDING SITE, designated SEQ ID:4030, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35585] Another function of GAM281 is therefore inhibition of 5'-nucleotidase, cytosolic ii (NT5C2, Accession NP_036361.1) . Accordingly, utilities of GAM281 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with NT5C2.

[35586] Nudix (nucleoside diphosphate linked moiety x)-type motif 4 (NUDT4, Accession NP_061967.2) is another GAM281 target gene, herein designated TARGET GENE. NUDT4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NUDT4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUDT4 BINDING SITE, designated SEQ ID:18879, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35587] Another function of GAM281 is therefore inhibition of Nudix (nucleoside diphosphate linked moiety x)-type motif 4 (NUDT4, Accession NP_061967.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUDT4.

[35588] NUP43 (Accession NP_078923.2) is another GAM281 target gene, herein designated TARGET GENE. NUP43 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NUP43, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUP43 BINDING SITE, designated SEQ ID:1900, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35589] Another function of GAM281 is therefore inhibition of NUP43 (Accession NP_078923.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUP43.

[35590] Nucleoredoxin (NXN, Accession NP_071908.1) is another GAM281 target gene, herein designated TARGET GENE. NXN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NXN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NXN BINDING SITE, designated SEQ ID:935, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35591] Another function of GAM281 is therefore inhibition of Nucleoredoxin (NXN, Accession NP_071908.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with NXN.

[35592] Olfactory receptor, family 51, subfamily e, member 2 (OR51E2, Accession NP_110401.1) is another GAM281 target gene, herein designated TARGET GENE. OR51E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OR51E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OR51E2 BINDING SITE, designated SEQ ID:4096, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35593] Another function of GAM281 is therefore inhibition of Olfactory receptor, family 51, subfamily e, member 2 (OR51E2, Accession NP_110401.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OR51E2.

[35594] Origin recognition complex, subunit 1-like (yeast) (ORC1L, Accession NP_004144.1) is another GAM281 target gene, herein designated TARGET GENE. ORC1L BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by ORC1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ORC1L BINDING SITE, designated SEQ ID:17969, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35595] Another function of GAM281 is therefore inhibition of Origin recognition complex, subunit 1-like (yeast) (ORC1L, Accession NP_004144.1), a gene which may be required for initiation of DNA replication. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ORC1L.

[35596] The function of ORC1L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Oxysterol binding protein-like 2 (OSBPL2, Accession NP_055650.1) is another GAM281 target gene, herein designated TARGET GENE. OSBPL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of OSBPL2 BINDING SITE, designated SEQ ID:7553, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35597] Another function of GAM281 is therefore inhibition of Oxysterol binding protein-like 2 (OSBPL2, Accession NP_055650.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL2.

[35598] Oxysterol binding protein-like 2 (OSBPL2, Accession NP_653081.1) is another GAM281 target gene, herein designated TARGET GENE. OSBPL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL2 BINDING SITE, designated SEQ ID:7553, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35599] Another function of GAM281 is therefore inhibition of Oxysterol binding protein-like 2 (OSBPL2, Accession NP_653081.1) . Accordingly, utilities of GAM281 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL2.

[35600] Otoancorin (OTOA, Accession NP_733764.1) is another GAM281 target gene, herein designated TARGET GENE. OTOA BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by OTOA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OTOA BINDING SITE, designated SEQ ID:18386, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35601] Another function of GAM281 is therefore inhibition of Otoancorin (OTOA, Accession NP_733764.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OTOA.

[35602] P24B (Accession NP_031390.1) is another GAM281 target gene, herein designated TARGET GENE. P24B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P24B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P24B BINDING SITE, designated SEQ ID:2381, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35603] Another function of GAM281 is therefore inhibition of P24B (Accession NP_031390.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P24B.

[35604] Purinergic receptor p2x, ligand-gated ion channel, 7 (P2RX7, Accession NP_803176.1) is another GAM281 target gene, herein designated TARGET GENE. P2RX7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by P2RX7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P2RX7 BINDING SITE, designated SEQ ID:7388, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35605] Another function of GAM281 is therefore inhibition of Purinergic receptor p2x, ligand-gated ion channel, 7 (P2RX7, Accession NP_803176.1), a gene which responsi-

ble for atp- dependent lysis of macrophages and therefore may be associated with Chronic lymphatic leukemia. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Chronic lymphatic leukemia, and of other diseases and clinical conditions associated with P2RX7.

[35606] The function of P2RX7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Purinergic receptor p2x, ligand-gated ion channel, 7 (P2RX7, Accession NP_002553.2) is another GAM281 target gene, herein designated TARGET GENE. P2RX7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by P2RX7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P2RX7 BINDING SITE, designated SEQ ID:7388, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35607] Another function of GAM281 is therefore inhibition of Purinergic receptor p2x, ligand-gated ion channel, 7 (P2RX7, Accession NP_002553.2), a gene which responsi-

ble for atp- dependent lysis of macrophages and therefore may be associated with Chronic lymphatic leukemia. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Chronic lymphatic leukemia, and of other diseases and clinical conditions associated with P2RX7.

[35608] The function of P2RX7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Purinergic receptor p2x-like 1, orphan receptor (P2RXL1, Accession NP_005437.1) is another GAM281 target gene, herein designated TARGET GENE. P2RXL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P2RXL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P2RXL1 BINDING SITE, designated SEQ ID:4425, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35609] Another function of GAM281 is therefore inhibition of Purinergic receptor p2x-like 1, orphan receptor (P2RXL1, Accession NP_005437.1) . Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RXL1.

[35610] P450RAI-2 (Accession NP_063938.1) is another GAM281 target gene, herein designated TARGET GENE. P450RAI-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P450RAI-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P450RAI-2 BINDING SITE, designated SEQ ID:18160, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35611] Another function of GAM281 is therefore inhibition of P450RAI-2 (Accession NP_063938.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P450RAI-2.

[35612] Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS, Accession NP_006443.1) is another GAM281 target gene, herein designated TARGET GENE. PAICS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PAICS, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PAICS BINDING SITE, designated SEQ ID:16852, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35613] Another function of GAM281 is therefore inhibition of Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS, Accession NP_006443.1), a gene which is required for purine biosynthesis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAICS.

[35614] The function of PAICS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) is another GAM281 target gene, herein designated TARGET GENE. PASK BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PASK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of PASK BINDING SITE, designated SEQ ID:2769, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35615] Another function of GAM281 is therefore inhibition of Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PASK.

[35616] Protocadherin alpha 9 (PCDHA9, Accession NP_054724.1) is another GAM281 target gene, herein designated TARGET GENE. PCDHA9 BINDING SITE1 and PCDHA9 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PCDHA9, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA9 BINDING SITE1 and PCDHA9 BINDING SITE2, designated SEQ ID:16048 and SEQ ID:10427 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35617] Another function of GAM281 is therefore inhibition of

Protocadherin alpha 9 (PCDHA9, Accession NP_054724.1), a gene which is a calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA9.

[35618] The function of PCDHA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Protocadherin beta 11 (PCDHB11, Accession NP_061754.1) is another GAM281 target gene, herein designated TARGET GENE. PCDHB11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB11 BINDING SITE, designated SEQ ID:10723, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35619] Another function of GAM281 is therefore inhibition of Protocadherin beta 11 (PCDHB11, Accession NP_061754.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PCDHB11.

[35620] Protocadherin beta 16 (PCDHB16, Accession NP_066008.1) is another GAM281 target gene, herein designated TARGET GENE. PCDHB16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB16 BINDING SITE, designated SEQ ID:4617, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35621] Another function of GAM281 is therefore inhibition of Protocadherin beta 16 (PCDHB16, Accession NP_066008.1), a gene which is a potential calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB16.

[35622] The function of PCDHB16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Protocadherin beta 9 (PCDHB9, Accession NP_061992.2) is another GAM281 target gene, herein

designated TARGET GENE. PCDHB9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB9 BINDING SITE, designated SEQ ID:11523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35623] Another function of GAM281 is therefore inhibition of Protocadherin beta 9 (PCDHB9, Accession NP_061992.2), a gene which is a potential calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB9.

[35624] The function of PCDHB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Phosducin-like (PDCL, Accession NP_005379.2) is another GAM281 target gene, herein designated TARGET GENE. PDCL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDCL, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDCL BINDING SITE, designated SEQ ID:4627, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35625] Another function of GAM281 is therefore inhibition of Phosducin-like (PDCL, Accession NP_005379.2), a gene which may regulate G- protein signaling and similar to phosducins. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDCL.

[35626] The function of PDCL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Phosphodiesterase 6b, cgmp-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NP_000274.1) is another GAM281 target gene, herein designated TARGET GENE. PDE6B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDE6B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of PDE6B BINDING SITE, designated SEQ ID:936, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35627] Another function of GAM281 is therefore inhibition of Phosphodiesterase 6b, cgmp-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NP_000274.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE6B.

[35628] Platelet derived growth factor c (PDGFC, Accession NP_057289.1) is another GAM281 target gene, herein designated TARGET GENE. PDGFC BINDING SITE1 through PDGFC BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PDGFC, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDGFC BINDING SITE1 through PDGFC BINDING SITE3, designated SEQ ID:12574, SEQ ID:7486 and SEQ ID:905 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35629] Another function of GAM281 is therefore inhibition of

Platelet derived growth factor c (PDGFC, Accession NP_057289.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFC.

[35630] Pdz and lim domain 2 (mystique) (PDLIM2, Accession NP_789847.1) is another GAM281 target gene, herein designated TARGET GENE. PDLIM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PDLIM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDLIM2 BINDING SITE, designated SEQ ID:14973, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35631] Another function of GAM281 is therefore inhibition of Pdz and lim domain 2 (mystique) (PDLIM2, Accession NP_789847.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDLIM2.

[35632] Pdz domain containing 1 (PDZK1, Accession NP_002605.2) is another GAM281 target gene, herein designated TARGET GENE. PDZK1 BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by PDZK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDZK1 BINDING SITE, designated SEQ ID:4194, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35633] Another function of GAM281 is therefore inhibition of Pdz domain containing 1 (PDZK1, Accession NP_002605.2), a gene which is a contains PDZ interaction domains, interacts with MAP17, a protein involved in control of cell proliferation. and therefore may be associated with Autosomal dominant hypophosphatemic rickets. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Autosomal dominant hypophosphatemic rickets, and of other diseases and clinical conditions associated with PDZK1.

[35634] The function of PDZK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.PDZRN1 (Accession NP_699202.1) is another GAM281 target gene, herein designated TARGET GENE. PDZRN1 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by PDZRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDZRN1 BINDING SITE, designated SEQ ID:5270, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35635] Another function of GAM281 is therefore inhibition of PDZRN1 (Accession NP_699202.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDZRN1.

[35636] Pellino homolog 1 (drosophila) (PELI1, Accession NP_065702.2) is another GAM281 target gene, herein designated TARGET GENE. PELI1 BINDING SITE1 through PELI1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PELI1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PELI1 BINDING SITE1 through PELI1 BINDING SITE3, designated SEQ ID:5491, SEQ ID:7382 and SEQ ID:14861 respectively, to the nucleotide sequence of GAM281 RNA,

herein designated GAM RNA, also designated SEQ ID:278.

[35637] Another function of GAM281 is therefore inhibition of Pellino homolog 1 (drosophila) (PELI1, Accession NP_065702.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PELI1.

[35638] PEPP3 (Accession NP_055750.1) is another GAM281 target gene, herein designated TARGET GENE. PEPP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PEPP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PEPP3 BINDING SITE, designated SEQ ID:5136, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35639] Another function of GAM281 is therefore inhibition of PEPP3 (Accession NP_055750.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEPP3.

[35640] Period homolog 2 (drosophila) (PER2, Accession NP_073728.1) is another GAM281 target gene, herein designated TARGET GENE. PER2 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PER2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PER2 BINDING SITE, designated SEQ ID:19703, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35641] Another function of GAM281 is therefore inhibition of Period homolog 2 (drosophila) (PER2, Accession NP_073728.1), a gene which Period homolog 2; putative circadian clock protein; has a PAS dimerization domain and therefore may be associated with Familial advanced sleep- phase syndrome. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Familial advanced sleep- phase syndrome, and of other diseases and clinical conditions associated with PER2.

[35642] The function of PER2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Phosphoribosylformylglycinamidine synthase (fgar amidotransferase) (PFAS, Accession NP_036525.1) is another GAM281 target gene, herein

designated TARGET GENE. PFAS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PFAS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PFAS BINDING SITE, designated SEQ ID:16261, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35643] Another function of GAM281 is therefore inhibition of Phosphoribosylformylglycinamidine synthase (fgar amidotransferase) (PFAS, Accession NP_036525.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFAS.

[35644] PHAX (Accession NP_115553.1) is another GAM281 target gene, herein designated TARGET GENE. PHAX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PHAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PHAX BINDING SITE, designated SEQ ID:12159, to the nucleotide se-

quence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35645] Another function of GAM281 is therefore inhibition of PHAX (Accession NP_115553.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHAX.

[35646] Phd finger protein 1 (PHF1, Accession NP_002627.1) is another GAM281 target gene, herein designated TARGET GENE. PHF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PHF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PHF1 BINDING SITE, designated SEQ ID:5036, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35647] Another function of GAM281 is therefore inhibition of Phd finger protein 1 (PHF1, Accession NP_002627.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHF1.

[35648] Phd finger protein 1 (PHF1, Accession NP_077084.1) is

another GAM281 target gene, herein designated TARGET GENE. PHF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PHF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PHF1 BINDING SITE, designated SEQ ID:5036, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35649] Another function of GAM281 is therefore inhibition of Phd finger protein 1 (PHF1, Accession NP_077084.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHF1.

[35650] Polymeric immunoglobulin receptor (PIGR, Accession NP_002635.2) is another GAM281 target gene, herein designated TARGET GENE. PIGR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIGR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIGR BINDING SITE, designated

SEQ ID:11059, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35651] Another function of GAM281 is therefore inhibition of Polymeric immunoglobulin receptor (PIGR, Accession NP_002635.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGR.

[35652] Phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B, Accession NP_002637.2) is another GAM281 target gene, herein designated TARGET GENE. PIK3C2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3C2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3C2B BINDING SITE, designated SEQ ID:10488, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35653] Another function of GAM281 is therefore inhibition of Phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B, Accession NP_002637.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PIK3C2B.

[35654] Phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD, Accession NP_005017.2) is another GAM281 target gene, herein designated TARGET GENE. PIK3CD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3CD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3CD BINDING SITE, designated SEQ ID:9545, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35655] Another function of GAM281 is therefore inhibition of Phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD, Accession NP_005017.2), a gene which regulating cell growth. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3CD.

[35656] The function of PIK3CD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Pbx/knotted 1 homeobox 1 (PKNOX1, Ac-

cession NP_004562.2) is another GAM281 target gene, herein designated TARGET GENE. PKNOX1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PKNOX1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PKNOX1 BINDING SITE, designated SEQ ID:8826, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35657] Another function of GAM281 is therefore inhibition of Pbx/knotted 1 homeobox 1 (PKNOX1, Accession NP_004562.2), a gene which may regulate gene expression and control cell differentiation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKNOX1.

[35658] The function of PKNOX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Pro-melanin-concentrating hormone-like 1 (PMCHL1, Accession NP_114093.1) is another GAM281 target gene, herein designated TARGET GENE. PMCHL1

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMCHL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMCHL1 BINDING SITE, designated SEQ ID:16917, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35659] Another function of GAM281 is therefore inhibition of Pro-melanin-concentrating hormone-like 1 (PMCHL1, Accession NP_114093.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMCHL1.

[35660] Pro-melanin-concentrating hormone-like 2 (PMCHL2, Accession NP_114094.1) is another GAM281 target gene, herein designated TARGET GENE. PMCHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMCHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMCHL2 BINDING SITE, designated SEQ ID:16917, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[35661] Another function of GAM281 is therefore inhibition of Pro-melanin-concentrating hormone-like 2 (PMCHL2, Accession NP_114094.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMCHL2.

[35662] PMPCA (Accession NP_055975.1) is another GAM281 target gene, herein designated TARGET GENE. PMPCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMPCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMPCA BINDING SITE, designated SEQ ID:7640, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35663] Another function of GAM281 is therefore inhibition of PMPCA (Accession NP_055975.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMPCA.

[35664] Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) is another GAM281 target gene, herein designated TARGET GENE. PNMA2 BINDING SITE1 and

PNMA2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PNMA2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PNMA2 BINDING SITE1 and PNMA2 BINDING SITE2, designated SEQ ID:8006 and SEQ ID:17067 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35665] Another function of GAM281 is therefore inhibition of Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNMA2.

[35666] Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) is another GAM281 target gene, herein designated TARGET GENE. POFUT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by POFUT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POFUT1 BINDING SITE, designated SEQ ID:11287, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35667] Another function of GAM281 is therefore inhibition of Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POFUT1.

[35668] Polymerase (dna directed), epsilon 3 (p17 subunit) (POLE3, Accession NP_059139.2) is another GAM281 target gene, herein designated TARGET GENE. POLE3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLE3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLE3 BINDING SITE, designated SEQ ID:6151, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35669] Another function of GAM281 is therefore inhibition of Polymerase (dna directed), epsilon 3 (p17 subunit) (POLE3, Accession NP_059139.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLE3.

[35670] Polymerase (rna) ii (dna directed) polypeptide d (POLR2D, Accession NP_004796.1) is another GAM281 target gene, herein designated TARGET GENE. POLR2D BINDING SITE1 and POLR2D BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by POLR2D, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLR2D BINDING SITE1 and POLR2D BINDING SITE2, designated SEQ ID:2798 and SEQ ID:5412 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35671] Another function of GAM281 is therefore inhibition of Polymerase (rna) ii (dna directed) polypeptide d (POLR2D, Accession NP_004796.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLR2D.

[35672] Paraoxonase 1 (PON1, Accession NP_000437.3) is another GAM281 target gene, herein designated TARGET GENE. PON1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PON1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of PON1 BINDING SITE, designated SEQ ID:2152, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35673] Another function of GAM281 is therefore inhibition of Paraoxonase 1 (PON1, Accession NP_000437.3), a gene which hydrolyzes the toxic metabolites of a variety of organophosphorus insecticides. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PON1.

[35674] The function of PON1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Pou domain, class 2, associating factor 1 (POU2AF1, Accession NP_006226.1) is another GAM281 target gene, herein designated TARGET GENE. POU2AF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POU2AF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POU2AF1 BINDING SITE, designated SEQ ID:20135, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[35675] Another function of GAM281 is therefore inhibition of Pou domain, class 2, associating factor 1 (POU2AF1, Accession NP_006226.1), a gene which is a transcriptional coactivator that specifically associates with either oct1 or oct2 and therefore may be associated with A form of b- cell leukemia. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of A form of b- cell leukemia, and of other diseases and clinical conditions associated with POU2AF1.

[35676] The function of POU2AF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Pou domain, class 2, transcription factor 3 (POU2F3, Accession NP_055167.1) is another GAM281 target gene, herein designated TARGET GENE. POU2F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POU2F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POU2F3 BINDING SITE, designated SEQ ID:16114, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[35677] Another function of GAM281 is therefore inhibition of Pou domain, class 2, transcription factor 3 (POU2F3, Accession NP_055167.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU2F3.

[35678] Pou domain, class 3, transcription factor 1 (POU3F1, Accession NP_002690.2) is another GAM281 target gene, herein designated TARGET GENE. POU3F1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POU3F1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POU3F1 BINDING SITE, designated SEQ ID:7918, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35679] Another function of GAM281 is therefore inhibition of Pou domain, class 3, transcription factor 1 (POU3F1, Accession NP_002690.2), a gene which involves in early embryogenesis and neurogenesis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU3F1.

[35680] The function of POU3F1 has been established by previous studies. The vertebrate class III POU transcription factors consist of 4 members: POU3F1 (Oct- 6), POU3F2 (OMIM Ref. No. 600494), POU3F3 (Brain- 1), and POU3F4 (Brain-4; 300039). The chromosomal locations of the murine class III POU genes were determined by interspecific back-cross analysis (Avraham et al., 1993; Xia et al., 1993). On the basis of mouse- human chromosomal homologies, human POU3F1 and POU3F3 were expected to map to 1p and 2q, respectively. Sumiyama et al. (1998) found that the location of POU3F1 was consistent with this position, mapping to 1p34.1 by FISH. Contrary to the prediction, however, POU3F3 was mapped to 3p14.2 by the same method. The human POU3F2 and POU3F4 genes map to 6q16 and Xq21.1, respectively. Thus, the 4 human class III POU genes map to different chromosomes. A phylogenetic tree of these 4 genes shows that they emerged in a common ancestor of vertebrates. Studies of the genome structure of vertebrates suggest that genome duplication occurred at least twice in the early stage of vertebrate evolution; 4 homologous complexes such as Hox and MHC are interspersed in the mammalian genome. The findings with the 4 class III POU genes are consistent with

the idea of 2 genome duplications. Xia et al. (1993) mapped the mouse homolog of the POU3F1 gene, called Tst1 by them, to chromosome 4. Most mice homozygous for a mutant Pou3f1 die soon after birth (Bermingham et al., 1996; Jaegle et al., 1996).

[35681]

[35682] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[35683] Sumiyama, K.; Washio- Watanabe, K.; Ono, T.; Yoshida, M. C.; Hayakawa, T.; Ueda, S. : Human class III POU genes, POU3F1 and POU3F3, map to chromosomes 1p34.1 and 3p14.1. Mammalian Genome 9: 180- 181, 1998. ; and

[35684] Xia, Y.- R.; Andersen, B.; Mehrabian, M.; Diep, A. T.; War- den, C. H.; Mohandas, T.; McEvilly, R. J.; Rosenfeld, M. G.; Lusis, A. J. : Chromosomal organization of mammalian POU domain facto.

[35685] Further studies establishing the function and utilities of POU3F1 are found in John Hopkins OMIM database record ID 602479, and in cited publications listed in Table 5, which are hereby incorporated by reference.PP1628 (Accession NP_079477.1) is another GAM281 target gene, herein designated TARGET GENE. PP1628 BINDING SITE is

a target binding site found in the 5` untranslated region of mRNA encoded by PP1628, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP1628 BINDING SITE, designated SEQ ID:10180, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35686] Another function of GAM281 is therefore inhibition of PP1628 (Accession NP_079477.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1628.

[35687] PP3111 (Accession NP_071439.2) is another GAM281 target gene, herein designated TARGET GENE. PP3111 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PP3111, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP3111 BINDING SITE, designated SEQ ID:10883, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35688] Another function of GAM281 is therefore inhibition of PP3111 (Accession NP_071439.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP3111.

[35689] PP3856 (Accession NP_660202.1) is another GAM281 target gene, herein designated TARGET GENE. PP3856 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PP3856, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP3856 BINDING SITE, designated SEQ ID:10744, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35690] Another function of GAM281 is therefore inhibition of PP3856 (Accession NP_660202.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP3856.

[35691] Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_803545.1) is another GAM281 target gene, herein designated TARGET GENE. PPAP2C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPAP2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPAP2C BINDING SITE, designated SEQ ID:7299, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35692] Another function of GAM281 is therefore inhibition of Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_803545.1) . Accordingly, utilities of GAM281 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with PPAP2C.

[35693] Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_808211.1) is another GAM281 target gene, herein designated TARGET GENE. PPAP2C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPAP2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPAP2C BINDING SITE, designated SEQ ID:7299, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35694] Another function of GAM281 is therefore inhibition of Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_808211.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPAP2C.

[35695] Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_003703.1) is another GAM281 target gene, herein designated TARGET GENE. PPAP2C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPAP2C, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPAP2C BINDING SITE, designated SEQ ID:7299, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35696] Another function of GAM281 is therefore inhibition of Phosphatidic acid phosphatase type 2c (PPAP2C, Accession NP_003703.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPAP2C.

[35697] Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690911.1) is another GAM281 target gene, herein designated TARGET GENE. PPEF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPEF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPEF2 BINDING SITE, designated SEQ ID:2954, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35698] Another function of GAM281 is therefore inhibition of

Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690911.1), a gene which is a homolog of Drosophila rdgC. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPEF2.

[35699] The function of PPEF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_006230.2) is another GAM281 target gene, herein designated TARGET GENE. PPEF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPEF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPEF2 BINDING SITE, designated SEQ ID:2954, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35700] Another function of GAM281 is therefore inhibition of Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_006230.2), a gene which is a homolog of Drosophila rdgC. Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPEF2.

[35701] The function of PPEF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690910.1) is another GAM281 target gene, herein designated TARGET GENE. PPEF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPEF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPEF2 BINDING SITE, designated SEQ ID:2954, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35702] Another function of GAM281 is therefore inhibition of Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690910.1), a gene which is a homolog of Drosophila rdgC. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPEF2.

[35703] The function of PPEF2 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Ptprf interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1, Accession NP_003613.2) is another GAM281 target gene, herein designated TARGET GENE. PPFIBP1 BINDING SITE1 through PPFIBP1 BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PPFIBP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPFIBP1 BINDING SITE1 through PPFIBP1 BINDING SITE3, designated SEQ ID:12217, SEQ ID:10708 and SEQ ID:8231 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35704] Another function of GAM281 is therefore inhibition of Ptprf interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1, Accession NP_003613.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPFIBP1.

[35705] Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession

NP_005029.1) is another GAM281 target gene, herein designated TARGET GENE. PPID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPID BINDING SITE, designated SEQ ID:7378, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35706] Another function of GAM281 is therefore inhibition of Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession NP_005029.1), a gene which catalyzes the cis- trans isomerization of proline imidic peptide bonds in oligopeptides. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPID.

[35707] The function of PPID and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) is another GAM281 target gene, herein designated TARGET GENE. PPIL2 BINDING SITE is a target binding site found in the 3` untranslated

region of multiple transcripts of mRNA encoded by PPIL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPIL2 BINDING SITE, designated SEQ ID:13122, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35708] Another function of GAM281 is therefore inhibition of Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPIL2.

[35709] Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) is another GAM281 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE1 and PPP1R12B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE1 and PPP1R12B BINDING SITE2, designated SEQ ID:13977 and SEQ ID:3861 respectively, to the nu-

cleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35710] Another function of GAM281 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[35711] Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_115288.1) is another GAM281 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE1 and PPP1R12B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE1 and PPP1R12B BINDING SITE2, designated SEQ ID:13977 and SEQ ID:3861 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35712] Another function of GAM281 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b

(PPP1R12B, Accession NP_115288.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[35713] Primase, polypeptide 2a, 58kda (PRIM2A, Accession NP_000938.1) is another GAM281 target gene, herein designated TARGET GENE. PRIM2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRIM2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRIM2A BINDING SITE, designated SEQ ID:10653, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35714] Another function of GAM281 is therefore inhibition of Primase, polypeptide 2a, 58kda (PRIM2A, Accession NP_000938.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRIM2A.

[35715] Protein kinase, interferon-inducible double stranded rna dependent (PRKR, Accession NP_002750.1) is another GAM281 target gene, herein designated TARGET GENE.

PRKR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKR BINDING SITE, designated SEQ ID:4790, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35716] Another function of GAM281 is therefore inhibition of Protein kinase, interferon-inducible double stranded rna dependent (PRKR, Accession NP_002750.1), a gene which catalyze the phosphorylation of the alpha subunit of eif2. and therefore may be associated with Huntington's disease. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Huntington's disease, and of other diseases and clinical conditions associated with PRKR.

[35717] The function of PRKR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Protein kinase, lysine deficient 3 (PRKWNK3, Accession NP_065973.1) is another GAM281 target gene, herein designated TARGET GENE. PRKWNK3 BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by PRKWNK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKWNK3 BINDING SITE, designated SEQ ID:14862, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35718] Another function of GAM281 is therefore inhibition of Protein kinase, lysine deficient 3 (PRKWNK3, Accession NP_065973.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKWNK3.

[35719] Protein kinase, y-linked (PRKY, Accession NP_002751.1) is another GAM281 target gene, herein designated TARGET GENE. PRKY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKY BINDING SITE, designated SEQ ID:6114, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35720] Another function of GAM281 is therefore inhibition of Protein kinase, y-linked (PRKY, Accession NP_002751.1), a gene which is a putative protein kinase. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKY.

[35721] The function of PRKY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Prion protein 2 (dublet) (PRND, Accession NP_036541.1) is another GAM281 target gene, herein designated TARGET GENE. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, designated SEQ ID:4170 and SEQ ID:1539 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35722] Another function of GAM281 is therefore inhibition of Prion protein 2 (dublet) (PRND, Accession NP_036541.1), a

gene which is similar to prion protein PRNP. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRND.

[35723] The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.PRO0297 (Accession NP_054800.1) is another GAM281 target gene, herein designated TARGET GENE. PRO0297 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0297, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0297 BINDING SITE, designated SEQ ID:10574, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35724] Another function of GAM281 is therefore inhibition of PRO0297 (Accession NP_054800.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0297.

[35725] PRO0365 (Accession NP_054845.1) is another GAM281 target gene, herein designated TARGET GENE. PRO0365 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0365, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0365 BINDING SITE, designated SEQ ID:18148, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35726] Another function of GAM281 is therefore inhibition of PRO0365 (Accession NP_054845.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0365.

[35727] PRO0456 (Accession NP_054846.1) is another GAM281 target gene, herein designated TARGET GENE. PRO0456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO0456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0456 BINDING SITE, designated SEQ ID:9064, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35728] Another function of GAM281 is therefore inhibition of PRO0456 (Accession NP_054846.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0456.

[35729] PRO1048 (Accession NP_060967.1) is another GAM281 target gene, herein designated TARGET GENE. PRO1048 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO1048, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO1048 BINDING SITE, designated SEQ ID:12596, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35730] Another function of GAM281 is therefore inhibition of PRO1048 (Accession NP_060967.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1048.

[35731] PRO2730 (Accession NP_079498.1) is another GAM281

target gene, herein designated TARGET GENE. PRO2730 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO2730, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO2730 BINDING SITE, designated SEQ ID:2048, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35732] Another function of GAM281 is therefore inhibition of PRO2730 (Accession NP_079498.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2730.

[35733] PROM2 (Accession NP_653308.1) is another GAM281 target gene, herein designated TARGET GENE. PROM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PROM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PROM2 BINDING SITE, designated SEQ ID:2147, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[35734] Another function of GAM281 is therefore inhibition of PROM2 (Accession NP_653308.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROM2.

[35735] Proteasome (prosome, macropain) 26s subunit, non-atpase, 9 (PSMD9, Accession NP_002804.2) is another GAM281 target gene, herein designated TARGET GENE. PSMD9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSMD9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSMD9 BINDING SITE, designated SEQ ID:17758, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35736] Another function of GAM281 is therefore inhibition of Proteasome (prosome, macropain) 26s subunit, non-atpase, 9 (PSMD9, Accession NP_002804.2), a gene which acts as a regulatory subunit of the 26 proteasome. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSMD9.

[35737] The function of PSMD9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Phosphoserine phosphatase (PSPH, Accession NP_004568.1) is another GAM281 target gene, herein designated TARGET GENE. PSPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSPH BINDING SITE, designated SEQ ID:15044, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35738] Another function of GAM281 is therefore inhibition of Phosphoserine phosphatase (PSPH, Accession NP_004568.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSPH.

[35739] Proline-serine-threonine phosphatase interacting protein 2 (PSTPIP2, Accession NP_077748.2) is another GAM281 target gene, herein designated TARGET GENE. PSTPIP2 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by PSTPIP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSTPIP2 BINDING SITE, designated SEQ ID:12057, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35740] Another function of GAM281 is therefore inhibition of Proline-serine-threonine phosphatase interacting protein 2 (PSTPIP2, Accession NP_077748.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSTPIP2.

[35741] Prostaglandin e synthase (PTGES, Accession NP_004869.1) is another GAM281 target gene, herein designated TARGET GENE. PTGES BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGES BINDING SITE, designated SEQ ID:16070, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ

ID:278.

[35742] Another function of GAM281 is therefore inhibition of Prostaglandin e synthase (PTGES, Accession NP_004869.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGES.

[35743] Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1) is another GAM281 target gene, herein designated TARGET GENE. PTGIS BINDING SITE1 and PTGIS BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PTGIS, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGIS BINDING SITE1 and PTGIS BINDING SITE2, designated SEQ ID:17361 and SEQ ID:10783 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35744] Another function of GAM281 is therefore inhibition of Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1), a gene which catalyzes the isomerization of prostaglandin h2 to prostacyclin (= prostaglandin i2). Accordingly, utilities of GAM281 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with PTGIS.

[35745] The function of PTGIS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Ptk2 protein tyrosine kinase 2 (PTK2, Accession NP_005598.3) is another GAM281 target gene, herein designated TARGET GENE. PTK2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PTK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTK2 BINDING SITE, designated SEQ ID:10355, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35746] Another function of GAM281 is therefore inhibition of Ptk2 protein tyrosine kinase 2 (PTK2, Accession NP_005598.3), a gene which involves in intracellular signal transduction pathway and is a putative homolog of chicken focal adhesion associated kinase. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with PTK2.

[35747] The function of PTK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.2.Protein tyrosine phosphatase, receptor type, t (PTPRT, Accession NP_008981.2) is another GAM281 target gene, herein designated TARGET GENE. PTPRT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTPRT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPRT BINDING SITE, designated SEQ ID:12157, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35748] Another function of GAM281 is therefore inhibition of Protein tyrosine phosphatase, receptor type, t (PTPRT, Accession NP_008981.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRT.

[35749] Protein tyrosine phosphatase, receptor type, t (PTPRT, Accession NP_573400.1) is another GAM281 target gene,

herein designated TARGET GENE. PTPRT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTPRT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPRT BINDING SITE, designated SEQ ID:12157, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35750] Another function of GAM281 is therefore inhibition of Protein tyrosine phosphatase, receptor type, t (PTPRT, Accession NP_573400.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRT.

[35751] Phosphorylase, glycogen; muscle (mcardle syndrome, glycogen storage disease type v) (PYGM, Accession NP_005600.1) is another GAM281 target gene, herein designated TARGET GENE. PYGM BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PYGM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PYGM BINDING SITE, designated

SEQ ID:15938, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35752] Another function of GAM281 is therefore inhibition of Phosphorylase, glycogen; muscle (mcardle syndrome, glycogen storage disease type v) (PYGM, Accession NP_005600.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PYGM.

[35753] Peptide yy (PYY, Accession NP_004151.1) is another GAM281 target gene, herein designated TARGET GENE. PYY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PYY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PYY BINDING SITE, designated SEQ ID:9133, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35754] Another function of GAM281 is therefore inhibition of Peptide yy (PYY, Accession NP_004151.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with PYY.

[35755] QRSL1 (Accession NP_060762.2) is another GAM281 target gene, herein designated TARGET GENE. QRSL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by QRSL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of QRSL1 BINDING SITE, designated SEQ ID:14971, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35756] Another function of GAM281 is therefore inhibition of QRSL1 (Accession NP_060762.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with QRSL1.

[35757] RAB11-FIP4 (Accession NP_116321.2) is another GAM281 target gene, herein designated TARGET GENE. RAB11-FIP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB11-FIP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB11-FIP4 BINDING SITE, designated SEQ ID:13848, to

the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35758] Another function of GAM281 is therefore inhibition of RAB11-FIP4 (Accession NP_116321.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB11-FIP4.

[35759] Rab21, member ras oncogene family (RAB21, Accession NP_055814.1) is another GAM281 target gene, herein designated TARGET GENE. RAB21 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB21 BINDING SITE, designated SEQ ID:7076, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35760] Another function of GAM281 is therefore inhibition of Rab21, member ras oncogene family (RAB21, Accession NP_055814.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB21.

[35761] Rab33b, member ras oncogene family (RAB33B, Accession

NP_112586.1) is another GAM281 target gene, herein designated TARGET GENE. RAB33B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB33B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB33B BINDING SITE, designated SEQ ID:7910, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35762] Another function of GAM281 is therefore inhibition of Rab33b, member ras oncogene family (RAB33B, Accession NP_112586.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB33B.

[35763] Rab36, member ras oncogene family (RAB36, Accession NP_004905.1) is another GAM281 target gene, herein designated TARGET GENE. RAB36 BINDING SITE1 and RAB36 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by RAB36, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

RAB36 BINDING SITE1 and RAB36 BINDING SITE2, designated SEQ ID:808 and SEQ ID:1652 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35764] Another function of GAM281 is therefore inhibition of Rab36, member ras oncogene family (RAB36, Accession NP_004905.1), a gene which is involved in protein transport. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB36.

[35765] The function of RAB36 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Rab39, member ras oncogene family (RAB39, Accession XP_084662.1) is another GAM281 target gene, herein designated TARGET GENE. RAB39 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB39, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB39 BINDING SITE, designated SEQ ID:3754, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[35766] Another function of GAM281 is therefore inhibition of Rab39, member ras oncogene family (RAB39, Accession XP_084662.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB39.

[35767] Rab4a, member ras oncogene family (RAB4A, Accession NP_004569.2) is another GAM281 target gene, herein designated TARGET GENE. RAB4A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAB4A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB4A BINDING SITE, designated SEQ ID:16568, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35768] Another function of GAM281 is therefore inhibition of Rab4a, member ras oncogene family (RAB4A, Accession NP_004569.2), a gene which is involved in protein transport. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB4A.

[35769] The function of RAB4A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.2.Rab, member of ras oncogene family-like 2a (RABL2A, Accession NP_038198.1) is another GAM281 target gene, herein designated TARGET GENE. RABL2A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RABL2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RABL2A BINDING SITE, designated SEQ ID:2648, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35770] Another function of GAM281 is therefore inhibition of Rab, member of ras oncogene family-like 2a (RABL2A, Accession NP_038198.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2A.

[35771] Rab, member of ras oncogene family-like 2b (RABL2B, Accession NP_009012.1) is another GAM281 target gene, herein designated TARGET GENE. RABL2B BINDING SITE is a target binding site found in the 3` untranslated region

of mRNA encoded by RABL2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RABL2B BINDING SITE, designated SEQ ID:2648, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35772] Another function of GAM281 is therefore inhibition of Rab, member of ras oncogene family-like 2b (RABL2B, Accession NP_009012.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2B.

[35773] RAI (Accession NP_006654.1) is another GAM281 target gene, herein designated TARGET GENE. RAI BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI BINDING SITE, designated SEQ ID:8937, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35774] Another function of GAM281 is therefore inhibition of RAI

(Accession NP_006654.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI.

[35775] Retinoic acid induced 17 (RAI17, Accession NP_065071.1) is another GAM281 target gene, herein designated TARGET GENE. RAI17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAI17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI17 BINDING SITE, designated SEQ ID:7523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35776] Another function of GAM281 is therefore inhibition of Retinoic acid induced 17 (RAI17, Accession NP_065071.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI17.

[35777] Retinoic acid induced 17 (RAI17, Accession XP_166091.2) is another GAM281 target gene, herein designated TARGET GENE. RAI17 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts

of mRNA encoded by RAI17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI17 BINDING SITE, designated SEQ ID:7523, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35778] Another function of GAM281 is therefore inhibition of Retinoic acid induced 17 (RAI17, Accession XP_166091.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI17.

[35779] Retinoic acid induced 3 (RAI3, Accession NP_003970.1) is another GAM281 target gene, herein designated TARGET GENE. RAI3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAI3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI3 BINDING SITE, designated SEQ ID:12784, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35780] Another function of GAM281 is therefore inhibition of

Retinoic acid induced 3 (RAI3, Accession NP_003970.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI3.

[35781] RAP140 (Accession NP_056039.1) is another GAM281 target gene, herein designated TARGET GENE. RAP140 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAP140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAP140 BINDING SITE, designated SEQ ID:16472, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35782] Another function of GAM281 is therefore inhibition of RAP140 (Accession NP_056039.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP140.

[35783] Retinoic acid receptor, gamma (RARG, Accession NP_000957.1) is another GAM281 target gene, herein designated TARGET GENE. RARG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA

encoded by RARG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RARG BINDING SITE, designated SEQ ID:11090, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35784] Another function of GAM281 is therefore inhibition of Retinoic acid receptor, gamma (RARG, Accession NP_000957.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RARG.

[35785] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739580.1) is another GAM281 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:19336, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35786] Another function of GAM281 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739580.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[35787] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739579.1) is another GAM281 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:19336, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35788] Another function of GAM281 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739579.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[35789] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_055552.1) is another GAM281 target gene,

herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:19336, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35790] Another function of GAM281 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_055552.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[35791] RBAK (Accession NP_066986.1) is another GAM281 target gene, herein designated TARGET GENE. RBAK BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RBAK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RBAK BINDING SITE, designated SEQ ID:12965, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[35792] Another function of GAM281 is therefore inhibition of RBAK (Accession NP_066986.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBAK.

[35793] Retinoblastoma binding protein 9 (RBBP9, Accession NP_006597.2) is another GAM281 target gene, herein designated TARGET GENE. RBBP9 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RBBP9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RBBP9 BINDING SITE, designated SEQ ID:16100, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35794] Another function of GAM281 is therefore inhibition of Retinoblastoma binding protein 9 (RBBP9, Accession NP_006597.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP9.

[35795] RCBTB1 (Accession NP_060661.2) is another GAM281 target gene, herein designated TARGET GENE. RCBTB1 BIND-

ING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RCBTB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RCBTB1 BINDING SITE, designated SEQ ID:13829, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35796] Another function of GAM281 is therefore inhibition of RCBTB1 (Accession NP_060661.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RCBTB1.

[35797] RCD-8 (Accession NP_055144.2) is another GAM281 target gene, herein designated TARGET GENE. RCD-8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RCD-8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RCD-8 BINDING SITE, designated SEQ ID:13335, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35798] Another function of GAM281 is therefore inhibition of RCD-8 (Accession NP_055144.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RCD-8.

[35799] RDH13 (Accession NP_612421.1) is another GAM281 target gene, herein designated TARGET GENE. RDH13 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RDH13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RDH13 BINDING SITE, designated SEQ ID:9713, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35800] Another function of GAM281 is therefore inhibition of RDH13 (Accession NP_612421.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RDH13.

[35801] REC14 (Accession NP_079510.1) is another GAM281 target gene, herein designated TARGET GENE. REC14 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by REC14, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of REC14 BINDING SITE, designated SEQ ID:5212, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35802] Another function of GAM281 is therefore inhibition of REC14 (Accession NP_079510.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with REC14.

[35803] Regenerating islet-derived-like, pancreatic stone protein-like, pancreatic thread protein-like (rat) (REGL, Accession NP_006499.1) is another GAM281 target gene, herein designated TARGET GENE. REGL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by REGL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of REGL BINDING SITE, designated SEQ ID:1455, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35804] Another function of GAM281 is therefore inhibition of Regenerating islet-derived-like, pancreatic stone protein-like, pancreatic thread protein-like (rat) (REGL, Accession

NP_006499.1), a gene which is a member of REG family with unknown function. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with REGL.

[35805] The function of REGL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Regulator of g-protein signalling 16 (RGS16, Accession NP_002919.1) is another GAM281 target gene, herein designated TARGET GENE. RGS16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RGS16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RGS16 BINDING SITE, designated SEQ ID:13380, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35806] Another function of GAM281 is therefore inhibition of Regulator of g-protein signalling 16 (RGS16, Accession NP_002919.1), a gene which inhibits signal transduction. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with RGS16.

[35807] The function of RGS16 has been established by previous studies. Snow et al. (1998) found that the RGS16 gene contains 5 exons. Northern blot analysis revealed that RGS16 is expressed at high levels in retina and at lower levels in all other tissues examined. By searching for retinal- specific RGS family members that might be involved in the phototransduction cascade, Chen et al. (1996) identified cDNAs encoding the mouse and rat homologs of RGS16, called Rgs- r by them. Northern blot analysis showed that rat Rgs16 is expressed predominantly in the retina. Chen et al. (1996) found that mouse Rgs16 enhances the rate of GTP- hydrolysis by transducin (see OMIM Ref. No. GNAT2; 139340), suggesting that Rgs16 may play a role in regulating the kinetics of signaling in the phototransduction cascade. The mouse and rat Rgs16 proteins have 94% amino acid sequence identity. Snow et al. (1998) reported that the mouse and human RGS16 proteins have 86% amino acid sequence identity

[35808]

[35809] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[35810] Snow, B. E.; Antonio, L.; Suggs, S.; Siderovski, D. P. : Cloning of a retinally abundant regulator of G- protein signaling (RGS- r/RGS16): genomic structure and chromosomal localization of the human gene. Gene 206: 247-253, 1998. ; and

[35811] Chen, C.- K.; Wieland, T.; Simon, M. I. : RGS- r, a retinal specific RGS protein, binds an intermediate conformation of transducin and enhances recycling. Proc. Nat. Acad. Sci. 93: 12885- 1288.

[35812] Further studies establishing the function and utilities of RGS16 are found in John Hopkins OMIM database record ID 602514, and in cited publications listed in Table 5, which are hereby incorporated by reference.Regulator of g-protein signalling 3 (RGS3, Accession NP_570613.1) is another GAM281 target gene, herein designated TARGET GENE. RGS3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by RGS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RGS3 BINDING SITE, designated SEQ ID:3344, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:278.

[35813] Another function of GAM281 is therefore inhibition of Regulator of g-protein signalling 3 (RGS3, Accession NP_570613.1), a gene which negatively regulates G protein- coupled receptor signalling. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS3.

[35814] The function of RGS3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM146.1.Rhesus blood group, d antigen (RHD, Accession NP_057208.2) is another GAM281 target gene, herein designated TARGET GENE. RHD BINDING SITE1 and RHD BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by RHD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE1 and RHD BINDING SITE2, designated SEQ ID:4143 and SEQ ID:13465 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35815] Another function of GAM281 is therefore inhibition of

Rhesus blood group, d antigen (RHD, Accession NP_057208.2), a gene which Major antigen of the RH system. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[35816] The function of RHD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Rhesus blood group, d antigen (RHD, Accession NP_057309.2) is another GAM281 target gene, herein designated TARGET GENE. RHD BINDING SITE1 and RHD BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by RHD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE1 and RHD BINDING SITE2, designated SEQ ID:4143 and SEQ ID:13465 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35817] Another function of GAM281 is therefore inhibition of Rhesus blood group, d antigen (RHD, Accession NP_057309.2), a gene which Major antigen of the RH sys-

tem. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[35818] The function of RHD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.RHPN2 (Accession NP_149094.2) is another GAM281 target gene, herein designated TARGET GENE. RHPN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RHPN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHPN2 BINDING SITE, designated SEQ ID:11803, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35819] Another function of GAM281 is therefore inhibition of RHPN2 (Accession NP_149094.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHPN2.

[35820] RNF137 (Accession NP_060543.4) is another GAM281 target gene, herein designated TARGET GENE. RNF137 BINDING SITE1 and RNF137 BINDING SITE2 are target binding

sites found in untranslated regions of mRNA encoded by RNF137, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF137 BINDING SITE1 and RNF137 BINDING SITE2, designated SEQ ID:16940 and SEQ ID:7446 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35821] Another function of GAM281 is therefore inhibition of RNF137 (Accession NP_060543.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF137.

[35822] RNF144 (Accession NP_055561.1) is another GAM281 target gene, herein designated TARGET GENE. RNF144 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF144, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF144 BINDING SITE, designated SEQ ID:13909, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35823] Another function of GAM281 is therefore inhibition of RNF144 (Accession NP_055561.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF144.

[35824] Ring finger protein (c3hc4 type) 8 (RNF8, Accession NP_003949.1) is another GAM281 target gene, herein designated TARGET GENE. RNF8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF8 BINDING SITE, designated SEQ ID:13778, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35825] Another function of GAM281 is therefore inhibition of Ring finger protein (c3hc4 type) 8 (RNF8, Accession NP_003949.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF8.

[35826] Rna binding protein s1, serine-rich domain (RNPS1, Accession NP_542161.1) is another GAM281 target gene,

herein designated TARGET GENE. RNPS1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RNPS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNPS1 BINDING SITE, designated SEQ ID:1646, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35827] Another function of GAM281 is therefore inhibition of Rna binding protein s1, serine-rich domain (RNPS1, Accession NP_542161.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNPS1.

[35828] Rna binding protein s1, serine-rich domain (RNPS1, Accession NP_006702.1) is another GAM281 target gene, herein designated TARGET GENE. RNPS1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RNPS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNPS1 BINDING SITE, designated SEQ ID:1646, to the nu-

cleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35829] Another function of GAM281 is therefore inhibition of Rna binding protein s1, serine-rich domain (RNPS1, Accession NP_006702.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNPS1.

[35830] Retinitis pigmentosa 2 (x-linked recessive) (RP2, Accession NP_008846.1) is another GAM281 target gene, herein designated TARGET GENE. RP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RP2 BINDING SITE, designated SEQ ID:6582, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35831] Another function of GAM281 is therefore inhibition of Retinitis pigmentosa 2 (x-linked recessive) (RP2, Accession NP_008846.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RP2.

[35832] Rabphilin 3a-like (without c2 domains) (RPH3AL, Acces-

sion NP_008918.1) is another GAM281 target gene, herein designated TARGET GENE. RPH3AL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RPH3AL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RPH3AL BINDING SITE, designated SEQ ID:2614, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35833] Another function of GAM281 is therefore inhibition of Rabphilin 3a-like (without c2 domains) (RPH3AL, Accession NP_008918.1), a gene which is a protein transporter. could play a role in neurotransmitter release by regulating membrane flow in the nerve terminal. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPH3AL.

[35834] The function of RPH3AL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.RPP30 (Accession NP_006404.1) is another GAM281 target gene, herein designated TARGET GENE.

RPP30 BINDING SITE1 and RPP30 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by RPP30, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RPP30 BINDING SITE1 and RPP30 BINDING SITE2, designated SEQ ID:19325 and SEQ ID:445 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35835] Another function of GAM281 is therefore inhibition of RPP30 (Accession NP_006404.1), a gene which is a component of ribonuclease p that processes 5' ends of precursor tRNAs. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPP30.

[35836] The function of RPP30 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.RRP40 (Accession NP_057126.1) is another GAM281 target gene, herein designated TARGET GENE. RRP40 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RRP40, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RRP40 BINDING SITE, designated SEQ ID:14169, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35837] Another function of GAM281 is therefore inhibition of RRP40 (Accession NP_057126.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RRP40.

[35838] S100A15 (Accession NP_789793.1) is another GAM281 target gene, herein designated TARGET GENE. S100A15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100A15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of S100A15 BINDING SITE, designated SEQ ID:19723, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35839] Another function of GAM281 is therefore inhibition of S100A15 (Accession NP_789793.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

S100A15.

[35840] SARM1 (Accession NP_055892.1) is another GAM281 target gene, herein designated TARGET GENE. SARM1 BINDING SITE1 and SARM1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SARM1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SARM1 BINDING SITE1 and SARM1 BINDING SITE2, designated SEQ ID:4282 and SEQ ID:7147 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35841] Another function of GAM281 is therefore inhibition of SARM1 (Accession NP_055892.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SARM1.

[35842] Sarcoma amplified sequence (SAS, Accession NP_005972.1) is another GAM281 target gene, herein designated TARGET GENE. SAS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SAS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of SAS BINDING SITE, designated SEQ ID:17726, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35843] Another function of GAM281 is therefore inhibition of Sarcoma amplified sequence (SAS, Accession NP_005972.1), a gene which is a member of the trans-membrane 4 superfamily (TM4SF) and may be involved in growth- related cellular processes T. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SAS.

[35844] The function of SAS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM88.1.SBLF (Accession NP_006864.2) is another GAM281 target gene, herein designated TARGET GENE. SBLF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SBLF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SBLF BINDING SITE, designated SEQ ID:14551, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[35845] Another function of GAM281 is therefore inhibition of SBLF (Accession NP_006864.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SBLF.

[35846] SCAMP-4 (Accession NP_524558.1) is another GAM281 target gene, herein designated TARGET GENE. SCAMP-4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCAMP-4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAMP-4 BINDING SITE, designated SEQ ID:2153, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35847] Another function of GAM281 is therefore inhibition of SCAMP-4 (Accession NP_524558.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP-4.

[35848] Scan domain containing 2 (SCAND2, Accession NP_071333.2) is another GAM281 target gene, herein designated TARGET GENE. SCAND2 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SCAND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAND2 BINDING SITE, designated SEQ ID:7179, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35849] Another function of GAM281 is therefore inhibition of Scan domain containing 2 (SCAND2, Accession NP_071333.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAND2.

[35850] SCAP (Accession NP_036367.1) is another GAM281 target gene, herein designated TARGET GENE. SCAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAP BINDING SITE, designated SEQ ID:9400, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35851] Another function of GAM281 is therefore inhibition of SCAP (Accession NP_036367.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAP.

[35852] Scavenger receptor class f, member 1 (SCARF1, Accession NP_003684.1) is another GAM281 target gene, herein designated TARGET GENE. SCARF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCARF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCARF1 BINDING SITE, designated SEQ ID:5158, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35853] Another function of GAM281 is therefore inhibition of Scavenger receptor class f, member 1 (SCARF1, Accession NP_003684.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCARF1.

[35854] Sex comb on midleg-like 2 (drosophila) (SCML2, Accession NP_006080.1) is another GAM281 target gene, herein designated TARGET GENE. SCML2 BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by SCML2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCML2 BINDING SITE, designated SEQ ID:3898, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35855] Another function of GAM281 is therefore inhibition of Sex comb on midleg-like 2 (drosophila) (SCML2, Accession NP_006080.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCML2.

[35856] SCN3B (Accession NP_060870.1) is another GAM281 target gene, herein designated TARGET GENE. SCN3B BINDING SITE1 and SCN3B BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SCN3B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCN3B BINDING SITE1 and SCN3B BINDING SITE2, designated SEQ ID:16355 and SEQ ID:4399 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35857] Another function of GAM281 is therefore inhibition of SCN3B (Accession NP_060870.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN3B.

[35858] SDS-RS1 (Accession NP_612441.1) is another GAM281 target gene, herein designated TARGET GENE. SDS-RS1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SDS-RS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SDS-RS1 BINDING SITE, designated SEQ ID:14127, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35859] Another function of GAM281 is therefore inhibition of SDS-RS1 (Accession NP_612441.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDS-RS1.

[35860] Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1) is another GAM281 target gene, herein designated TARGET GENE. SEDL BINDING SITE1 through SEDL BINDING SITE4 are target binding sites found in un-

translated regions of mRNA encoded by SEDL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEDL BINDING SITE1 through SEDL BINDING SITE4, designated SEQ ID:11591, SEQ ID:16937, SEQ ID:15576 and SEQ ID:926 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35861] Another function of GAM281 is therefore inhibition of Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1), a gene which may play role in vesicular transport from endoplasmic reticulum to golgi. and therefore may be associated with Spondyloepiphyseal dysplasia. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Spondyloepiphyseal dysplasia, and of other diseases and clinical conditions associated with SEDL.

[35862] The function of SEDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.SELH (Accession NP_734467.1) is another GAM281 target gene, herein designated TARGET GENE.

SELH BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SELH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SELH BINDING SITE, designated SEQ ID:13030, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35863] Another function of GAM281 is therefore inhibition of SELH (Accession NP_734467.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SELH.

[35864] Sema domain, immunoglobulin domain (ig), short basic domain, secreted, (semaphorin) 3b (SEMA3B, Accession NP_004627.1) is another GAM281 target gene, herein designated TARGET GENE. SEMA3B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEMA3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEMA3B BINDING SITE, designated SEQ ID:17810, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[35865] Another function of GAM281 is therefore inhibition of Sema domain, immunoglobulin domain (ig), short basic domain, secreted, (semaphorin) 3b (SEMA3B, Accession NP_004627.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA3B.

[35866] Sema domain, immunoglobulin domain (ig), short basic domain, secreted, (semaphorin) 3e (SEMA3E, Accession NP_036563.1) is another GAM281 target gene, herein designated TARGET GENE. SEMA3E BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEMA3E, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEMA3E BINDING SITE, designated SEQ ID:13353, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35867] Another function of GAM281 is therefore inhibition of Sema domain, immunoglobulin domain (ig), short basic domain, secreted, (semaphorin) 3e (SEMA3E, Accession NP_036563.1) . Accordingly, utilities of GAM281 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA3E.

[35868] Selenoprotein n, 1 (SEPN1, Accession NP_065184.1) is another GAM281 target gene, herein designated TARGET GENE. SEPN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEPN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEPN1 BINDING SITE, designated SEQ ID:18255, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35869] Another function of GAM281 is therefore inhibition of Selenoprotein n, 1 (SEPN1, Accession NP_065184.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEPN1.

[35870] Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) is another GAM281 target gene, herein designated TARGET GENE. SERF1A BINDING SITE1 and SERF1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERF1A, corresponding to target binding sites such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1A BINDING SITE1 and SERF1A BINDING SITE2, designated SEQ ID:9219 and SEQ ID:15849 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35871] Another function of GAM281 is therefore inhibition of Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1A.

[35872] Small edrk-rich factor 1b (centromeric) (SERF1B, Accession NP_075267.1) is another GAM281 target gene, herein designated TARGET GENE. SERF1B BINDING SITE1 and SERF1B BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERF1B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1B BINDING SITE1 and SERF1B BINDING SITE2, designated SEQ ID:15849 and SEQ ID:9219 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35873] Another function of GAM281 is therefore inhibition of Small edrk-rich factor 1b (centromeric) (SERF1B, Accession NP_075267.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1B.

[35874] Small edrk-rich factor 2 (SERF2, Accession NP_005761.2) is another GAM281 target gene, herein designated TARGET GENE. SERF2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SERF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF2 BINDING SITE, designated SEQ ID:16210, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35875] Another function of GAM281 is therefore inhibition of Small edrk-rich factor 2 (SERF2, Accession NP_005761.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF2.

[35876] Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 8 (SERPINB8, Accession

NP_002631.1) is another GAM281 target gene, herein designated TARGET GENE. SERPINB8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERPINB8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERPINB8 BINDING SITE, designated SEQ ID:20173, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35877] Another function of GAM281 is therefore inhibition of Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 8 (SERPINB8, Accession NP_002631.1), a gene which protease inhibitors; may be a serpin serine protease inhibitor that binds thrombin. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB8.

[35878] The function of SERPINB8 has been established by previous studies. High molecular weight serine proteinase inhibitors (serpins) are a large superfamily of proteins which bind to and inactivate serine proteinases. These interactions are involved in many cellular processes including

coagulation, fibrinolysis, complement fixation, matrix remodeling, and apoptosis. Sprecher et al. (1995) cloned 2 novel serpins, termed PI8 and PI9 (OMIM Ref. No. 601799), from a human placenta cDNA library. Sequence analysis showed that PI8 encodes a 376- amino acid polypeptide with over 60% identity to PI6 (OMIM Ref. No. 173321). Using Northern blotting, they observed that PI8 was expressed as 2 transcripts of 1.4 and 3.8 kb. The 1.4- kb transcript was most abundant in liver and lung while the 3.8- kb transcript was most abundant in skeletal muscle and heart. They showed that PI8 was localized to the cytoplasm of transfected cells and that it was able to form an SDS- insoluble complex with human thrombin (OMIM Ref. No. 176930). Serpins are characterized by a well- conserved tertiary structure that consists of 3 beta sheets and 8 or 9 alpha helices (Huber and Carrell, 1989). A critical portion of the molecule, the reactive center loop, connects beta sheets A and C and, in most cases, serves as bait for a target serine proteinase. Bartuski et al. (1997) stated that more than 100 members of the serpin superfamily are known, including C1 esterase inhibitor (C1NH; 606860), antithrombin III (AT3; 107300), protease inhibitor 7 (PI7; 177010), and maspin (PI5; 154790), which

are involved in complement activation, coagulation, cell differentiation, and tumor suppression, respectively, as well as many others. The ovalbumin- type serpins (ov-serpins) are a subset of the serpin superfamily and are characterized by their high degree of homology to chicken ovalbumin, the lack of N- and C- terminal extensions, the absence of a signal peptide, and a serine rather than an asparagine residue at the penultimate position. Four members of the ov- serpin family had been mapped to a 300- kb region within 18q21.3: PI5, SCCA1 (OMIM Ref. No. 600517), SCCA2 (OMIM Ref. No. 600518), and PAI2 (OMIM Ref. No. 173390). Using a panel of 18q21.3 YAC clones, PCR, and DNA blotting, Bartuski et al. (1997) mapped 2 additional ov- serpins, cytoplasmic antiproteinase 2 (CAP2 or PI8) and bone marrow- associated serpin bomapin (PI10; 602058), to the same region. Three of the serpins (PI8, PI10, and PAI2) mapped to the same YACs. Bartuski et al. (1997) estimated that the size of the 18q21.3 serpin cluster spans approximately 500 kb and contains at least 6 serpin genes. The gene order is cen- - PI5- - SCCA2- - SCCA1- - PAI2- - PI10- - PI8- - tel. The characterization of the serpin gene cluster at 18q21 provided new opportunities to study coordinate gene regula-

tion and the evolution of gene families.

[35879]

[35880] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[35881] Bartuski, A. J.; Kamachi, Y.; Schick, C.; Overhauser, J.; Silverman, G. A. : Cytoplasmic antiproteinase 2 (PI8) and bomapin (PI10) map to the serpin cluster at 18q21.3. Genomics 43: 321- 328, 1997. ; and

[35882] Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.; Schrader, S. K.; Foster, D. C.; Kisiel, W. : Molecular cloning, expression, and partial characterization of two novel m.

[35883] Further studies establishing the function and utilities of SERPINB8 are found in John Hopkins OMIM database record ID 601697, and in cited publications listed in Table 5, which are hereby incorporated by reference.Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 9 (SERPINB9, Accession NP_004146.1) is another GAM281 target gene, herein designated TARGET GENE. SERPINB9 BINDING SITE1 and SERPINB9 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERPINB9, corresponding to target

binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERPINB9 BINDING SITE1 and SERPINB9 BINDING SITE2, designated SEQ ID:4363 and SEQ ID:9152 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35884] Another function of GAM281 is therefore inhibition of Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 9 (SERPINB9, Accession NP_004146.1), a gene which may be a serpin serine protease inhibitor that interacts with granzyme B (GZMB). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB9.

[35885] The function of SERPINB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM88.2.Sideroflexin 2 (SFXN2, Accession NP_849189.1) is another GAM281 target gene, herein designated TARGET GENE. SFXN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SFXN2, correspond-

ing to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SFXN2 BINDING SITE, designated SEQ ID:3678, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35886] Another function of GAM281 is therefore inhibition of Sideroflexin 2 (SFXN2, Accession NP_849189.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN2.

[35887] Sideroflexin 2 (SFXN2, Accession XP_058359.2) is another GAM281 target gene, herein designated TARGET GENE. SFXN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SFXN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SFXN2 BINDING SITE, designated SEQ ID:3678, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35888] Another function of GAM281 is therefore inhibition of Sideroflexin 2 (SFXN2, Accession XP_058359.2) . Accord-

ingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN2.

[35889] Sideroflexin 5 (SFXN5, Accession NP_653180.1) is another GAM281 target gene, herein designated TARGET GENE. SFXN5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SFXN5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SFXN5 BINDING SITE, designated SEQ ID:11307, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35890] Another function of GAM281 is therefore inhibition of Sideroflexin 5 (SFXN5, Accession NP_653180.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN5.

[35891] Sh3-domain binding protein 2 (SH3BP2, Accession NP_003014.2) is another GAM281 target gene, herein designated TARGET GENE. SH3BP2 BINDING SITE1 and SH3BP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SH3BP2, corre-

sponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SH3BP2 BINDING SITE1 and SH3BP2 BINDING SITE2, designated SEQ ID:3836 and SEQ ID:9440 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35892] Another function of GAM281 is therefore inhibition of Sh3-domain binding protein 2 (SH3BP2, Accession NP_003014.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BP2.

[35893] Split hand/foot malformation (ectrodactyly) type 3 (SHFM3, Accession NP_071322.1) is another GAM281 target gene, herein designated TARGET GENE. SHFM3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SHFM3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SHFM3 BINDING SITE, designated SEQ ID:2197, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35894] Another function of GAM281 is therefore inhibition of Split hand/foot malformation (ectrodactyly) type 3 (SHFM3, Accession NP_071322.1), a gene which probably binds to some phosphorylated proteins and promotes their degradation. and therefore may be associated with Split- hand/split- foot malformation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Split- hand/split- foot malformation, and of other diseases and clinical conditions associated with SHFM3.

[35895] The function of SHFM3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Short stature homeobox (SHOX, Accession NP_006874.1) is another GAM281 target gene, herein designated TARGET GENE. SHOX BINDING SITE1 and SHOX BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by SHOX, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SHOX BINDING SITE1 and SHOX BINDING SITE2, designated SEQ ID:4375 and SEQ ID:16527 respectively, to the nucleotide sequence of GAM281 RNA,

herein designated GAM RNA, also designated SEQ ID:278.

[35896] Another function of GAM281 is therefore inhibition of Short stature homeobox (SHOX, Accession NP_006874.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHOX.

[35897] Sialic acid binding ig-like lectin 8 (SIGLEC8, Accession NP_055257.1) is another GAM281 target gene, herein designated TARGET GENE. SIGLEC8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIGLEC8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIGLEC8 BINDING SITE, designated SEQ ID:4513, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35898] Another function of GAM281 is therefore inhibition of Sialic acid binding ig-like lectin 8 (SIGLEC8, Accession NP_055257.1), a gene which is a cell adhesion molecule for postnatal neural development. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIGLEC8.

[35899] The function of SIGLEC8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Tal1 (scl) interrupting locus (SIL, Accession NP_003026.1) is another GAM281 target gene, herein designated TARGET GENE. SIL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIL BINDING SITE, designated SEQ ID:12411, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35900] Another function of GAM281 is therefore inhibition of Tal1 (scl) interrupting locus (SIL, Accession NP_003026.1), a gene which may be required for axial development and left- right specification and therefore may be associated with Prominent midline neural tube defects, abnormal left- right development. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Prominent midline neural tube defects, abnormal left- right development, and of other diseases and clinical conditions associated with SIL.

[35901] The function of SIL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Signal-regulatory protein beta 1 (SIRPB1, Accession NP_006056.1) is another GAM281 target gene, herein designated TARGET GENE. SIRPB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIRPB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIRPB1 BINDING SITE, designated SEQ ID:14771, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35902] Another function of GAM281 is therefore inhibition of Signal-regulatory protein beta 1 (SIRPB1, Accession NP_006056.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIRPB1.

[35903] Src-like-adaptor 2 (SLA2, Accession NP_778252.1) is another GAM281 target gene, herein designated TARGET GENE. SLA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of

mRNA encoded by SLA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLA2 BINDING SITE, designated SEQ ID:19573, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35904] Another function of GAM281 is therefore inhibition of Src-like-adaptor 2 (SLA2, Accession NP_778252.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA2.

[35905] Src-like-adaptor 2 (SLA2, Accession NP_115590.1) is another GAM281 target gene, herein designated TARGET GENE. SLA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLA2 BINDING SITE, designated SEQ ID:19573, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35906] Another function of GAM281 is therefore inhibition of Src-like-adaptor 2 (SLA2, Accession NP_115590.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA2.

[35907] Solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8, Accession NP_078904.1) is another GAM281 target gene, herein designated TARGET GENE. SLC12A8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC12A8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC12A8 BINDING SITE, designated SEQ ID:5190, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35908] Another function of GAM281 is therefore inhibition of Solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8, Accession NP_078904.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC12A8.

[35909] Solute carrier family 13 (sodium/sulfate symporters),

member 1 (SLC13A1, Accession NP_071889.2) is another GAM281 target gene, herein designated TARGET GENE. SLC13A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC13A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC13A1 BINDING SITE, designated SEQ ID:4370, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35910] Another function of GAM281 is therefore inhibition of Solute carrier family 13 (sodium/sulfate symporters), member 1 (SLC13A1, Accession NP_071889.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC13A1.

[35911] Solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (SLC13A3, Accession NP_073740.2) is another GAM281 target gene, herein designated TARGET GENE. SLC13A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC13A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC13A3 BINDING SITE, designated SEQ ID:7448, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35912] Another function of GAM281 is therefore inhibition of Solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (SLC13A3, Accession NP_073740.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC13A3.

[35913] Solute carrier family 14 (urea transporter), member 2 (SLC14A2, Accession NP_009094.2) is another GAM281 target gene, herein designated TARGET GENE. SLC14A2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC14A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC14A2 BINDING SITE, designated SEQ ID:4514, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35914] Another function of GAM281 is therefore inhibition of So-

lute carrier family 14 (urea transporter), member 2 (SLC14A2, Accession NP_009094.2), a gene which is a renal urea transporter 2. and therefore may be associated with Orthostatic hypotension. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Orthostatic hypotension, and of other diseases and clinical conditions associated with SLC14A2.

[35915] The function of SLC14A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM97.1.Solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1, Accession NP_005064.1) is another GAM281 target gene, herein designated TARGET GENE. SLC15A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC15A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC15A1 BINDING SITE, designated SEQ ID:18930, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35916] Another function of GAM281 is therefore inhibition of So-

lute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1, Accession NP_005064.1), a gene which is a H(+)- coupled peptide transporter. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC15A1.

[35917] The function of SLC15A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Solute carrier family 16 (monocarboxylic acid transporters), member 4 (SLC16A4, Accession NP_004687.1) is another GAM281 target gene, herein designated TARGET GENE. SLC16A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC16A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A4 BINDING SITE, designated SEQ ID:611, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35918] Another function of GAM281 is therefore inhibition of Solute carrier family 16 (monocarboxylic acid transporters),

member 4 (SLC16A4, Accession NP_004687.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A4.

[35919] Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) is another GAM281 target gene, herein designated TARGET GENE. SLC16A6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC16A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A6 BINDING SITE, designated SEQ ID:5302, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35920] Another function of GAM281 is therefore inhibition of Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A6.

[35921] Solute carrier family 19, member 3 (SLC19A3, Accession NP_079519.1) is another GAM281 target gene, herein

designated TARGET GENE. SLC19A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC19A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC19A3 BINDING SITE, designated SEQ ID:6713, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35922] Another function of GAM281 is therefore inhibition of Solute carrier family 19, member 3 (SLC19A3, Accession NP_079519.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC19A3.

[35923] Solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5, Accession NP_005619.1) is another GAM281 target gene, herein designated TARGET GENE. SLC1A5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC1A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC1A5 BINDING SITE, designated SEQ ID:1277, to the

nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35924] Another function of GAM281 is therefore inhibition of Solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5, Accession NP_005619.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC1A5.

[35925] Solute carrier family 21 (prostaglandin transporter), member 2 (SLC21A2, Accession NP_005621.1) is another GAM281 target gene, herein designated TARGET GENE. SLC21A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC21A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC21A2 BINDING SITE, designated SEQ ID:18939, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35926] Another function of GAM281 is therefore inhibition of Solute carrier family 21 (prostaglandin transporter), member 2 (SLC21A2, Accession NP_005621.1), a gene which is a Prostaglandin transporter. Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC21A2.

[35927] The function of SLC21A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM148.1.Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1, Accession NP_004718.1) is another GAM281 target gene, herein designated TARGET GENE. SLC24A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC24A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC24A1 BINDING SITE, designated SEQ ID:10966, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35928] Another function of GAM281 is therefore inhibition of Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1, Accession NP_004718.1), a gene which is a critical component of the visual transduction cascade, controlling the calcium concentration of outer segments during light and darkness. Accordingly,

utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC24A1.

[35929] The function of SLC24A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.SLC30A5 (Accession NP_076960.1) is another GAM281 target gene, herein designated TARGET GENE. SLC30A5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLC30A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC30A5 BINDING SITE, designated SEQ ID:3692, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35930] Another function of GAM281 is therefore inhibition of SLC30A5 (Accession NP_076960.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC30A5.

[35931] SLC30A6 (Accession NP_060434.2) is another GAM281

target gene, herein designated TARGET GENE. SLC30A6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC30A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC30A6 BINDING SITE, designated SEQ ID:5362, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35932] Another function of GAM281 is therefore inhibition of SLC30A6 (Accession NP_060434.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC30A6.

[35933] SLC35E2 (Accession XP_049733.6) is another GAM281 target gene, herein designated TARGET GENE. SLC35E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC35E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC35E2 BINDING SITE, designated SEQ ID:13336, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[35934] Another function of GAM281 is therefore inhibition of SLC35E2 (Accession XP_049733.6) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35E2.

[35935] Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2) is another GAM281 target gene, herein designated TARGET GENE. SLC39A1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC39A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC39A1 BINDING SITE, designated SEQ ID:9528, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35936] Another function of GAM281 is therefore inhibition of Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2), a gene which is a divalent (zinc/iron) metal ion transporter. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

SLC39A1.

[35937] The function of SLC39A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.1.Solute carrier family 39 (zinc transporter), member 3 (SLC39A3, Accession NP_653165.1) is another GAM281 target gene, herein designated TARGET GENE. SLC39A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC39A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC39A3 BINDING SITE, designated SEQ ID:20136, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35938] Another function of GAM281 is therefore inhibition of Solute carrier family 39 (zinc transporter), member 3 (SLC39A3, Accession NP_653165.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC39A3.

[35939] Solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14, Accession NP_009162.1) is another

GAM281 target gene, herein designated TARGET GENE. SLC6A14 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC6A14 BINDING SITE, designated SEQ ID:13830, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35940] Another function of GAM281 is therefore inhibition of Solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14, Accession NP_009162.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A14.

[35941] Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (SLC6A3, Accession NP_001035.1) is another GAM281 target gene, herein designated TARGET GENE. SLC6A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of SLC6A3 BINDING SITE, designated SEQ ID:12941, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35942] Another function of GAM281 is therefore inhibition of Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (SLC6A3, Accession NP_001035.1), a gene which terminates the action of dopamine by its high affinity sodium- dependent reuptake into presynaptic terminals. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A3.

[35943] The function of SLC6A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.SMAC (Accession NP_620308.1) is another GAM281 target gene, herein designated TARGET GENE. SMAC BINDING SITE1 and SMAC BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by SMAC, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMAC BIND-

ING SITE1 and SMAC BINDING SITE2, designated SEQ ID:1861 and SEQ ID:18165 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35944] Another function of GAM281 is therefore inhibition of SMAC (Accession NP_620308.1), a gene which promotes apoptosis via caspase activation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMAC.

[35945] The function of SMAC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Smith-magenis syndrome chromosome region, candidate 5 (SMCR5, Accession NP_658987.1) is another GAM281 target gene, herein designated TARGET GENE. SMCR5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SMCR5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMCR5 BINDING SITE, designated SEQ ID:8677, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35946] Another function of GAM281 is therefore inhibition of Smith-magenis syndrome chromosome region, candidate 5 (SMCR5, Accession NP_658987.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMCR5.

[35947] Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_003816.2) is another GAM281 target gene, herein designated TARGET GENE. SNAP23 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNAP23, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP23 BINDING SITE, designated SEQ ID:19007, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35948] Another function of GAM281 is therefore inhibition of Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_003816.2), a gene which is essential component of the high affinity receptor for the general membrane fusion machinery. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP23.

[35949] The function of SNAP23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_570710.1) is another GAM281 target gene, herein designated TARGET GENE. SNAP23 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNAP23, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP23 BINDING SITE, designated SEQ ID:19007, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35950] Another function of GAM281 is therefore inhibition of Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_570710.1), a gene which is essential component of the high affinity receptor for the general membrane fusion machinery. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP23.

[35951] The function of SNAP23 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.SNARK (Accession NP_112214.1) is another GAM281 target gene, herein designated TARGET GENE. SNARK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNARK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNARK BINDING SITE, designated SEQ ID:18622, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35952] Another function of GAM281 is therefore inhibition of SNARK (Accession NP_112214.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNARK.

[35953] Syntaphilin (SNPH, Accession NP_055538.1) is another GAM281 target gene, herein designated TARGET GENE. SNPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

SNPH BINDING SITE, designated SEQ ID:15041, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35954] Another function of GAM281 is therefore inhibition of Syntaphilin (SNPH, Accession NP_055538.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNPH.

[35955] Sorting nexin 15 (SNX15, Accession NP_037438.2) is another GAM281 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:7625, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35956] Another function of GAM281 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NP_037438.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with SNX15.

[35957] Sorting nexin 15 (SNX15, Accession NP_680086.1) is another GAM281 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:7625, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35958] Another function of GAM281 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NP_680086.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15.

[35959] SNX22 (Accession NP_079074.1) is another GAM281 target gene, herein designated TARGET GENE. SNX22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNX22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of SNX22 BINDING SITE, designated SEQ ID:13596, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35960] Another function of GAM281 is therefore inhibition of SNX22 (Accession NP_079074.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX22.

[35961] SNX27 (Accession NP_112180.4) is another GAM281 target gene, herein designated TARGET GENE. SNX27 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNX27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX27 BINDING SITE, designated SEQ ID:16941, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35962] Another function of GAM281 is therefore inhibition of SNX27 (Accession NP_112180.4) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX27.

[35963] Sialophorin (gpl115, leukosialin, cd43) (SPN, Accession

NP_003114.1) is another GAM281 target gene, herein designated TARGET GENE. SPN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPN BINDING SITE, designated SEQ ID:16209, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35964] Another function of GAM281 is therefore inhibition of Sialophorin (gpl115, leukosialin, cd43) (SPN, Accession NP_003114.1), a gene which plays a role in the physico-chemical properties of the t- cell surface and in lectin binding. presents carbohydrate ligands to selectins. . and therefore may be associated with Wiskott- aldrich syndrome. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Wiskott- aldrich syndrome, and of other diseases and clinical conditions associated with SPN.

[35965] The function of SPN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM130.1.Speckle-type poz protein (SPOP, Accession NP_003554.1) is another GAM281 target gene, herein designated TARGET GENE. SPOP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SPOP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPOP BINDING SITE, designated SEQ ID:5610, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35966] Another function of GAM281 is therefore inhibition of Speckle-type poz protein (SPOP, Accession NP_003554.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPOP.

[35967] SQV7L (Accession XP_047287.1) is another GAM281 target gene, herein designated TARGET GENE. SQV7L BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SQV7L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SQV7L BINDING SITE, designated SEQ ID:7375, to the nucleotide se-

quence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35968] Another function of GAM281 is therefore inhibition of SQV7L (Accession XP_047287.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SQV7L.

[35969] Sarcalumenin (SRL, Accession XP_064152.3) is another GAM281 target gene, herein designated TARGET GENE. SRL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SRL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRL BINDING SITE, designated SEQ ID:6681, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35970] Another function of GAM281 is therefore inhibition of Sarcalumenin (SRL, Accession XP_064152.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRL.

[35971] Serine/arginine repetitive matrix 2 (SRRM2, Accession NP_057417.2) is another GAM281 target gene, herein

designated TARGET GENE. SRRM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SRRM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRRM2 BINDING SITE, designated SEQ ID:18975, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35972] Another function of GAM281 is therefore inhibition of Serine/arginine repetitive matrix 2 (SRRM2, Accession NP_057417.2), a gene which RELATED NUCLEAR MATRIX PROTEIN. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRRM2.

[35973] The function of SRRM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1) is another GAM281 target gene, herein designated TARGET GENE. SS18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SS18, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SS18 BINDING SITE, designated SEQ ID:17762, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35974] Another function of GAM281 is therefore inhibition of Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1), a gene which is a putative transcriptional activator. and therefore is associated with Human synovial sarcomas. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Human synovial sarcomas., and of other diseases and clinical conditions associated with SS18.

[35975] The function of SS18 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.STAF65(gamma) (Accession NP_055675.1) is another GAM281 target gene, herein designated TARGET GENE. STAF65(gamma) BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STAF65(gamma), corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAF65(gamma) BINDING SITE, designated SEQ ID:2196, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35976] Another function of GAM281 is therefore inhibition of STAF65(gamma) (Accession NP_055675.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAF65(gamma).

[35977] Signal transducing adaptor molecule (sh3 domain and itam motif) 2 (STAM2, Accession NP_005834.3) is another GAM281 target gene, herein designated TARGET GENE. STAM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STAM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAM2 BINDING SITE, designated SEQ ID:5301, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35978] Another function of GAM281 is therefore inhibition of Signal transducing adaptor molecule (sh3 domain and itam

motif) 2 (STAM2, Accession NP_005834.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAM2.

[35979] Staufen, rna binding protein (drosophila) (STAU, Accession NP_004593.1) is another GAM281 target gene, herein designated TARGET GENE. STAU BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by STAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAU BINDING SITE, designated SEQ ID:3950, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35980] Another function of GAM281 is therefore inhibition of Staufen, rna binding protein (drosophila) (STAU, Accession NP_004593.1), a gene which may play a role in specific positioning of mrnas at given sites in the cell and in stimulating their translation at the site. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAU.

[35981] The function of STAU and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM37.1.Sulfotransferase, estrogen-preferring (STE, Accession NP_005411.1) is another GAM281 target gene, herein designated TARGET GENE. STE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STE BINDING SITE, designated SEQ ID:3303, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35982] Another function of GAM281 is therefore inhibition of Sulfotransferase, estrogen-preferring (STE, Accession NP_005411.1), a gene which sulfates estrone and dehydroepiandrosterone, but not dopamine. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STE.

[35983] The function of STE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Six transmembrane epithelial antigen of

prostate 2 (STEAP2, Accession NP_694544.1) is another GAM281 target gene, herein designated TARGET GENE. STEAP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STEAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STEAP2 BINDING SITE, designated SEQ ID:9147, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35984] Another function of GAM281 is therefore inhibition of Six transmembrane epithelial antigen of prostate 2 (STEAP2, Accession NP_694544.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STEAP2.

[35985] Serine/threonine kinase 10 (STK10, Accession NP_005981.1) is another GAM281 target gene, herein designated TARGET GENE. STK10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STK10 BINDING SITE, designated

SEQ ID:2481, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35986] Another function of GAM281 is therefore inhibition of Serine/threonine kinase 10 (STK10, Accession NP_005981.1), a gene which can act on substrates such as myelin basic protein and histone iia on serine and threonine residues. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK10.

[35987] The function of STK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.Stomatin (STOM, Accession NP_004090.3) is another GAM281 target gene, herein designated TARGET GENE. STOM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STOM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STOM BINDING SITE, designated SEQ ID:2907, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35988] Another function of GAM281 is therefore inhibition of

Stomatin (STOM, Accession NP_004090.3) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STOM.

[35989] Synaptotagmin xi (SYT11, Accession NP_689493.2) is another GAM281 target gene, herein designated TARGET GENE. SYT11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYT11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYT11 BINDING SITE, designated SEQ ID:9033, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35990] Another function of GAM281 is therefore inhibition of Synaptotagmin xi (SYT11, Accession NP_689493.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT11.

[35991] Synaptotagmin xiii (SYT13, Accession NP_065877.1) is another GAM281 target gene, herein designated TARGET GENE. SYT13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYT13,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYT13 BINDING SITE, designated SEQ ID:15294, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35992] Another function of GAM281 is therefore inhibition of Synaptotagmin xiii (SYT13, Accession NP_065877.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT13.

[35993] TADA3L (Accession NP_597814.1) is another GAM281 target gene, herein designated TARGET GENE. TADA3L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TADA3L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TADA3L BINDING SITE, designated SEQ ID:9087, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35994] Another function of GAM281 is therefore inhibition of TADA3L (Accession NP_597814.1) . Accordingly, utilities

of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TADA3L.

[35995] Taf11 rna polymerase ii, tata box binding protein (tbp)-associated factor, 28kda (TAF11, Accession NP_005634.1) is another GAM281 target gene, herein designated TARGET GENE. TAF11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TAF11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAF11 BINDING SITE, designated SEQ ID:1997, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35996] Another function of GAM281 is therefore inhibition of Taf11 rna polymerase ii, tata box binding protein (tbp)-associated factor, 28kda (TAF11, Accession NP_005634.1), a gene which plays a central role in mediating promoter responses to various activators and repressors. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAF11.

[35997] The function of TAF11 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.T-cell acute lymphocytic leukemia 1 (TAL1, Accession NP_003180.1) is another GAM281 target gene, herein designated TARGET GENE. TAL1 BINDING SITE1 and TAL1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TAL1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAL1 BINDING SITE1 and TAL1 BINDING SITE2, designated SEQ ID:18260 and SEQ ID:3146 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[35998] Another function of GAM281 is therefore inhibition of T-cell acute lymphocytic leukemia 1 (TAL1, Accession NP_003180.1), a gene which may help control cell growth and differentiation. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAL1.

[35999] The function of TAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM30.1.Tap binding protein (tapasin) (TAPBP, Accession NP_003181.3) is another GAM281 target gene, herein designated TARGET GENE. TAPBP BINDING SITE1 through TAPBP BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TAPBP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAPBP BINDING SITE1 through TAPBP BINDING SITE3, designated SEQ ID:12247, SEQ ID:11523 and SEQ ID:16940 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36000] Another function of GAM281 is therefore inhibition of Tap binding protein (tapasin) (TAPBP, Accession NP_003181.3), a gene which is involved in MHC class I-restricted antigen processing. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAPBP.

[36001] The function of TAPBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Tyrosine aminotransferase (TAT, Accession

NP_000344.1) is another GAM281 target gene, herein designated TARGET GENE. TAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAT BINDING SITE, designated SEQ ID:18942, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36002] Another function of GAM281 is therefore inhibition of Tyrosine aminotransferase (TAT, Accession NP_000344.1), a gene which is tyrosine aminotransferase and strongly similar to rat Rn.9947, which plays a role in gluconeogenesis. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAT.

[36003] The function of TAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Tafazzin (cardiomyopathy, dilated 3a (x-linked); endocardial fibroelastosis 2; barth syndrome) (TAZ, Accession NP_851831.1) is another GAM281 target

gene, herein designated TARGET GENE. TAZ BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TAZ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAZ BINDING SITE, designated SEQ ID:9257, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36004] Another function of GAM281 is therefore inhibition of Tafazzin (cardiomyopathy, dilated 3a (x-linked); endocardial fibroelastosis 2; barth syndrome) (TAZ, Accession NP_851831.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAZ.

[36005] Tbc1 domain family, member 5 (TBC1D5, Accession NP_055559.1) is another GAM281 target gene, herein designated TARGET GENE. TBC1D5 BINDING SITE1 and TBC1D5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TBC1D5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

TBC1D5 BINDING SITE1 and TBC1D5 BINDING SITE2, designated SEQ ID:16449 and SEQ ID:14859 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36006] Another function of GAM281 is therefore inhibition of Tbc1 domain family, member 5 (TBC1D5, Accession NP_055559.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBC1D5.

[36007] Transcription factor 2, hepatic; lf-b3; variant hepatic nuclear factor (TCF2, Accession NP_006472.1) is another GAM281 target gene, herein designated TARGET GENE. TCF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TCF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCF2 BINDING SITE, designated SEQ ID:625, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36008] Another function of GAM281 is therefore inhibition of Transcription factor 2, hepatic; lf-b3; variant hepatic nuclear factor (TCF2, Accession NP_006472.1), a gene which

probably binds to the inverted palindrome 5'- gttaatnat-taac- 3'. and therefore is associated with Maturity- onset diabetes of the young type 5 (mody5), familial hypoplastic glomerulocystic kidney disease (gckd). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Maturity- onset diabetes of the young type 5 (mody5), familial hypoplastic glomerulocystic kidney disease (gckd), and of other diseases and clinical conditions associated with TCF2.

[36009] The function of TCF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.T-cell leukemia/lymphoma 6 (TCL6, Accession NP_055233.1) is another GAM281 target gene, herein designated TARGET GENE. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TCL6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:17450 and SEQ ID:17450 respectively, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[36010] Another function of GAM281 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_055233.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[36011] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065577.2) is another GAM281 target gene, herein designated TARGET GENE. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TCL6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:17450 and SEQ ID:9387 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36012] Another function of GAM281 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065577.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[36013] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065578.2) is another GAM281 target gene, herein designated TARGET GENE. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TCL6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:9387 and SEQ ID:17450 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36014] Another function of GAM281 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065578.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[36015] Teratocarcinoma-derived growth factor 1 (TDGF1, Accession NP_003203.1) is another GAM281 target gene, herein designated TARGET GENE. TDGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TDGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TDGF1 BINDING SITE, designated SEQ ID:8563, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36016] Another function of GAM281 is therefore inhibition of Teratocarcinoma-derived growth factor 1 (TDGF1, Accession NP_003203.1), a gene which can play a role in the determination of the epiblastic cells that subsequently give rise to the mesoderm. and therefore may be associated with Forebrain defects. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Forebrain defects, and of other diseases and clinical conditions associated with TDGF1.

[36017] The function of TDGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.TERA (Accession NP_067061.1) is another GAM281 target gene, herein designated TARGET GENE. TERA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TERA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

TERA BINDING SITE, designated SEQ ID:17755, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36018] Another function of GAM281 is therefore inhibition of TERA (Accession NP_067061.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERA.

[36019] Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_003209.1) is another GAM281 target gene, herein designated TARGET GENE. TERF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TERF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF1 BINDING SITE, designated SEQ ID:1745, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36020] Another function of GAM281 is therefore inhibition of Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_003209.1), a gene which negatively regulates telomere length, involves in regulation of the mitotic spindle. Accordingly, utilities of GAM281 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF1.

[36021] The function of TERF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_059523.1) is another GAM281 target gene, herein designated TARGET GENE. TERF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TERF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF1 BINDING SITE, designated SEQ ID:1745, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36022] Another function of GAM281 is therefore inhibition of Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_059523.1), a gene which negatively regulates telomere length, involves in regulation of the mitotic spindle. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with TERF1.

[36023] The function of TERF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Telomeric repeat binding factor 2 (TERF2, Accession NP_005643.1) is another GAM281 target gene, herein designated TARGET GENE. TERF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TERF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF2 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36024] Another function of GAM281 is therefore inhibition of Telomeric repeat binding factor 2 (TERF2, Accession NP_005643.1), a gene which plays a key role in the protective activity of telomeres. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF2.

[36025] The function of TERF2 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM133.2.Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) is another GAM281 target gene, herein designated TARGET GENE. TGIF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGIF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGIF2 BINDING SITE, designated SEQ ID:6881, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36026] Another function of GAM281 is therefore inhibition of Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGIF2.

[36027] Thioesterase, adipose associated (THEA, Accession NP_671517.1) is another GAM281 target gene, herein designated TARGET GENE. THEA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by THEA, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of THEA BINDING SITE, designated SEQ ID:14452, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36028] Another function of GAM281 is therefore inhibition of Thioesterase, adipose associated (THEA, Accession NP_671517.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THEA.

[36029] Tigger transposable element derived 6 (TIGD6, Accession NP_112215.1) is another GAM281 target gene, herein designated TARGET GENE. TIGD6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TIGD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TIGD6 BINDING SITE, designated SEQ ID:4933, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36030] Another function of GAM281 is therefore inhibition of Tigger transposable element derived 6 (TIGD6, Accession NP_112215.1) . Accordingly, utilities of GAM281 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with TIGD6.

[36031] TIM50L (Accession XP_053074.2) is another GAM281 target gene, herein designated TARGET GENE. TIM50L BINDING SITE1 and TIM50L BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TIM50L, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TIM50L BINDING SITE1 and TIM50L BINDING SITE2, designated SEQ ID:10157 and SEQ ID:5989 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36032] Another function of GAM281 is therefore inhibition of TIM50L (Accession XP_053074.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIM50L.

[36033] Thymidine kinase 2, mitochondrial (TK2, Accession NP_004605.1) is another GAM281 target gene, herein designated TARGET GENE. TK2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TK2 BINDING SITE, designated SEQ ID:3160, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36034] Another function of GAM281 is therefore inhibition of Thymidine kinase 2, mitochondrial (TK2, Accession NP_004605.1), a gene which phosphorylates thymidine, deoxycytidine, deoxyuridine, and also anti- viral and anti-cancer nucleoside analogs and therefore may be associated with Mitochondrial dna depletion myopathy. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Mitochondrial dna depletion myopathy, and of other diseases and clinical conditions associated with TK2.

[36035] The function of TK2 has been established by previous studies. Johansson and Karlsson (1997) cloned cDNAs encoding human TK2. The gene encodes a 234- amino acid polypeptide. Although TK2 is believed to reside in mitochondria, it contains no mitochondrial translocation signal sequence. Northern blot analysis revealed that TK2 was ubiquitously expressed as 2 transcripts of 2.4 and 4 kb. Expression of the TK2 cDNA revealed a 60- kD protein with phosphorylation activity similar to purified human

TK2. Based on the partial protein sequence of human TK2, Wang et al. (1999) isolated a human brain TK2 cDNA. These authors noted that although the cDNA they isolated corresponds to the full- length mature protein, it is likely to be incomplete because it lacks the coding region for a mitochondrial target presequence. They reported that the predicted protein sequence matched that of purified TK2, but differed at the N- terminus and at amino acid 28 from the TK2 sequence deduced by Johansson and Karlsson (1997). TK2 shares approximately 40% identity with deoxycytidine kinase (OMIM Ref. No. 125450) and deoxyguanosine kinase (OMIM Ref. No. 601465) on the amino acid level. Wang et al. (1999) characterized both recombinant and native TK2 forms and found that the enzyme has broad substrate specificity and complex kinetics, suggesting that it may play a role in the activation of chemotherapeutic nucleoside analogs. Northern blot analysis indicated that the TK2 gene was expressed as multiple transcripts, some of which show a tissue- specific pattern. The highest levels of expression were observed in testis and ovary. Saada et al. (2001) identified 2 mutations in TK2, his90 to asn (188250.0001) and ile181 to asn (188250.0002), in 4 individuals who developed devastat-

ing myopathy and depletion of muscular mtDNA in infancy. In these individuals, the activity of TK2 in muscle mitochondria was reduced to 14 to 45% of the mean value in healthy control individuals. Mandel et al. (2001) identified mutations in the DGUOK gene in another form of mtDNA depletion syndrome, the hepatocerebral form (see OMIM Ref. No. 251880). They noted that the main supply of dNTPs for mtDNA synthesis comes from the salvage pathway initiated by DGK and TK2. The association of mtDNA depletion with mutations in the genes encoding these 2 kinases suggested that the salvage pathway enzymes are involved in the maintenance of balanced mitochondrial dNTP pools.

[36036]

[36037] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[36038] Wang, L.; Munch- Petersen, B.; Herrstrom Sjoberg, A.; Hellman, U.; Bergman, T.; Jornvall, H.; Eriksson, S. : Human thymidine kinase 2: molecular cloning and characterisation of the enzyme activity with antiviral and cytostatic nucleoside substrates. FEBS Lett. 443: 170- 174, 1999. ; and

[36039] Saada, A.; Shaag, A.; Mandel, H.; Nevo, Y.; Eriksson, S.; Elpeleg, O. : Mutant mitochondrial thymidine kinase in mitochondrial DNA depletion myopathy. Nature Genet. 29: 342- 344, 2001.

[36040] Further studies establishing the function and utilities of TK2 are found in John Hopkins OMIM database record ID 188250, and in cited publications listed in Table 5, which are hereby incorporated by reference.Toll-like receptor 5 (TLR5, Accession NP_003259.2) is another GAM281 target gene, herein designated TARGET GENE. TLR5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TLR5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLR5 BINDING SITE, designated SEQ ID:16229, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36041] Another function of GAM281 is therefore inhibition of Toll-like receptor 5 (TLR5, Accession NP_003259.2), a gene which participates in the innate immune response to bacterial flagellins. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with TLR5.

[36042] The function of TLR5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Transmembrane, cochlear expressed, 1 (TMC1, Accession NP_619636.2) is another GAM281 target gene, herein designated TARGET GENE. TMC1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TMC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMC1 BINDING SITE, designated SEQ ID:2152, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36043] Another function of GAM281 is therefore inhibition of Transmembrane, cochlear expressed, 1 (TMC1, Accession NP_619636.2), a gene which is required for normal function of cochlear hair cells and therefore may be associated with Autosomal recessive nonsyndromic neurosensory deafness and autosomal dominant nonsyndromic sensorineural hearing loss . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Autosomal

recessive nonsyndromic neurosensory deafness and autosomal dominant nonsyndromic sensorineural hearing loss ., and of other diseases and clinical conditions associated with TMC1.

[36044] The function of TMC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.TMEM14A (Accession NP_054770.1) is another GAM281 target gene, herein designated TARGET GENE. TMEM14A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TMEM14A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMEM14A BINDING SITE, designated SEQ ID:5271, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36045] Another function of GAM281 is therefore inhibition of TMEM14A (Accession NP_054770.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEM14A.

[36046] Transmembrane protease, serine 3 (TMPRSS3, Accession

NP_076927.1) is another GAM281 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE, designated SEQ ID:6625, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36047] Another function of GAM281 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_076927.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[36048] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115780.1) is another GAM281 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

TMPRSS3 BINDING SITE, designated SEQ ID:6625, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36049] Another function of GAM281 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115780.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[36050] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115777.1) is another GAM281 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE, designated SEQ ID:6625, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36051] Another function of GAM281 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115777.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with TMPRSS3.

[36052] Tumor necrosis factor, alpha-induced protein 2 (TNFAIP2, Accession NP_006282.2) is another GAM281 target gene, herein designated TARGET GENE. TNFAIP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFAIP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFAIP2 BINDING SITE, designated SEQ ID:17621, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36053] Another function of GAM281 is therefore inhibition of Tumor necrosis factor, alpha-induced protein 2 (TNFAIP2, Accession NP_006282.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFAIP2.

[36054] Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_003833.3) is another GAM281 target gene, herein designated TARGET GENE. TNFRSF10B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF10B, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE, designated SEQ ID:4398, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36055] Another function of GAM281 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_003833.3), a gene which forms complex that induces apoptosis. and therefore may be associated with Squamous cell carcinoma . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Squamous cell carcinoma ., and of other diseases and clinical conditions associated with TNFRSF10B.

[36056] The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_671716.1) is another GAM281 target gene, herein designated TARGET GENE. TNFRSF10B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF10B, corresponding to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE, designated SEQ ID:4398, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36057] Another function of GAM281 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_671716.1), a gene which forms complex that induces apoptosis. and therefore may be associated with Squamous cell carcinoma . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Squamous cell carcinoma ., and of other diseases and clinical conditions associated with TNFRSF10B.

[36058] The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tumor necrosis factor receptor superfamily, member 11a, activator of nfkb (TNFRSF11A, Accession NP_003830.1) is another GAM281 target gene, herein designated TARGET GENE. TNFRSF11A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF11A, corresponding to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF11A BINDING SITE, designated SEQ ID:2200, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36059] Another function of GAM281 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 11a, activator of nfkb (TNFRSF11A, Accession NP_003830.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF11A.

[36060] Tumor necrosis factor receptor superfamily, member 18 (TNFRSF18, Accession NP_683700.1) is another GAM281 target gene, herein designated TARGET GENE. TNFRSF18 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF18 BINDING SITE, designated SEQ ID:8120, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36061] Another function of GAM281 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 18 (TNFRSF18, Accession NP_683700.1), a gene which interacts between activated t lymphocytes and endothelial cells. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF18.

[36062] The function of TNFRSF18 has been established by previous studies. Members of the tumor necrosis factor (TNF; 191160) and TNF receptor (TNFR) superfamilies regulate diverse biologic functions, including cell proliferation, differentiation, and survival. See 191190. Using differential display to identify T cell mRNAs induced by the synthetic glucocorticoid hormone dexamethasone, Nocentini et al. (1997) identified a mouse cDNA encoding a novel member of the TNFR family. They designated the corresponding gene Gitr for 'glucocorticoid- induced TNFR family- related gene.' Like other TNFRs, the predicted Gitr protein contains cysteine- rich repeats in the extracellular domain. In addition, the intracellular domain of Gitr shares significant homology with those of the mouse and human TNFRs 4- 1BB (OMIM Ref. No. 602250) and CD27 (OMIM Ref. No. 186711). Nocentini et al. (1997) demonstrated

that the Gitr gene is induced in T cells by dexamethasone as well as by other cell- activating stimuli. Gitr expression protected T cells from apoptosis induced by treatment with anti- CD3 (OMIM Ref. No. 186790) antibodies, but not by other apoptotic agents. The authors concluded that Gitr is a new member of the TNFR family involved in the regulation of T cell receptor- mediated cell death. Kwon et al. (1999) isolated cDNAs encoding the human Gitr homolog and the Gitr ligand (OMIM Ref. No. 603898), which they designated AITR (activation- inducible TNFR family member) and AITRL, respectively. These authors reported that the predicted 234- amino acid AITR protein is a type I transmembrane protein with a signal peptide and a single transmembrane region. AITR and mouse Gitr proteins are 55% identical. As with other TNFR family members, when expressed in mammalian cells, AITR mediated NF- kappa- B (see OMIM Ref. No. 164011) activation via TRAF2 (OMIM Ref. No. 601895). TRAF1 (OMIM Ref. No. 601711) and TRAF3 (OMIM Ref. No. 601896) appeared to downregulate AITR- induced NF- kappa- B activation. Northern blot analysis revealed that the 1.25- kb AITR mRNA is expressed in lymph node, peripheral blood leukocytes, and, weakly, in spleen. Expression of AITR, like that of other

TNFRs, was upregulated in peripheral mononuclear cells after antigen stimulation. AITRL was constitutively expressed in an endothelial cell line, leading the authors to suggest that AITR and its ligand may be important for interactions between activated T lymphocytes and endothelial cells. Independently, Gurney et al. (1999) identified cDNAs encoding AITR and AITRL, which they called GITR and GITRL, respectively. Coexpression of ligand and receptor protected Jurkat T cells against antigen receptor-induced cell death, suggesting that GITRL and GITR may modulate T lymphocyte survival in peripheral tissues.

[36063]

[36064] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[36065] Gurney, A. L.; Marsters, S. A.; Huang, A.; Pitti, R. M.; Mark, M.; Baldwin, D. T.; Gray, A. M.; Dowd, P.; Brush, J.; Heldens, S.; Schow, P.; Goddard, A. D.; Wood, W. I.; Baker, K. P.; Godowski, P. J.; Ashkenazi, A. : Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR. Curr. Biol. 9: 215- 218, 1999. ; and

[36066] Kwon, B.; Yu, K.- Y.; Ni, J.; Yu, G.- L.; Jang, I.- K.; Kim, Y.-

J.; Xing, L.; Liu, D.; Wang, S.- X.; Kwon, B. S. : Identification of a novel activation- inducible protein of the tumor necro.

[36067] Further studies establishing the function and utilities of TNFRSF18 are found in John Hopkins OMIM database record ID 603905, and in cited publications listed in Table 5, which are hereby incorporated by reference.Tumor necrosis factor receptor superfamily, member 18 (TNFRSF18, Accession NP_004186.1) is another GAM281 target gene, herein designated TARGET GENE. TNFRSF18 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF18 BINDING SITE, designated SEQ ID:8120, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36068] Another function of GAM281 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 18 (TNFRSF18, Accession NP_004186.1), a gene which interacts between activated t lymphocytes and endothelial cells. Accordingly, utilities of GAM281 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with TNFRSF18.

[36069] The function of TNFRSF18 has been established by previous studies. Members of the tumor necrosis factor (TNF; 191160) and TNF receptor (TNFR) superfamilies regulate diverse biologic functions, including cell proliferation, differentiation, and survival. See 191190. Using differential display to identify T cell mRNAs induced by the synthetic glucocorticoid hormone dexamethasone, Nocentini et al. (1997) identified a mouse cDNA encoding a novel member of the TNFR family. They designated the corresponding gene Gitr for 'glucocorticoid- induced TNFR family- related gene.' Like other TNFRs, the predicted Gitr protein contains cysteine- rich repeats in the extracellular domain. In addition, the intracellular domain of Gitr shares significant homology with those of the mouse and human TNFRs 4- 1BB (OMIM Ref. No. 602250) and CD27 (OMIM Ref. No. 186711). Nocentini et al. (1997) demonstrated that the Gitr gene is induced in T cells by dexamethasone as well as by other cell- activating stimuli. Gitr expression protected T cells from apoptosis induced by treatment with anti- CD3 (OMIM Ref. No. 186790) antibodies, but not by other apoptotic agents. The authors concluded that

Gitr is a new member of the TNFR family involved in the regulation of T cell receptor- mediated cell death. Kwon et al. (1999) isolated cDNAs encoding the human Gitr homolog and the Gitr ligand (OMIM Ref. No. 603898), which they designated AITR (activation- inducible TNFR family member) and AITRL, respectively. These authors reported that the predicted 234- amino acid AITR protein is a type I transmembrane protein with a signal peptide and a single transmembrane region. AITR and mouse Gitr proteins are 55% identical. As with other TNFR family members, when expressed in mammalian cells, AITR mediated NF- kappa-B (see OMIM Ref. No. 164011) activation via TRAF2 (OMIM Ref. No. 601895). TRAF1 (OMIM Ref. No. 601711) and TRAF3 (OMIM Ref. No. 601896) appeared to downregulate AITR- induced NF- kappa- B activation. Northern blot analysis revealed that the 1.25- kb AITR mRNA is expressed in lymph node, peripheral blood leukocytes, and, weakly, in spleen. Expression of AITR, like that of other TNFRs, was upregulated in peripheral mononuclear cells after antigen stimulation. AITRL was constitutively expressed in an endothelial cell line, leading the authors to suggest that AITR and its ligand may be important for interactions between activated T lymphocytes and endothe-

lial cells. Independently, Gurney et al. (1999) identified cDNAs encoding AITR and AITRL, which they called GITR and GITRL, respectively. Coexpression of ligand and receptor protected Jurkat T cells against antigen receptor-induced cell death, suggesting that GITRL and GITR may modulate T lymphocyte survival in peripheral tissues.

[36070]

[36071] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[36072] Gurney, A. L.; Marsters, S. A.; Huang, A.; Pitti, R. M.; Mark, M.; Baldwin, D. T.; Gray, A. M.; Dowd, P.; Brush, J.; Heldens, S.; Schow, P.; Goddard, A. D.; Wood, W. I.; Baker, K. P.; Godowski, P. J.; Ashkenazi, A. : Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR. Curr. Biol. 9: 215- 218, 1999. ; and

[36073] Kwon, B.; Yu, K.- Y.; Ni, J.; Yu, G.- L.; Jang, I.- K.; Kim, Y.- J.; Xing, L.; Liu, D.; Wang, S.- X.; Kwon, B. S. : Identification of a novel activation- inducible protein of the tumor necro.

[36074] Further studies establishing the function and utilities of TNFRSF18 are found in John Hopkins OMIM database

record ID 603905, and in cited publications listed in Table 5, which are hereby incorporated by reference.Tumor necrosis factor receptor superfamily, member 18 (TNFRSF18, Accession NP_683699.1) is another GAM281 target gene, herein designated TARGET GENE. TNFRSF18 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF18 BINDING SITE, designated SEQ ID:8120, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36075] Another function of GAM281 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 18 (TNFRSF18, Accession NP_683699.1), a gene which interacts between activated t lymphocytes and endothelial cells. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF18.

[36076] The function of TNFRSF18 has been established by previous studies. Members of the tumor necrosis factor (TNF; 191160) and TNF receptor (TNFR) superfamilies regulate

diverse biologic functions, including cell proliferation, differentiation, and survival. See 191190. Using differential display to identify T cell mRNAs induced by the synthetic glucocorticoid hormone dexamethasone, Nocentini et al. (1997) identified a mouse cDNA encoding a novel member of the TNFR family. They designated the corresponding gene Gitr for 'glucocorticoid- induced TNFR family- related gene.' Like other TNFRs, the predicted Gitr protein contains cysteine- rich repeats in the extracellular domain. In addition, the intracellular domain of Gitr shares significant homology with those of the mouse and human TNFRs 4- 1BB (OMIM Ref. No. 602250) and CD27 (OMIM Ref. No. 186711). Nocentini et al. (1997) demonstrated that the Gitr gene is induced in T cells by dexamethasone as well as by other cell- activating stimuli. Gitr expression protected T cells from apoptosis induced by treatment with anti- CD3 (OMIM Ref. No. 186790) antibodies, but not by other apoptotic agents. The authors concluded that Gitr is a new member of the TNFR family involved in the regulation of T cell receptor- mediated cell death. Kwon et al. (1999) isolated cDNAs encoding the human Gitr homolog and the Gitr ligand (OMIM Ref. No. 603898), which they designated AITR (activation- inducible TNFR family

member) and AITRL, respectively. These authors reported that the predicted 234- amino acid AITR protein is a type I transmembrane protein with a signal peptide and a single transmembrane region. AITR and mouse Gitr proteins are 55% identical. As with other TNFR family members, when expressed in mammalian cells, AITR mediated NF- kappa-B (see OMIM Ref. No. 164011) activation via TRAF2 (OMIM Ref. No. 601895). TRAF1 (OMIM Ref. No. 601711) and TRAF3 (OMIM Ref. No. 601896) appeared to downregulate AITR- induced NF- kappa- B activation. Northern blot analysis revealed that the 1.25- kb AITR mRNA is expressed in lymph node, peripheral blood leukocytes, and, weakly, in spleen. Expression of AITR, like that of other TNFRs, was upregulated in peripheral mononuclear cells after antigen stimulation. AITRL was constitutively expressed in an endothelial cell line, leading the authors to suggest that AITR and its ligand may be important for interactions between activated T lymphocytes and endothelial cells. Independently, Gurney et al. (1999) identified cDNAs encoding AITR and AITRL, which they called GITR and GITRL, respectively. Coexpression of ligand and receptor protected Jurkat T cells against antigen receptor-induced cell death, suggesting that GITRL and GITR may

modulate T lymphocyte survival in peripheral tissues.

[36077]

[36078] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[36079] Gurney, A. L.; Marsters, S. A.; Huang, A.; Pitti, R. M.; Mark, M.; Baldwin, D. T.; Gray, A. M.; Dowd, P.; Brush, J.; Heldens, S.; Schow, P.; Goddard, A. D.; Wood, W. I.; Baker, K. P.; Godowski, P. J.; Ashkenazi, A. : Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR. Curr. Biol. 9: 215- 218, 1999. ; and

[36080] Kwon, B.; Yu, K.- Y.; Ni, J.; Yu, G.- L.; Jang, I.- K.; Kim, Y.- J.; Xing, L.; Liu, D.; Wang, S.- X.; Kwon, B. S. : Identification of a novel activation- inducible protein of the tumor necro.

[36081] Further studies establishing the function and utilities of TNFRSF18 are found in John Hopkins OMIM database record ID 603905, and in cited publications listed in Table 5, which are hereby incorporated by reference.Tumor necrosis factor receptor superfamily, member 9 (TNFRSF9, Accession NP_001552.2) is another GAM281 target gene, herein designated TARGET GENE. TNFRSF9 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF9 BINDING SITE, designated SEQ ID:13464, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36082] Another function of GAM281 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 9 (TNFRSF9, Accession NP_001552.2), a gene which inhibits proliferation of activated T lymphocytes. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF9.

[36083] The function of TNFRSF9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Tnfaip3 interacting protein 3 (TNIP3, Accession NP_079149.2) is another GAM281 target gene, herein designated TARGET GENE. TNIP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNIP3, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNIP3 BINDING SITE, designated SEQ ID:15713, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36084] Another function of GAM281 is therefore inhibition of Tnfaip3 interacting protein 3 (TNIP3, Accession NP_079149.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNIP3.

[36085] TOLLIP (Accession NP_061882.2) is another GAM281 target gene, herein designated TARGET GENE. TOLLIP BINDING SITE1 and TOLLIP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TOLLIP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOLLIP BINDING SITE1 and TOLLIP BINDING SITE2, designated SEQ ID:9557 and SEQ ID:13694 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36086] Another function of GAM281 is therefore inhibition of

TOLLIP (Accession NP_061882.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOLLIP.

[36087] Torsin family 1, member b (torsin b) (TOR1B, Accession NP_055321.1) is another GAM281 target gene, herein designated TARGET GENE. TOR1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TOR1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOR1B BINDING SITE, designated SEQ ID:14221, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36088] Another function of GAM281 is therefore inhibition of Torsin family 1, member b (torsin b) (TOR1B, Accession NP_055321.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOR1B.

[36089] Tumor protein p53 (li-fraumeni syndrome) (TP53, Accession NP_000537.2) is another GAM281 target gene, herein designated TARGET GENE. TP53 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by TP53, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TP53 BINDING SITE, designated SEQ ID:4654, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36090] Another function of GAM281 is therefore inhibition of Tumor protein p53 (li-fraumeni syndrome) (TP53, Accession NP_000537.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53.

[36091] Thiopurine s-methyltransferase (TPMT, Accession NP_000358.1) is another GAM281 target gene, herein designated TARGET GENE. TPMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TPMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPMT BINDING SITE, designated SEQ ID:19670, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36092] Another function of GAM281 is therefore inhibition of

Thiopurine s-methyltransferase (TPMT, Accession NP_000358.1), a gene which catalyzes the s- methylation of thiopurine drugs such as 6- mercaptopurine. and therefore may be associated with Thiopurine s- methyl-transferase polymorphism. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Thiopurine s- methyltransferase polymorphism, and of other diseases and clinical conditions associated with TPMT.

[36093] The function of TPMT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Tnf receptor-associated factor 2 (TRAF2, Accession NP_663770.1) is another GAM281 target gene, herein designated TARGET GENE. TRAF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRAF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF2 BINDING SITE, designated SEQ ID:778, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36094] Another function of GAM281 is therefore inhibition of Tnf receptor-associated factor 2 (TRAF2, Accession NP_663770.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF2.

[36095] Tnf receptor-associated factor 2 (TRAF2, Accession NP_066961.2) is another GAM281 target gene, herein designated TARGET GENE. TRAF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRAF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF2 BINDING SITE, designated SEQ ID:778, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36096] Another function of GAM281 is therefore inhibition of Tnf receptor-associated factor 2 (TRAF2, Accession NP_066961.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF2.

[36097] Tnf receptor-associated factor 5 (TRAF5, Accession NP_665702.1) is another GAM281 target gene, herein

designated TARGET GENE. TRAF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRAF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:7045, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36098] Another function of GAM281 is therefore inhibition of Tnf receptor-associated factor 5 (TRAF5, Accession NP_665702.1), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5.

[36099] The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Tnf receptor-associated factor 5 (TRAF5, Accession NP_004610.1) is another GAM281 target gene, herein designated TARGET GENE. TRAF5 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by TRAF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:7045, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36100] Another function of GAM281 is therefore inhibition of Tnf receptor-associated factor 5 (TRAF5, Accession NP_004610.1), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5.

[36101] The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.TRAP150 (Accession NP_005110.1) is another GAM281 target gene, herein designated TARGET GENE. TRAP150 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRAP150, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of TRAP150 BINDING SITE, designated SEQ ID:4929, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36102] Another function of GAM281 is therefore inhibition of TRAP150 (Accession NP_005110.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAP150.

[36103] Three prime repair exonuclease 1 (TREX1, Accession NP_338598.1) is another GAM281 target gene, herein designated TARGET GENE. TREX1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TREX1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TREX1 BINDING SITE, designated SEQ ID:8479, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36104] Another function of GAM281 is therefore inhibition of Three prime repair exonuclease 1 (TREX1, Accession NP_338598.1) . Accordingly, utilities of GAM281 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with TREX1.

[36105] Tripartite motif-containing 16 (TRIM16, Accession NP_006461.2) is another GAM281 target gene, herein designated TARGET GENE. TRIM16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRIM16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM16 BINDING SITE, designated SEQ ID:4601, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36106] Another function of GAM281 is therefore inhibition of Tripartite motif-containing 16 (TRIM16, Accession NP_006461.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM16.

[36107] Tripartite motif-containing 5 (TRIM5, Accession NP_149023.1) is another GAM281 target gene, herein designated TARGET GENE. TRIM5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRIM5, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM5 BINDING SITE, designated SEQ ID:5879, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36108] Another function of GAM281 is therefore inhibition of Tripartite motif-containing 5 (TRIM5, Accession NP_149023.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM5.

[36109] Tripartite motif-containing 6 (TRIM6, Accession NP_477514.1) is another GAM281 target gene, herein designated TARGET GENE. TRIM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRIM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM6 BINDING SITE, designated SEQ ID:13572, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36110] Another function of GAM281 is therefore inhibition of Tri-

partite motif-containing 6 (TRIM6, Accession NP_477514.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM6.

[36111] Transient receptor potential cation channel, subfamily m, member 6 (TRPM6, Accession NP_060132.3) is another GAM281 target gene, herein designated TARGET GENE. TRPM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPM6 BINDING SITE, designated SEQ ID:18177, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36112] Another function of GAM281 is therefore inhibition of Transient receptor potential cation channel, subfamily m, member 6 (TRPM6, Accession NP_060132.3), a gene which contains a predicted ion channel domain and a protein kinase domain. and therefore is associated with Hypomagnesemia with secondary hypocalcemia. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Hypomagnesemia with secondary hypocalcemia,

and of other diseases and clinical conditions associated with TRPM6.

[36113] The function of TRPM6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1) is another GAM281 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:19833 and SEQ ID:16980 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36114] Another function of GAM281 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with TRPV1.

[36115] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_061197.3) is another GAM281 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:16980 and SEQ ID:19833 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36116] Another function of GAM281 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_061197.3), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[36117] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542435.1) is another GAM281 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:19833 and SEQ ID:16980 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36118] Another function of GAM281 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542435.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[36119] The function of TRPV1 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542437.1) is another GAM281 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:19833 and SEQ ID:16980 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36120] Another function of GAM281 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542437.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[36121] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM130.1.Tuberous sclerosis 1 (TSC1, Accession NP_000359.1) is another GAM281 target gene, herein designated TARGET GENE. TSC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TSC1 BINDING SITE, designated SEQ ID:15082, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36122] Another function of GAM281 is therefore inhibition of Tuberous sclerosis 1 (TSC1, Accession NP_000359.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSC1.

[36123] Tspy-like (TSPYL, Accession XP_166325.1) is another GAM281 target gene, herein designated TARGET GENE. TSPYL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSPYL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of TSPYL BINDING SITE, designated SEQ ID:15042, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36124] Another function of GAM281 is therefore inhibition of Tspy-like (TSPYL, Accession XP_166325.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSPYL.

[36125] Tetratricopeptide repeat domain 4 (TTC4, Accession NP_004614.1) is another GAM281 target gene, herein designated TARGET GENE. TTC4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TTC4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TTC4 BINDING SITE, designated SEQ ID:9587, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36126] Another function of GAM281 is therefore inhibition of Tetratricopeptide repeat domain 4 (TTC4, Accession NP_004614.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with TTC4.

[36127] TTY7 (Accession NP_114132.1) is another GAM281 target gene, herein designated TARGET GENE. TTY7 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TTY7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TTY7 BINDING SITE, designated SEQ ID:1016, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36128] Another function of GAM281 is therefore inhibition of TTY7 (Accession NP_114132.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTY7.

[36129] TU12B1-TY (Accession NP_057659.1) is another GAM281 target gene, herein designated TARGET GENE. TU12B1-TY BINDING SITE1 through TU12B1-TY BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by TU12B1-TY, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TU12B1-TY

BINDING SITE1 through TU12B1-TY BINDING SITE3, designated SEQ ID:16036, SEQ ID:15780 and SEQ ID:4256 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36130] Another function of GAM281 is therefore inhibition of TU12B1-TY (Accession NP_057659.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TU12B1-TY.

[36131] TUCAN (Accession NP_055774.1) is another GAM281 target gene, herein designated TARGET GENE. TUCAN BINDING SITE1 through TUCAN BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by TUCAN, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUCAN BINDING SITE1 through TUCAN BINDING SITE3, designated SEQ ID:9530, SEQ ID:7106 and SEQ ID:13395 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36132] Another function of GAM281 is therefore inhibition of TUCAN (Accession NP_055774.1) . Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUCAN.

[36133] Tuftelin 1 (TUFT1, Accession NP_064512.1) is another GAM281 target gene, herein designated TARGET GENE. TUFT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TUFT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUFT1 BINDING SITE, designated SEQ ID:6115, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36134] Another function of GAM281 is therefore inhibition of Tuftelin 1 (TUFT1, Accession NP_064512.1), a gene which appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and capping. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUFT1.

[36135] The function of TUFT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.TXL-2 (Accession NP_835231.1) is another

GAM281 target gene, herein designated TARGET GENE. TXL-2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TXL-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TXL-2 BINDING SITE, designated SEQ ID:15381, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36136] Another function of GAM281 is therefore inhibition of TXL-2 (Accession NP_835231.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TXL-2.

[36137] Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) is another GAM281 target gene, herein designated TARGET GENE. TXNL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TXNL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TXNL2 BINDING SITE, designated SEQ ID:9147, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36138] Another function of GAM281 is therefore inhibition of Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TXNL2.

[36139] U1SNRNPBP (Accession NP_851030.1) is another GAM281 target gene, herein designated TARGET GENE. U1SNRNPBP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by U1SNRNPBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of U1SNRNPBP BINDING SITE, designated SEQ ID:9590, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36140] Another function of GAM281 is therefore inhibition of U1SNRNPBP (Accession NP_851030.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U1SNRNPBP.

[36141] U1SNRNPBP (Accession NP_851034.1) is another GAM281 target gene, herein designated TARGET GENE. U1SNRNPBP

BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by U1SNRNPBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of U1SNRNPBP BINDING SITE, designated SEQ ID:9590, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36142] Another function of GAM281 is therefore inhibition of U1SNRNPBP (Accession NP_851034.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U1SNRNPBP.

[36143] U1SNRNPBP (Accession NP_008951.1) is another GAM281 target gene, herein designated TARGET GENE. U1SNRNPBP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by U1SNRNPBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of U1SNRNPBP BINDING SITE, designated SEQ ID:9590, to the nucleotide sequence of

GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36144] Another function of GAM281 is therefore inhibition of U1SNRNPBP (Accession NP_008951.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U1SNRNPBP.

[36145] UCK1 (Accession NP_113620.1) is another GAM281 target gene, herein designated TARGET GENE. UCK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UCK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UCK1 BINDING SITE, designated SEQ ID:14148, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36146] Another function of GAM281 is therefore inhibition of UCK1 (Accession NP_113620.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UCK1.

[36147] Udp-glucose dehydrogenase (UGDH, Accession NP_003350.1) is another GAM281 target gene, herein

designated TARGET GENE. UGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGDH BINDING SITE, designated SEQ ID:7909, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36148] Another function of GAM281 is therefore inhibition of Udp-glucose dehydrogenase (UGDH, Accession NP_003350.1), a gene which is an UDP- glucose dehydrogenase. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGDH.

[36149] The function of UGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Udp glycosyltransferase 1 family, polypeptide a1 (UGT1A1, Accession NP_000454.1) is another GAM281 target gene, herein designated TARGET GENE. UGT1A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A1, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A1 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36150] Another function of GAM281 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a1 (UGT1A1, Accession NP_000454.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT1A1.

[36151] Udp glycosyltransferase 1 family, polypeptide a10 (UGT1A10, Accession NP_061948.1) is another GAM281 target gene, herein designated TARGET GENE. UGT1A10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A10 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36152] Another function of GAM281 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a10 (UGT1A10,

Accession NP_061948.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT1A10.

[36153] Udp glycosyltransferase 1 family, polypeptide a4 (UGT1A4, Accession NP_009051.1) is another GAM281 target gene, herein designated TARGET GENE. UGT1A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A4 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36154] Another function of GAM281 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a4 (UGT1A4, Accession NP_009051.1), a gene which is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds. and therefore may be associated with Gilbert's syndrome, crigler- najjar. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Gilbert's syndrome, crigler- najjar, and of other diseases and clinical

conditions associated with UGT1A4.

[36155] The function of UGT1A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Udp glycosyltransferase 1 family, polypeptide a6 (UGT1A6, Accession NP_001063.1) is another GAM281 target gene, herein designated TARGET GENE. UGT1A6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A6 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36156] Another function of GAM281 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a6 (UGT1A6, Accession NP_001063.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT1A6.

[36157] Udp glycosyltransferase 1 family, polypeptide a8 (UGT1A8, Accession NP_061949.3) is another GAM281 target gene, herein designated TARGET GENE. UGT1A8

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGT1A8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A8 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36158] Another function of GAM281 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a8 (UGT1A8, Accession NP_061949.3), a gene which is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT1A8.

[36159] The function of UGT1A8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Udp glycosyltransferase 1 family, polypeptide a9 (UGT1A9, Accession NP_066307.1) is another GAM281 target gene, herein designated TARGET GENE. UGT1A9 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by UGT1A9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGT1A9 BINDING SITE, designated SEQ ID:10967, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36160] Another function of GAM281 is therefore inhibition of Udp glycosyltransferase 1 family, polypeptide a9 (UGT1A9, Accession NP_066307.1), a gene which is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGT1A9.

[36161] The function of UGT1A9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS, Accession NP_000364.1) is another GAM281 target gene, herein designated TARGET GENE. UMPS BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by UMPS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UMPS BINDING SITE, designated SEQ ID:2144, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36162] Another function of GAM281 is therefore inhibition of Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS, Accession NP_000364.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UMPS.

[36163] Unc-84 homolog a (c. elegans) (UNC84B, Accession XP_039332.1) is another GAM281 target gene, herein designated TARGET GENE. UNC84B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UNC84B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UNC84B BINDING SITE, designated SEQ ID:13541, to the nucleotide sequence of GAM281 RNA, herein designated

GAM RNA, also designated SEQ ID:278.

[36164] Another function of GAM281 is therefore inhibition of Unc-84 homolog a (c. elegans) (UNC84B, Accession XP_039332.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC84B.

[36165] Unc-84 homolog a (c. elegans) (UNC84B, Accession NP_056189.1) is another GAM281 target gene, herein designated TARGET GENE. UNC84B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UNC84B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UNC84B BINDING SITE, designated SEQ ID:13541, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36166] Another function of GAM281 is therefore inhibition of Unc-84 homolog a (c. elegans) (UNC84B, Accession NP_056189.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC84B.

[36167] URG4 (Accession NP_060390.2) is another GAM281 target

gene, herein designated TARGET GENE. URG4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by URG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of URG4 BINDING SITE, designated SEQ ID:6788, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36168] Another function of GAM281 is therefore inhibition of URG4 (Accession NP_060390.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with URG4.

[36169] Ubiquitin specific protease 22 (USP22, Accession XP_042698.2) is another GAM281 target gene, herein designated TARGET GENE. USP22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by USP22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of USP22 BINDING SITE, designated SEQ ID:11288, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ

ID:278.

[36170] Another function of GAM281 is therefore inhibition of Ubiquitin specific protease 22 (USP22, Accession XP_042698.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP22.

[36171] VDU1 (Accession NP_055832.2) is another GAM281 target gene, herein designated TARGET GENE. VDU1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VDU1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VDU1 BINDING SITE, designated SEQ ID:3187, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36172] Another function of GAM281 is therefore inhibition of VDU1 (Accession NP_055832.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VDU1.

[36173] Vent-like homeobox 2 (VENTX2, Accession NP_055283.1) is another GAM281 target gene, herein designated TARGET GENE. VENTX2 BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by VENTX2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VENTX2 BINDING SITE, designated SEQ ID:19331, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36174] Another function of GAM281 is therefore inhibition of Vent-like homeobox 2 (VENTX2, Accession NP_055283.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VENTX2.

[36175] Von hippel-lindau syndrome (VHL, Accession NP_000542.1) is another GAM281 target gene, herein designated TARGET GENE. VHL BINDING SITE1 and VHL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by VHL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VHL BINDING SITE1 and VHL BINDING SITE2, designated SEQ ID:3873 and SEQ ID:8786 respectively, to the nucleotide sequence

of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36176] Another function of GAM281 is therefore inhibition of Von hippel-lindau syndrome (VHL, Accession NP_000542.1), a gene which may control rna stability through the selective degradation of rna- bound proteins. and therefore is associated with Von hippel- lindau disease. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Von hippel- lindau disease, and of other diseases and clinical conditions associated with VHL.

[36177] The function of VHL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Vasoactive intestinal peptide receptor 2 (VIPR2, Accession NP_003373.2) is another GAM281 target gene, herein designated TARGET GENE. VIPR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VIPR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VIPR2 BINDING SITE, designated SEQ ID:7754, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA,

also designated SEQ ID:278.

[36178] Another function of GAM281 is therefore inhibition of Vasoactive intestinal peptide receptor 2 (VIPR2, Accession NP_003373.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIPR2.

[36179] Vacuolar protein sorting 33a (yeast) (VPS33A, Accession NP_075067.2) is another GAM281 target gene, herein designated TARGET GENE. VPS33A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VPS33A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VPS33A BINDING SITE, designated SEQ ID:16690, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36180] Another function of GAM281 is therefore inhibition of Vacuolar protein sorting 33a (yeast) (VPS33A, Accession NP_075067.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS33A.

[36181] Vesicle transport through interaction with t-snares ho-

molog 1a (yeast) (VTI1A, Accession NP_660207.1) is another GAM281 target gene, herein designated TARGET GENE. VTI1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VTI1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VTI1A BINDING SITE, designated SEQ ID:2313, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36182] Another function of GAM281 is therefore inhibition of Vesicle transport through interaction with t-snares homolog 1a (yeast) (VTI1A, Accession NP_660207.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VTI1A.

[36183] Williams-beuren syndrome chromosome region 1 (WBSCR1, Accession NP_071496.1) is another GAM281 target gene, herein designated TARGET GENE. WBSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WBSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR1 BINDING SITE, designated SEQ ID:11337, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36184] Another function of GAM281 is therefore inhibition of Williams-beuren syndrome chromosome region 1 (WBSCR1, Accession NP_071496.1), a gene which stimulates protein translation and therefore may be associated with Williams syndrome. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Williams syndrome, and of other diseases and clinical conditions associated with WBSCR1.

[36185] The function of WBSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Williams-beuren syndrome chromosome region 1 (WBSCR1, Accession NP_114381.1) is another GAM281 target gene, herein designated TARGET GENE. WBSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WBSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR1 BINDING SITE, designated SEQ ID:11337, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36186] Another function of GAM281 is therefore inhibition of Williams-beuren syndrome chromosome region 1 (WBSCR1, Accession NP_114381.1), a gene which stimulates protein translation and therefore may be associated with Williams syndrome. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Williams syndrome, and of other diseases and clinical conditions associated with WBSCR1.

[36187] The function of WBSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Williams beuren syndrome chromosome region 18 (WBSCR18, Accession NP_115693.2) is another GAM281 target gene, herein designated TARGET GENE. WBSCR18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WBSCR18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR18 BINDING SITE, designated SEQ ID:2152, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36188] Another function of GAM281 is therefore inhibition of Williams beuren syndrome chromosome region 18 (WBSCR18, Accession NP_115693.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR18.

[36189] Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_579889.1) is another GAM281 target gene, herein designated TARGET GENE. WHSC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WHSC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE, designated SEQ ID:9245, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36190] Another function of GAM281 is therefore inhibition of Wolf-hirschhorn syndrome candidate 1 (WHSC1, Acces-

sion NP_579889.1), a gene which binds covalently to and repairs g/t mismatches. and therefore may be associated with Wolf- hirschhorn syndrome. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of Wolf- hirschhorn syndrome, and of other diseases and clinical conditions associated with WHSC1.

[36191] The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Wnt1 inducible signaling pathway protein 2 (WISP2, Accession NP_003872.1) is another GAM281 target gene, herein designated TARGET GENE. WISP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WISP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WISP2 BINDING SITE, designated SEQ ID:6412, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36192] Another function of GAM281 is therefore inhibition of Wnt1 inducible signaling pathway protein 2 (WISP2, Accession NP_003872.1) . Accordingly, utilities of GAM281

include diagnosis, prevention and treatment of diseases and clinical conditions associated with WISP2.

[36193] X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1) is another GAM281 target gene, herein designated TARGET GENE. XRCC2 BINDING SITE1 through XRCC2 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by XRCC2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of XRCC2 BINDING SITE1 through XRCC2 BINDING SITE3, designated SEQ ID:12605, SEQ ID:10148 and SEQ ID:9688 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36194] Another function of GAM281 is therefore inhibition of X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1), a gene which involves in the homologous recombination repair (hrr) pathway of double- stranded dna. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XRCC2.

[36195] The function of XRCC2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.V-yes-1 yamaguchi sarcoma viral oncogene homolog 1 (YES1, Accession NP_005424.1) is another GAM281 target gene, herein designated TARGET GENE. YES1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by YES1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of YES1 BINDING SITE, designated SEQ ID:16112, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36196] Another function of GAM281 is therefore inhibition of V-yes-1 yamaguchi sarcoma viral oncogene homolog 1 (YES1, Accession NP_005424.1), a gene which is a putative protein- tyrosine kinase. Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YES1.

[36197] The function of YES1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM30.1.ZAK (Accession NP_598407.1) is another GAM281 target gene, herein designated TARGET GENE. ZAK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZAK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAK BINDING SITE, designated SEQ ID:7294, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36198] Another function of GAM281 is therefore inhibition of ZAK (Accession NP_598407.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAK.

[36199] ZAP (Accession NP_064504.2) is another GAM281 target gene, herein designated TARGET GENE. ZAP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAP BINDING SITE, designated SEQ ID:3071, to the nucleotide sequence of GAM281 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:278.

[36200] Another function of GAM281 is therefore inhibition of ZAP (Accession NP_064504.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAP.

[36201] Z-dna binding protein 1 (ZBP1, Accession NP_110403.1) is another GAM281 target gene, herein designated TARGET GENE. ZBP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZBP1 BINDING SITE, designated SEQ ID:16276, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36202] Another function of GAM281 is therefore inhibition of Z-dna binding protein 1 (ZBP1, Accession NP_110403.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZBP1.

[36203] ZFP30 (Accession NP_055713.1) is another GAM281 target gene, herein designated TARGET GENE. ZFP30 BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by ZFP30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP30 BINDING SITE, designated SEQ ID:9331, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36204] Another function of GAM281 is therefore inhibition of ZFP30 (Accession NP_055713.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP30.

[36205] ZFP42 (Accession NP_777560.1) is another GAM281 target gene, herein designated TARGET GENE. ZFP42 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZFP42, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP42 BINDING SITE, designated SEQ ID:10587, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36206] Another function of GAM281 is therefore inhibition of ZFP42 (Accession NP_777560.1) . Accordingly, utilities of

GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP42.

[36207] Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_060667.1) is another GAM281 target gene, herein designated TARGET GENE. ZFP64 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP64, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP64 BINDING SITE, designated SEQ ID:15043, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36208] Another function of GAM281 is therefore inhibition of Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_060667.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP64.

[36209] Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_071371.2) is another GAM281 target gene, herein designated TARGET GENE. ZFP64 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP64, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP64 BINDING SITE, designated SEQ ID:15043, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36210] Another function of GAM281 is therefore inhibition of Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_071371.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP64.

[36211] ZFYVE26 (Accession XP_031077.1) is another GAM281 target gene, herein designated TARGET GENE. ZFYVE26 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZFYVE26, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFYVE26 BINDING SITE, designated SEQ ID:12160, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36212] Another function of GAM281 is therefore inhibition of ZFYVE26 (Accession XP_031077.1) . Accordingly, utilities

of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFYVE26.

[36213] ZMYND17 (Accession NP_848546.1) is another GAM281 target gene, herein designated TARGET GENE. ZMYND17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZMYND17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZMYND17 BINDING SITE, designated SEQ ID:456, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36214] Another function of GAM281 is therefore inhibition of ZMYND17 (Accession NP_848546.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZMYND17.

[36215] Zinc finger protein 253 (ZNF253, Accession NP_066385.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF253 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF253, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF253 BINDING SITE, designated SEQ ID:19746, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36216] Another function of GAM281 is therefore inhibition of Zinc finger protein 253 (ZNF253, Accession NP_066385.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF253.

[36217] Zinc finger protein 264 (ZNF264, Accession NP_003408.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF264 BINDING SITE1 and ZNF264 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ZNF264, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF264 BINDING SITE1 and ZNF264 BINDING SITE2, designated SEQ ID:3319 and SEQ ID:9147 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36218] Another function of GAM281 is therefore inhibition of Zinc finger protein 264 (ZNF264, Accession NP_003408.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF264.

[36219] Zinc finger protein 273 (ZNF273, Accession XP_088082.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF273 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF273, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF273 BINDING SITE, designated SEQ ID:18868, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36220] Another function of GAM281 is therefore inhibition of Zinc finger protein 273 (ZNF273, Accession XP_088082.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF273.

[36221] Zinc finger protein 289, id1 regulated (ZNF289, Accession NP_115765.2) is another GAM281 target gene, herein

designated TARGET GENE. ZNF289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF289 BINDING SITE, designated SEQ ID:13159, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36222] Another function of GAM281 is therefore inhibition of Zinc finger protein 289, id1 regulated (ZNF289, Accession NP_115765.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF289.

[36223] Zinc finger protein 305 (ZNF305, Accession NP_055539.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF305 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF305, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF305 BINDING SITE, designated SEQ ID:18505, to the nucleotide sequence of GAM281

RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36224] Another function of GAM281 is therefore inhibition of Zinc finger protein 305 (ZNF305, Accession NP_055539.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF305.

[36225] Zinc finger protein 334 (ZNF334, Accession NP_060572.2) is another GAM281 target gene, herein designated TARGET GENE. ZNF334 BINDING SITE1 and ZNF334 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ZNF334, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF334 BINDING SITE1 and ZNF334 BINDING SITE2, designated SEQ ID:5064 and SEQ ID:9628 respectively, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36226] Another function of GAM281 is therefore inhibition of Zinc finger protein 334 (ZNF334, Accession NP_060572.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with ZNF334.

[36227] Zinc finger protein 339 (ZNF339, Accession NP_067043.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF339 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF339, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF339 BINDING SITE, designated SEQ ID:1729, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36228] Another function of GAM281 is therefore inhibition of Zinc finger protein 339 (ZNF339, Accession NP_067043.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF339.

[36229] Zinc finger protein 345 (ZNF345, Accession NP_003410.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF345 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF345, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of ZNF345 BINDING SITE, designated SEQ ID:1011, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36230] Another function of GAM281 is therefore inhibition of Zinc finger protein 345 (ZNF345, Accession NP_003410.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF345.

[36231] Zinc finger protein 347 (ZNF347, Accession NP_115973.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF347 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF347, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF347 BINDING SITE, designated SEQ ID:8447, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36232] Another function of GAM281 is therefore inhibition of Zinc finger protein 347 (ZNF347, Accession NP_115973.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF347.

[36233] Zinc finger protein 398 (ZNF398, Accession NP_065832.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF398 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ZNF398, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF398 BINDING SITE, designated SEQ ID:8530, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36234] Another function of GAM281 is therefore inhibition of Zinc finger protein 398 (ZNF398, Accession NP_065832.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF398.

[36235] ZNF431 (Accession XP_086098.2) is another GAM281 target gene, herein designated TARGET GENE. ZNF431 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF431, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF431

BINDING SITE, designated SEQ ID:8477, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36236] Another function of GAM281 is therefore inhibition of ZNF431 (Accession XP_086098.2) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF431.

[36237] ZNF432 (Accession NP_055465.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF432 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF432, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF432 BINDING SITE, designated SEQ ID:5065, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36238] Another function of GAM281 is therefore inhibition of ZNF432 (Accession NP_055465.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF432.

[36239] ZNF440 (Accession NP_689570.1) is another GAM281 tar-

get gene, herein designated TARGET GENE. ZNF440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF440 BINDING SITE, designated SEQ ID:1744, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36240] Another function of GAM281 is therefore inhibition of ZNF440 (Accession NP_689570.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF440.

[36241] Zinc finger protein 70 (cos17) (ZNF70, Accession NP_068735.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF70 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZNF70, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF70 BINDING SITE, designated SEQ ID:17076, to the nu-

cleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36242] Another function of GAM281 is therefore inhibition of Zinc finger protein 70 (cos17) (ZNF70, Accession NP_068735.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF70.

[36243] Zinc finger protein 70 (cos17) (ZNF70, Accession NP_852101.1) is another GAM281 target gene, herein designated TARGET GENE. ZNF70 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZNF70, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF70 BINDING SITE, designated SEQ ID:17076, to the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, also designated SEQ ID:278.

[36244] Another function of GAM281 is therefore inhibition of Zinc finger protein 70 (cos17) (ZNF70, Accession NP_852101.1) . Accordingly, utilities of GAM281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF70.

[36245]

[36246] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 391 (GAM391), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36247] GAM391 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM391 was detected is described hereinabove with reference to Figs. 8-15.

[36248] GAM391 gene, herein designated GAM GENE, and GAM391 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[36249] GAM391 gene encodes a GAM391 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM391 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM391 precursor RNA is designated SEQ ID:199, and is provided hereinbelow with reference to the sequence listing part.

[36250] GAM391 precursor RNA folds onto itself, forming GAM391

folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36251] GAM391 precursor RNA folds onto itself, forming GAM391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[36252] Nucleotide sequence of GAM391 precursor RNA, designated SEQ-ID: 199, and a schematic representation of a predicted secondary folding of GAM391 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[36253] An enzyme complex designated DICER COMPLEX, `dices`

the GAM391 folded precursor RNA into GAM391 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM391 RNA is designated SEQ ID:326, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[36254] GAM391 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM391 target RNA, herein designated GAM TARGET RNA. GAM391 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[36255] GAM391 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM391 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM391

RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM391 RNA may have a different number of target binding sites in untranslated regions of a GAM391 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[36256] The complementary binding of GAM391 RNA, herein designated GAM RNA, to target binding sites on GAM391 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM391 target RNA into GAM391 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36257] It is appreciated that GAM391 target gene, herein designated TARGET GENE, in fact represents a plurality of

GAM391 target genes. The mRNA of each one of this plurality of GAM391 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM391 RNA, herein designated GAM RNA, and which when bound by GAM391 RNA causes inhibition of translation of respective one or more GAM391 target proteins.

[36258] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM391 gene, herein designated GAM GENE, on one or more GAM391 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36259] It is appreciated that specific functions and accordingly utilities of GAM391 correlate with, and may be deduced from, the identity of the target genes which GAM391 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36260]

[36261]

[36262] 5'OY11.1 (Accession NP_542942.1) is a GAM391 target gene, herein designated TARGET GENE. 5'OY11.1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by 5'OY11.1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of 5'OY11.1 BINDING SITE, designated SEQ ID:5923, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36263] A function of GAM391 is therefore inhibition of 5'OY11.1 (Accession NP_542942.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 5'OY11.1.

[36264] APBB3 (Accession NP_573422.1) is another GAM391 target

gene, herein designated TARGET GENE. APBB3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APBB3 BINDING SITE, designated SEQ ID:539, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36265] Another function of GAM391 is therefore inhibition of APBB3 (Accession NP_573422.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APBB3.

[36266] APBB3 (Accession NP_573421.1) is another GAM391 target gene, herein designated TARGET GENE. APBB3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APBB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APBB3 BINDING SITE, designated SEQ ID:539, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36267] Another function of GAM391 is therefore inhibition of APBB3 (Accession NP_573421.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APBB3.

[36268] Amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2, Accession NP_006371.2) is another GAM391 target gene, herein designated TARGET GENE. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APPBP2 BINDING SITE, designated SEQ ID:1844, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36269] Another function of GAM391 is therefore inhibition of Amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2, Accession NP_006371.2), a gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore may be associated with Alzheimer's disease. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of Alzheimer's disease, and of other diseases and clinical conditions as-

sociated with APPBP2.

[36270] The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Ankyrin repeat and socs box-containing 1 (ASB1, Accession NP_057198.1) is another GAM391 target gene, herein designated TARGET GENE. ASB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB1 BINDING SITE, designated SEQ ID:11800, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36271] Another function of GAM391 is therefore inhibition of Ankyrin repeat and socs box-containing 1 (ASB1, Accession NP_057198.1), a gene which May mediate protein-protein interactions. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB1.

[36272] The function of ASB1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM47.1.Atpase, class i, type 8b, member 2 (ATP8B2, Accession XP_290875.1) is another GAM391 target gene, herein designated TARGET GENE. ATP8B2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ATP8B2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP8B2 BINDING SITE, designated SEQ ID:11976, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36273] Another function of GAM391 is therefore inhibition of Atpase, class i, type 8b, member 2 (ATP8B2, Accession XP_290875.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8B2.

[36274] Axotrophin (AXOT, Accession NP_073737.1) is another GAM391 target gene, herein designated TARGET GENE. AXOT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AXOT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of AXOT BINDING SITE, designated SEQ ID:3201, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36275] Another function of GAM391 is therefore inhibition of Axotrophin (AXOT, Accession NP_073737.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXOT.

[36276] C14orf78 (Accession XP_290629.1) is another GAM391 target gene, herein designated TARGET GENE. C14orf78 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C14orf78, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf78 BINDING SITE, designated SEQ ID:3928, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36277] Another function of GAM391 is therefore inhibition of C14orf78 (Accession XP_290629.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

C14orf78.

[36278] Chromosome 1 open reading frame 24 (C1orf24, Accession NP_071366.1) is another GAM391 target gene, herein designated TARGET GENE. C1orf24 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C1orf24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:1181, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36279] Another function of GAM391 is therefore inhibition of Chromosome 1 open reading frame 24 (C1orf24, Accession NP_071366.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24.

[36280] Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) is another GAM391 target gene, herein designated TARGET GENE. C1orf24 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C1orf24, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:1181, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36281] Another function of GAM391 is therefore inhibition of Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24.

[36282] Chromosome 21 open reading frame 82 (C21orf82, Accession NP_715632.1) is another GAM391 target gene, herein designated TARGET GENE. C21orf82 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C21orf82, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C21orf82 BINDING SITE, designated SEQ ID:5611, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36283] Another function of GAM391 is therefore inhibition of Chromosome 21 open reading frame 82 (C21orf82, Ac-

cession NP_715632.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf82.

[36284] Reserved (C8orf6, Accession NP_663631.1) is another GAM391 target gene, herein designated TARGET GENE. C8orf6 BINDING SITE1 and C8orf6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C8orf6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C8orf6 BINDING SITE1 and C8orf6 BINDING SITE2, designated SEQ ID:6819 and SEQ ID:16546 respectively, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36285] Another function of GAM391 is therefore inhibition of Reserved (C8orf6, Accession NP_663631.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf6.

[36286] Chromosome 9 open reading frame 25 (C9orf25, Accession NP_671735.1) is another GAM391 target gene, herein designated TARGET GENE. C9orf25 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by C9orf25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C9orf25 BINDING SITE, designated SEQ ID:2377, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36287] Another function of GAM391 is therefore inhibition of Chromosome 9 open reading frame 25 (C9orf25, Accession NP_671735.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf25.

[36288] Chemokine (c-c motif) receptor 2 (CCR2, Accession NP_000638.1) is another GAM391 target gene, herein designated TARGET GENE. CCR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CCR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCR2 BINDING SITE, designated SEQ ID:9391, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA,

also designated SEQ ID:326.

[36289] Another function of GAM391 is therefore inhibition of Chemokine (c-c motif) receptor 2 (CCR2, Accession NP_000638.1), a gene which binds chemokines and transduces a signal by increasing the intracellular calcium ions level. and therefore may be associated with Hiv- 1 infection. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of Hiv- 1 infection, and of other diseases and clinical conditions associated with CCR2.

[36290] The function of CCR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.1.Cat eye syndrome chromosome region, candidate 6 (CECR6, Accession NP_114096.1) is another GAM391 target gene, herein designated TARGET GENE. CECR6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CECR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR6 BINDING SITE, designated SEQ ID:1794, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36291] Another function of GAM391 is therefore inhibition of Cat eye syndrome chromosome region, candidate 6 (CECR6, Accession NP_114096.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR6.

[36292] Centaurin, delta 2 (CENTD2, Accession NP_056057.1) is another GAM391 target gene, herein designated TARGET GENE. CENTD2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CENTD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENTD2 BINDING SITE, designated SEQ ID:12112, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36293] Another function of GAM391 is therefore inhibition of Centaurin, delta 2 (CENTD2, Accession NP_056057.1), a gene which involved in cell signaling/communication. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENTD2.

[36294] The function of CENTD2 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.CGI-127 (Accession NP_057145.1) is another GAM391 target gene, herein designated TARGET GENE. CGI-127 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CGI-127, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-127 BINDING SITE, designated SEQ ID:16833, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36295] Another function of GAM391 is therefore inhibition of CGI-127 (Accession NP_057145.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-127.

[36296] Calcium homeostasis endoplasmic reticulum protein (CHERP, Accession NP_006378.2) is another GAM391 target gene, herein designated TARGET GENE. CHERP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHERP, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHERP BINDING SITE, designated SEQ ID:18403, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36297] Another function of GAM391 is therefore inhibition of Calcium homeostasis endoplasmic reticulum protein (CHERP, Accession NP_006378.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHERP.

[36298] Cholinergic receptor, nicotinic, beta polypeptide 4 (CHRNB4, Accession NP_000741.1) is another GAM391 target gene, herein designated TARGET GENE. CHRNB4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHRNB4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHRNB4 BINDING SITE, designated SEQ ID:20038, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36299] Another function of GAM391 is therefore inhibition of Cholinergic receptor, nicotinic, beta polypeptide 4

(CHRNB4, Accession NP_000741.1), a gene which mediates fast signal transmission at synapses. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRNB4.

[36300] The function of CHRNB4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM76.1.Dab2 interacting protein (DAB2IP, Accession NP_115941.1) is another GAM391 target gene, herein designated TARGET GENE. DAB2IP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DAB2IP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DAB2IP BINDING SITE, designated SEQ ID:8058, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36301] Another function of GAM391 is therefore inhibition of Dab2 interacting protein (DAB2IP, Accession NP_115941.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAB2IP.

[36302] Damage-specific dna binding protein 1, 127kda (DDB1, Accession NP_001914.2) is another GAM391 target gene, herein designated TARGET GENE. DDB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DDB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDB1 BINDING SITE, designated SEQ ID:4279, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36303] Another function of GAM391 is therefore inhibition of Damage-specific dna binding protein 1, 127kda (DDB1, Accession NP_001914.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDB1.

[36304] DKFZP434O047 (Accession NP_056409.1) is another GAM391 target gene, herein designated TARGET GENE. DKFZP434O047 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP434O047, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of DKFZP434O047 BINDING SITE, designated SEQ ID:13168, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36305] Another function of GAM391 is therefore inhibition of DKFZP434O047 (Accession NP_056409.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434O047.

[36306] DKFZP434P211 (Accession NP_055364.1) is another GAM391 target gene, herein designated TARGET GENE. DKFZP434P211 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434P211, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434P211 BINDING SITE, designated SEQ ID:7211, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36307] Another function of GAM391 is therefore inhibition of DKFZP434P211 (Accession NP_055364.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with DKFZP434P211.

[36308] E2f transcription factor 3 (E2F3, Accession NP_001940.1) is another GAM391 target gene, herein designated TARGET GENE. E2F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by E2F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of E2F3 BINDING SITE, designated SEQ ID:16925, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36309] Another function of GAM391 is therefore inhibition of E2f transcription factor 3 (E2F3, Accession NP_001940.1), a gene which binds dna and controls cell- cycle progression from g1 to s phase. and therefore may be associated with Hereditary autosomal dominant myoclonus dystonia. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of Hereditary autosomal dominant myoclonus dystonia, and of other diseases and clinical conditions associated with E2F3.

[36310] The function of E2F3 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM44.1.Erythrocyte membrane protein band 4.1 like 4b (EPB41L4B, Accession NP_060894.1) is another GAM391 target gene, herein designated TARGET GENE. EPB41L4B BINDING SITE1 and EPB41L4B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by EPB41L4B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EPB41L4B BINDING SITE1 and EPB41L4B BINDING SITE2, designated SEQ ID:16985 and SEQ ID:5606 respectively, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36311] Another function of GAM391 is therefore inhibition of Erythrocyte membrane protein band 4.1 like 4b (EPB41L4B, Accession NP_060894.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPB41L4B.

[36312] Ellis van creveld syndrome (EVC, Accession NP_714928.1) is another GAM391 target gene, herein designated TARGET GENE. EVC BINDING SITE1 and EVC BINDING SITE2 are target binding sites found in untranslated regions of mul-

tiple transcripts of mRNA encoded by EVC, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE1 and EVC BINDING SITE2, designated SEQ ID:8983 and SEQ ID:672 respectively, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36313] Another function of GAM391 is therefore inhibition of Ellis van creveld syndrome (EVC, Accession NP_714928.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC.

[36314] FLJ10350 (Accession NP_060537.2) is another GAM391 target gene, herein designated TARGET GENE. FLJ10350 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10350, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10350 BINDING SITE, designated SEQ ID:5633, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36315] Another function of GAM391 is therefore inhibition of FLJ10350 (Accession NP_060537.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10350.

[36316] FLJ10702 (Accession NP_060654.1) is another GAM391 target gene, herein designated TARGET GENE. FLJ10702 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10702, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10702 BINDING SITE, designated SEQ ID:3052, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36317] Another function of GAM391 is therefore inhibition of FLJ10702 (Accession NP_060654.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10702.

[36318] FLJ12409 (Accession NP_079381.1) is another GAM391 target gene, herein designated TARGET GENE. FLJ12409 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ12409, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12409 BINDING SITE, designated SEQ ID:3246, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36319] Another function of GAM391 is therefore inhibition of FLJ12409 (Accession NP_079381.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12409.

[36320] FLJ14260 (Accession NP_079303.2) is another GAM391 target gene, herein designated TARGET GENE. FLJ14260 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ14260, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14260 BINDING SITE, designated SEQ ID:17291, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36321] Another function of GAM391 is therefore inhibition of

FLJ14260 (Accession NP_079303.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14260.

[36322] FLJ20275 (Accession NP_060207.1) is another GAM391 target gene, herein designated TARGET GENE. FLJ20275 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20275, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20275 BINDING SITE, designated SEQ ID:518, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36323] Another function of GAM391 is therefore inhibition of FLJ20275 (Accession NP_060207.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20275.

[36324] FLJ39005 (Accession NP_848616.1) is another GAM391 target gene, herein designated TARGET GENE. FLJ39005 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ39005, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39005 BINDING SITE, designated SEQ ID:3674, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36325] Another function of GAM391 is therefore inhibition of FLJ39005 (Accession NP_848616.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39005.

[36326] Forkhead box m1 (FOXM1, Accession NP_068772.1) is another GAM391 target gene, herein designated TARGET GENE. FOXM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOXM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXM1 BINDING SITE, designated SEQ ID:11174, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36327] Another function of GAM391 is therefore inhibition of

Forkhead box m1 (FOXM1, Accession NP_068772.1), a gene which may play a role in the control of cell proliferation. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXM1.

[36328] The function of FOXM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.Forkhead box p1 (FOXP1, Accession NP_116071.2) is another GAM391 target gene, herein designated TARGET GENE. FOXP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FOXP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXP1 BINDING SITE, designated SEQ ID:4841, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36329] Another function of GAM391 is therefore inhibition of Forkhead box p1 (FOXP1, Accession NP_116071.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXP1.

[36330] GALNACT-2 (Accession NP_061060.3) is another GAM391 target gene, herein designated TARGET GENE. GALNACT-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GALNACT-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GALNACT-2 BINDING SITE, designated SEQ ID:11066, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36331] Another function of GAM391 is therefore inhibition of GALNACT-2 (Accession NP_061060.3) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNACT-2.

[36332] Gata binding protein 2 (GATA2, Accession NP_116027.2) is another GAM391 target gene, herein designated TARGET GENE. GATA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GATA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GATA2 BINDING SITE, designated

SEQ ID:12989, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36333] Another function of GAM391 is therefore inhibition of Gata binding protein 2 (GATA2, Accession NP_116027.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GATA2.

[36334] GEMIN7 (Accession NP_078983.1) is another GAM391 target gene, herein designated TARGET GENE. GEMIN7 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GEMIN7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GEMIN7 BINDING SITE, designated SEQ ID:6579, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36335] Another function of GAM391 is therefore inhibition of GEMIN7 (Accession NP_078983.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GEMIN7.

[36336] Glutamate receptor, ionotropic, n-methyl d-aspartate 2b (GRIN2B, Accession NP_000825.1) is another GAM391 target gene, herein designated TARGET GENE. GRIN2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRIN2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRIN2B BINDING SITE, designated SEQ ID:14110, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36337] Another function of GAM391 is therefore inhibition of Glutamate receptor, ionotropic, n-methyl d-aspartate 2b (GRIN2B, Accession NP_000825.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIN2B.

[36338] Hairy/enhancer-of-split related with yrpw motif-like (HEYL, Accession NP_055386.1) is another GAM391 target gene, herein designated TARGET GENE. HEYL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HEYL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HEYL BINDING SITE, designated SEQ ID:11546, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36339] Another function of GAM391 is therefore inhibition of Hairy/enhancer-of-split related with yrpw motif-like (HEYL, Accession NP_055386.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEYL.

[36340] Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) is another GAM391 target gene, herein designated TARGET GENE. INMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INMT BINDING SITE, designated SEQ ID:9915, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36341] Another function of GAM391 is therefore inhibition of Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) . Accordingly, utilities of GAM391 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with INMT.

[36342] Jumonji homolog (mouse) (JMJ, Accession NP_004964.2) is another GAM391 target gene, herein designated TARGET GENE. JMJ BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JMJ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JMJ BINDING SITE, designated SEQ ID:2359, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36343] Another function of GAM391 is therefore inhibition of Jumonji homolog (mouse) (JMJ, Accession NP_004964.2), a gene which participates in the negative regulation of cell growth. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JMJ.

[36344] The function of JMJ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5, Accession

NP_002225.2) is another GAM391 target gene, herein designated TARGET GENE. KCNA5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KCNA5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNA5 BINDING SITE, designated SEQ ID:3000, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36345] Another function of GAM391 is therefore inhibition of Potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5, Accession NP_002225.2), a gene which mediates the voltage- dependent potassium ion permeability of excitable membranes. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNA5.

[36346] The function of KCNA5 has been established by previous studies. Potassium channels play an important role in the regulation of pancreatic beta cells in response to glucose and the sulfonylurea oral hypoglycemic agents. Philipson et al. (1991) used a rat brain potassium channel probe to screen a human insulinoma cDNA library for clones en-

coding voltage- gated potassium channels. They isolated a series of cDNA clones which were then used to isolate and sequence a potassium channel gene, designated PCN1. Microinjection of synthetic RNA encoding PCN1 was accomplished in order to determine the electrophysiologic characteristics of the protein. These experiments demonstrated that the PCN1 potassium channel has the electrophysiologic characteristics of delayed- rectifier type channels. Tamkun et al. (1991) isolated human heart cDNAs encoding PCN1, which they called HK2, and HK1 (KCNA4; 176266). They reported that the predicted 605- amino acid HK2 protein shares the characteristics of voltage-gated potassium channels, with 6 potential membrane-spanning domains and a positively charged region in the fourth membrane- spanning domain. Northern blot analysis revealed that HK2 is expressed as a major 2.5- and a minor 1.5- kb mRNA in human atrium and ventricle. By study of somatic cell hybrids, McPherson et al. (1991) mapped a Shaker- related potassium voltage- gated channel gene to chromosome 12. Designated here KCNA5, the gene was identified with probe Kv1 from the rat. By multipoint linkage analysis of 8 CEPH families, Phromchotikul et al. (1993) mapped the KCNA5 gene to

12p and determined its position relative to 4 DNA markers. Using interspecific backcrosses between Mus musculus and Mus spretus, Klocke et al. (1993) mapped the Kcna5 gene to a cluster with the Kcna1 and Kcna6 (OMIM Ref. No. 176257) genes and the mouse homolog of TPI1 (OMIM Ref. No. 190450). Since TPI1 is located on band 12p13 in the human, the 3 K(+)- channel genes was predicted to be in the same band. Curran et al. (1992) mapped the KCNA5 gene, which they erroneously referred to as the KCNA1 gene, to chromosome 12 by use of human- rodent somatic cell panels and narrowed the localization to the distal short arm by in situ hybridization. Linkage studies had shown a maximum lod score of 2.72 at a recombination fraction of 0.05 between KCNA5 and the von Willebrand locus (VWF; 193400). Albrecht et al. (1995) determined that a 300- kb cluster on chromosome 12p13 contains the human KCNA6, KCNA1, and KCNA5 genes arranged in tandem

[36347]

[36348] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[36349] Albrecht, B.; Weber, K.; Pongs, O. : Characterization of a

voltage- activated K- channel gene cluster on human chromosome 12p13. Receptors Channels 3: 213- 220, 1995. ; and

[36350] Curran, M. E.; Landes, G. M.; Keating, M. T. : Molecular cloning, characterization, and genomic localization of a human potassium channel gene. Genomics 12: 729- 737, 1992.

[36351] Further studies establishing the function and utilities of KCNA5 are found in John Hopkins OMIM database record ID 176267, and in cited publications listed in Table 5, which are hereby incorporated by reference.KIAA0276 (Accession XP_048199.1) is another GAM391 target gene, herein designated TARGET GENE. KIAA0276 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0276, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0276 BINDING SITE, designated SEQ ID:13253, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36352] Another function of GAM391 is therefore inhibition of KIAA0276 (Accession XP_048199.1) . Accordingly, utilities

of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0276.

[36353] KIAA0376 (Accession XP_037759.2) is another GAM391 target gene, herein designated TARGET GENE. KIAA0376 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0376, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0376 BINDING SITE, designated SEQ ID:5037, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36354] Another function of GAM391 is therefore inhibition of KIAA0376 (Accession XP_037759.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0376.

[36355] KIAA0773 (Accession NP_055505.1) is another GAM391 target gene, herein designated TARGET GENE. KIAA0773 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0773, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0773 BINDING SITE, designated SEQ ID:7493, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36356] Another function of GAM391 is therefore inhibition of KIAA0773 (Accession NP_055505.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0773.

[36357] KIAA0937 (Accession XP_166213.1) is another GAM391 target gene, herein designated TARGET GENE. KIAA0937 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0937, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0937 BINDING SITE, designated SEQ ID:11761, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36358] Another function of GAM391 is therefore inhibition of KIAA0937 (Accession XP_166213.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA0937.

[36359] KIAA1462 (Accession XP_166132.1) is another GAM391 target gene, herein designated TARGET GENE. KIAA1462 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1462, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1462 BINDING SITE, designated SEQ ID:16373, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36360] Another function of GAM391 is therefore inhibition of KIAA1462 (Accession XP_166132.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1462.

[36361] KIAA1951 (Accession XP_057401.1) is another GAM391 target gene, herein designated TARGET GENE. KIAA1951 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1951, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA1951 BINDING SITE, designated SEQ ID:13357, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36362] Another function of GAM391 is therefore inhibition of KIAA1951 (Accession XP_057401.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1951.

[36363] KIFC2 (Accession NP_665697.1) is another GAM391 target gene, herein designated TARGET GENE. KIFC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIFC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIFC2 BINDING SITE, designated SEQ ID:6714, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36364] Another function of GAM391 is therefore inhibition of KIFC2 (Accession NP_665697.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIFC2.

[36365] Kringle containing transmembrane protein 1 (KREMEN1, Accession NP_114434.3) is another GAM391 target gene, herein designated TARGET GENE. KREMEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KREMEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KREMEN1 BINDING SITE, designated SEQ ID:7291, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36366] Another function of GAM391 is therefore inhibition of Kringle containing transmembrane protein 1 (KREMEN1, Accession NP_114434.3) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KREMEN1.

[36367] Lim domain binding 3 (LDB3, Accession XP_084376.6) is another GAM391 target gene, herein designated TARGET GENE. LDB3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LDB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of LDB3 BINDING SITE, designated SEQ ID:2117, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36368] Another function of GAM391 is therefore inhibition of Lim domain binding 3 (LDB3, Accession XP_084376.6), a gene which could play a role during mating. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LDB3.

[36369] The function of LDB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.LOC125061 (Accession XP_058889.3) is another GAM391 target gene, herein designated TARGET GENE. LOC125061 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC125061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC125061 BINDING SITE, designated SEQ ID:19284, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36370] Another function of GAM391 is therefore inhibition of LOC125061 (Accession XP_058889.3) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125061.

[36371] LOC139201 (Accession XP_208439.1) is another GAM391 target gene, herein designated TARGET GENE. LOC139201 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC139201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC139201 BINDING SITE, designated SEQ ID:11240, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36372] Another function of GAM391 is therefore inhibition of LOC139201 (Accession XP_208439.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139201.

[36373] LOC143310 (Accession XP_084485.1) is another GAM391 target gene, herein designated TARGET GENE. LOC143310 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC143310, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143310 BINDING SITE, designated SEQ ID:12539, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36374] Another function of GAM391 is therefore inhibition of LOC143310 (Accession XP_084485.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143310.

[36375] LOC145660 (Accession XP_085200.1) is another GAM391 target gene, herein designated TARGET GENE. LOC145660 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145660, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145660 BINDING SITE, designated SEQ ID:10556, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36376] Another function of GAM391 is therefore inhibition of

LOC145660 (Accession XP_085200.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145660.

[36377] LOC145820 (Accession XP_085246.1) is another GAM391 target gene, herein designated TARGET GENE. LOC145820 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145820, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145820 BINDING SITE, designated SEQ ID:1993, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36378] Another function of GAM391 is therefore inhibition of LOC145820 (Accession XP_085246.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145820.

[36379] LOC146243 (Accession XP_096956.1) is another GAM391 target gene, herein designated TARGET GENE. LOC146243 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146243, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146243 BINDING SITE, designated SEQ ID:11896, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36380] Another function of GAM391 is therefore inhibition of LOC146243 (Accession XP_096956.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146243.

[36381] LOC146517 (Accession XP_085491.1) is another GAM391 target gene, herein designated TARGET GENE. LOC146517 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146517, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146517 BINDING SITE, designated SEQ ID:18098, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36382] Another function of GAM391 is therefore inhibition of LOC146517 (Accession XP_085491.1) . Accordingly, utili-

ties of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146517.

[36383] LOC148709 (Accession XP_086281.1) is another GAM391 target gene, herein designated TARGET GENE. LOC148709 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148709, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148709 BINDING SITE, designated SEQ ID:17147, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36384] Another function of GAM391 is therefore inhibition of LOC148709 (Accession XP_086281.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148709.

[36385] LOC150174 (Accession XP_086802.2) is another GAM391 target gene, herein designated TARGET GENE. LOC150174 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150174, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150174 BINDING SITE, designated SEQ ID:7211, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36386] Another function of GAM391 is therefore inhibition of LOC150174 (Accession XP_086802.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150174.

[36387] LOC150213 (Accession XP_059324.1) is another GAM391 target gene, herein designated TARGET GENE. LOC150213 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150213, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150213 BINDING SITE, designated SEQ ID:7211, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36388] Another function of GAM391 is therefore inhibition of LOC150213 (Accession XP_059324.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC150213.

[36389] LOC151068 (Accession XP_098000.1) is another GAM391 target gene, herein designated TARGET GENE. LOC151068 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151068, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151068 BINDING SITE, designated SEQ ID:6116, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36390] Another function of GAM391 is therefore inhibition of LOC151068 (Accession XP_098000.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151068.

[36391] LOC151124 (Accession XP_098006.1) is another GAM391 target gene, herein designated TARGET GENE. LOC151124 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151124, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC151124 BINDING SITE, designated SEQ ID:6464, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36392] Another function of GAM391 is therefore inhibition of LOC151124 (Accession XP_098006.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151124.

[36393] LOC151877 (Accession XP_098132.1) is another GAM391 target gene, herein designated TARGET GENE. LOC151877 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151877, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151877 BINDING SITE, designated SEQ ID:9078, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36394] Another function of GAM391 is therefore inhibition of LOC151877 (Accession XP_098132.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC151877.

[36395] LOC157531 (Accession XP_212210.1) is another GAM391 target gene, herein designated TARGET GENE. LOC157531 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC157531, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157531 BINDING SITE, designated SEQ ID:9551, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36396] Another function of GAM391 is therefore inhibition of LOC157531 (Accession XP_212210.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157531.

[36397] LOC196988 (Accession XP_113795.1) is another GAM391 target gene, herein designated TARGET GENE. LOC196988 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC196988, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC196988 BINDING SITE, designated SEQ ID:19127, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36398] Another function of GAM391 is therefore inhibition of LOC196988 (Accession XP_113795.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196988.

[36399] LOC199718 (Accession XP_113998.1) is another GAM391 target gene, herein designated TARGET GENE. LOC199718 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC199718, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199718 BINDING SITE, designated SEQ ID:10043, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36400] Another function of GAM391 is therefore inhibition of LOC199718 (Accession XP_113998.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC199718.

[36401] LOC200225 (Accession XP_117206.2) is another GAM391 target gene, herein designated TARGET GENE. LOC200225 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200225, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200225 BINDING SITE, designated SEQ ID:12207, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36402] Another function of GAM391 is therefore inhibition of LOC200225 (Accession XP_117206.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200225.

[36403] LOC221922 (Accession XP_166555.2) is another GAM391 target gene, herein designated TARGET GENE. LOC221922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC221922 BINDING SITE, designated SEQ ID:14906, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36404] Another function of GAM391 is therefore inhibition of LOC221922 (Accession XP_166555.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221922.

[36405] LOC254099 (Accession XP_173023.1) is another GAM391 target gene, herein designated TARGET GENE. LOC254099 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC254099, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254099 BINDING SITE, designated SEQ ID:1936, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36406] Another function of GAM391 is therefore inhibition of LOC254099 (Accession XP_173023.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254099.

[36407] LOC283030 (Accession XP_210858.1) is another GAM391 target gene, herein designated TARGET GENE. LOC283030 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283030, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283030 BINDING SITE, designated SEQ ID:19606, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36408] Another function of GAM391 is therefore inhibition of LOC283030 (Accession XP_210858.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283030.

[36409] LOC283049 (Accession XP_210868.1) is another GAM391 target gene, herein designated TARGET GENE. LOC283049 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283049, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283049 BINDING SITE, designated SEQ ID:7277, to

the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36410] Another function of GAM391 is therefore inhibition of LOC283049 (Accession XP_210868.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283049.

[36411] LOC283530 (Accession XP_211079.1) is another GAM391 target gene, herein designated TARGET GENE. LOC283530 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283530, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283530 BINDING SITE, designated SEQ ID:9689, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36412] Another function of GAM391 is therefore inhibition of LOC283530 (Accession XP_211079.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283530.

[36413] LOC283624 (Accession XP_211126.1) is another GAM391

target gene, herein designated TARGET GENE. LOC283624 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283624, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283624 BINDING SITE, designated SEQ ID:480, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36414] Another function of GAM391 is therefore inhibition of LOC283624 (Accession XP_211126.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283624.

[36415] LOC284167 (Accession XP_208171.1) is another GAM391 target gene, herein designated TARGET GENE. LOC284167 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284167 BINDING SITE, designated SEQ ID:6945, to the nucleotide sequence of GAM391 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:326.

[36416] Another function of GAM391 is therefore inhibition of LOC284167 (Accession XP_208171.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284167.

[36417] LOC284313 (Accession XP_209116.1) is another GAM391 target gene, herein designated TARGET GENE. LOC284313 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284313, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284313 BINDING SITE, designated SEQ ID:3674, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36418] Another function of GAM391 is therefore inhibition of LOC284313 (Accession XP_209116.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284313.

[36419] LOC284591 (Accession XP_211529.1) is another GAM391 target gene, herein designated TARGET GENE. LOC284591

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284591, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284591 BINDING SITE, designated SEQ ID:19633, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36420] Another function of GAM391 is therefore inhibition of LOC284591 (Accession XP_211529.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284591.

[36421] LOC284791 (Accession XP_211633.1) is another GAM391 target gene, herein designated TARGET GENE. LOC284791 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284791, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284791 BINDING SITE, designated SEQ ID:11856, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36422] Another function of GAM391 is therefore inhibition of LOC284791 (Accession XP_211633.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284791.

[36423] LOC285043 (Accession XP_211742.1) is another GAM391 target gene, herein designated TARGET GENE. LOC285043 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285043, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285043 BINDING SITE, designated SEQ ID:1586, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36424] Another function of GAM391 is therefore inhibition of LOC285043 (Accession XP_211742.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285043.

[36425] LOC285151 (Accession XP_211782.1) is another GAM391 target gene, herein designated TARGET GENE. LOC285151 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC285151, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285151 BINDING SITE, designated SEQ ID:9288, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36426] Another function of GAM391 is therefore inhibition of LOC285151 (Accession XP_211782.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285151.

[36427] LOC285452 (Accession XP_209615.1) is another GAM391 target gene, herein designated TARGET GENE. LOC285452 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285452 BINDING SITE, designated SEQ ID:14330, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36428] Another function of GAM391 is therefore inhibition of

LOC285452 (Accession XP_209615.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285452.

[36429] LOC285687 (Accession XP_211985.1) is another GAM391 target gene, herein designated TARGET GENE. LOC285687 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285687 BINDING SITE, designated SEQ ID:15156, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36430] Another function of GAM391 is therefore inhibition of LOC285687 (Accession XP_211985.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285687.

[36431] LOC285996 (Accession XP_212128.1) is another GAM391 target gene, herein designated TARGET GENE. LOC285996 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285996, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285996 BINDING SITE, designated SEQ ID:8402, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36432] Another function of GAM391 is therefore inhibition of LOC285996 (Accession XP_212128.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285996.

[36433] LOC286220 (Accession XP_209954.1) is another GAM391 target gene, herein designated TARGET GENE. LOC286220 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286220, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286220 BINDING SITE, designated SEQ ID:1222, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36434] Another function of GAM391 is therefore inhibition of LOC286220 (Accession XP_209954.1) . Accordingly, utili-

ties of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286220.

[36435] LOC286372 (Accession XP_212294.1) is another GAM391 target gene, herein designated TARGET GENE. LOC286372 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286372, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286372 BINDING SITE, designated SEQ ID:16638, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36436] Another function of GAM391 is therefore inhibition of LOC286372 (Accession XP_212294.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286372.

[36437] LOC339568 (Accession XP_295008.1) is another GAM391 target gene, herein designated TARGET GENE. LOC339568 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339568, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339568 BINDING SITE, designated SEQ ID:12947, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36438] Another function of GAM391 is therefore inhibition of LOC339568 (Accession XP_295008.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339568.

[36439] LOC340731 (Accession XP_291690.2) is another GAM391 target gene, herein designated TARGET GENE. LOC340731 BINDING SITE1 through LOC340731 BINDING SITE5 are target binding sites found in untranslated regions of mRNA encoded by LOC340731, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340731 BINDING SITE1 through LOC340731 BINDING SITE5, designated SEQ ID:6111, SEQ ID:9019, SEQ ID:17313, SEQ ID:10106 and SEQ ID:1668 respectively, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36440] Another function of GAM391 is therefore inhibition of LOC340731 (Accession XP_291690.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340731.

[36441] LOC348461 (Accession XP_302764.1) is another GAM391 target gene, herein designated TARGET GENE. LOC348461 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348461, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348461 BINDING SITE, designated SEQ ID:13888, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36442] Another function of GAM391 is therefore inhibition of LOC348461 (Accession XP_302764.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348461.

[36443] LOC349408 (Accession XP_303044.1) is another GAM391 target gene, herein designated TARGET GENE. LOC349408 BINDING SITE1 through LOC349408 BINDING SITE3 are

target binding sites found in untranslated regions of mRNA encoded by LOC349408, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349408 BINDING SITE1 through LOC349408 BINDING SITE3, designated SEQ ID:6295, SEQ ID:10334 and SEQ ID:5729 respectively, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36444] Another function of GAM391 is therefore inhibition of LOC349408 (Accession XP_303044.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349408.

[36445] LOC349999 (Accession XP_303713.1) is another GAM391 target gene, herein designated TARGET GENE. LOC349999 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349999 BINDING SITE, designated SEQ ID:12995, to the nucleotide sequence of GAM391 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:326.

[36446] Another function of GAM391 is therefore inhibition of LOC349999 (Accession XP_303713.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349999.

[36447] LOC90246 (Accession XP_030283.1) is another GAM391 target gene, herein designated TARGET GENE. LOC90246 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90246, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90246 BINDING SITE, designated SEQ ID:7361, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36448] Another function of GAM391 is therefore inhibition of LOC90246 (Accession XP_030283.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90246.

[36449] LOC90719 (Accession XP_033704.1) is another GAM391 target gene, herein designated TARGET GENE. LOC90719

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90719 BINDING SITE, designated SEQ ID:16755, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36450] Another function of GAM391 is therefore inhibition of LOC90719 (Accession XP_033704.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90719.

[36451] LOC90906 (Accession XP_034809.1) is another GAM391 target gene, herein designated TARGET GENE. LOC90906 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90906, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90906 BINDING SITE, designated SEQ ID:17746, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36452] Another function of GAM391 is therefore inhibition of LOC90906 (Accession XP_034809.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90906.

[36453] Mitogen-activated protein kinase 8 interacting protein 3 (MAPK8IP3, Accession NP_203750.1) is another GAM391 target gene, herein designated TARGET GENE. MAPK8IP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK8IP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPK8IP3 BINDING SITE, designated SEQ ID:6962, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36454] Another function of GAM391 is therefore inhibition of Mitogen-activated protein kinase 8 interacting protein 3 (MAPK8IP3, Accession NP_203750.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK8IP3.

[36455] MGC10772 (Accession NP_085044.2) is another GAM391

target gene, herein designated TARGET GENE. MGC10772 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10772, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10772 BINDING SITE, designated SEQ ID:3496, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36456] Another function of GAM391 is therefore inhibition of MGC10772 (Accession NP_085044.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10772.

[36457] MGC10870 (Accession NP_115677.1) is another GAM391 target gene, herein designated TARGET GENE. MGC10870 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10870, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10870 BINDING SITE, designated SEQ ID:17365, to the nucleotide sequence of GAM391 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:326.

[36458] Another function of GAM391 is therefore inhibition of MGC10870 (Accession NP_115677.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10870.

[36459] MGC11102 (Accession NP_115701.2) is another GAM391 target gene, herein designated TARGET GENE. MGC11102 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC11102, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC11102 BINDING SITE, designated SEQ ID:17225, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36460] Another function of GAM391 is therefore inhibition of MGC11102 (Accession NP_115701.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11102.

[36461] MGC17299 (Accession NP_653227.1) is another GAM391 target gene, herein designated TARGET GENE. MGC17299

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC17299, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC17299 BINDING SITE, designated SEQ ID:14020, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36462] Another function of GAM391 is therefore inhibition of MGC17299 (Accession NP_653227.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC17299.

[36463] MGC2306 (Accession NP_002041.2) is another GAM391 target gene, herein designated TARGET GENE. MGC2306 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2306, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2306 BINDING SITE, designated SEQ ID:12989, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36464] Another function of GAM391 is therefore inhibition of MGC2306 (Accession NP_002041.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2306.

[36465] MGC2508 (Accession NP_077303.1) is another GAM391 target gene, herein designated TARGET GENE. MGC2508 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2508, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2508 BINDING SITE, designated SEQ ID:11605, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36466] Another function of GAM391 is therefore inhibition of MGC2508 (Accession NP_077303.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2508.

[36467] MTO1 (Accession NP_598400.1) is another GAM391 target gene, herein designated TARGET GENE. MTO1 BINDING SITE is a target binding site found in the 3` untranslated

region of multiple transcripts of mRNA encoded by MTO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTO1 BINDING SITE, designated SEQ ID:17745, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36468] Another function of GAM391 is therefore inhibition of MTO1 (Accession NP_598400.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTO1.

[36469] Myosin, light polypeptide kinase (MYLK, Accession NP_444253.1) is another GAM391 target gene, herein designated TARGET GENE. MYLK BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MYLK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYLK BINDING SITE, designated SEQ ID:11895, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36470] Another function of GAM391 is therefore inhibition of

Myosin, light polypeptide kinase (MYLK, Accession NP_444253.1), a gene which is involved in contraction of smooth muscle. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLK.

[36471] The function of MYLK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Myosin, light polypeptide kinase (MYLK, Accession NP_444256.1) is another GAM391 target gene, herein designated TARGET GENE. MYLK BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MYLK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYLK BINDING SITE, designated SEQ ID:11895, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36472] Another function of GAM391 is therefore inhibition of Myosin, light polypeptide kinase (MYLK, Accession NP_444256.1), a gene which is involved in contraction of smooth muscle. Accordingly, utilities of GAM391 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLK.

[36473] The function of MYLK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Myosin, light polypeptide kinase (MYLK, Accession NP_444255.1) is another GAM391 target gene, herein designated TARGET GENE. MYLK BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MYLK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYLK BINDING SITE, designated SEQ ID:11895, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36474] Another function of GAM391 is therefore inhibition of Myosin, light polypeptide kinase (MYLK, Accession NP_444255.1), a gene which is involved in contraction of smooth muscle. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLK.

[36475] The function of MYLK and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Myosin, light polypeptide kinase (MYLK, Accession NP_444254.1) is another GAM391 target gene, herein designated TARGET GENE. MYLK BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MYLK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYLK BINDING SITE, designated SEQ ID:11895, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36476] Another function of GAM391 is therefore inhibition of Myosin, light polypeptide kinase (MYLK, Accession NP_444254.1), a gene which is involved in contraction of smooth muscle. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLK.

[36477] The function of MYLK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Myosin, light polypeptide kinase (MYLK, Ac-

cession NP_444257.1) is another GAM391 target gene, herein designated TARGET GENE. MYLK BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MYLK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYLK BINDING SITE, designated SEQ ID:11895, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36478] Another function of GAM391 is therefore inhibition of Myosin, light polypeptide kinase (MYLK, Accession NP_444257.1), a gene which is involved in contraction of smooth muscle. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLK.

[36479] The function of MYLK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.N33 (Accession NP_006756.2) is another GAM391 target gene, herein designated TARGET GENE. N33 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA en-

coded by N33, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of N33 BINDING SITE, designated SEQ ID:6148, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36480] Another function of GAM391 is therefore inhibition of N33 (Accession NP_006756.2), a gene which is a putative integral membrane protein. and therefore may be associated with Metastatic prostate cancer. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of Metastatic prostate cancer., and of other diseases and clinical conditions associated with N33.

[36481] The function of N33 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Nucleoporin 54kda (NUP54, Accession NP_059122.2) is another GAM391 target gene, herein designated TARGET GENE. NUP54 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NUP54, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of NUP54 BINDING SITE, designated SEQ ID:7998, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36482] Another function of GAM391 is therefore inhibition of Nucleoporin 54kda (NUP54, Accession NP_059122.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUP54.

[36483] Orthopedia homolog (drosophila) (OTP, Accession NP_115485.1) is another GAM391 target gene, herein designated TARGET GENE. OTP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OTP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OTP BINDING SITE, designated SEQ ID:18727, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36484] Another function of GAM391 is therefore inhibition of Orthopedia homolog (drosophila) (OTP, Accession NP_115485.1), a gene which involves in the development of the forebrain and spinal cord. Accordingly, utilities of

GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OTP.

[36485] The function of OTP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM148.1.Progesterone receptor membrane component 2 (PGRMC2, Accession NP_006311.1) is another GAM391 target gene, herein designated TARGET GENE. PGRMC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PGRMC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PGRMC2 BINDING SITE, designated SEQ ID:742, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36486] Another function of GAM391 is therefore inhibition of Progesterone receptor membrane component 2 (PGRMC2, Accession NP_006311.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGRMC2.

[36487] Preimplantation protein 3 (PREI3, Accession NP_056202.1) is another GAM391 target gene, herein designated TAR-

GET GENE. PREI3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PREI3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PREI3 BINDING SITE, designated SEQ ID:13783, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36488] Another function of GAM391 is therefore inhibition of Preimplantation protein 3 (PREI3, Accession NP_056202.1). Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PREI3.

[36489] PRO2859 (Accession NP_061013.1) is another GAM391 target gene, herein designated TARGET GENE. PRO2859 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO2859, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO2859 BINDING SITE, designated SEQ ID:16593, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36490] Another function of GAM391 is therefore inhibition of PRO2859 (Accession NP_061013.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2859.

[36491] Protease, serine, 11 (igf binding) (PRSS11, Accession NP_002766.1) is another GAM391 target gene, herein designated TARGET GENE. PRSS11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRSS11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRSS11 BINDING SITE, designated SEQ ID:15793, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36492] Another function of GAM391 is therefore inhibition of Protease, serine, 11 (igf binding) (PRSS11, Accession NP_002766.1), a gene which stimulates the proliferation and differentiation of a vast number of cell types. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRSS11.

[36493] The function of PRSS11 has been established by previous studies. Insulin- like growth factors (IGFs; OMIM Ref. No. 147440) stimulate the proliferation and differentiation of a vast number of cell types. The action of the growth factors is mediated and controlled by a complex system of components, including at least 2 different forms of IGF, 2 IGF receptors (e.g., 147370), 7 different IGF- binding proteins (IGFBPs; OMIM Ref. No. 146730), and several proteases that cleave the IGFBPs. CLONING Zumbrunn and Trueb (1996) cloned the cDNA for a human protein, termed L56 by them, that seemed to be part of the IGF signaling system. The predicted protein encodes a 480- amino acid polypeptide with a molecular mass of 51 kD. Zumbrunn and Trueb (1996) found that PRSS11 contains a secretory signal sequence, an IGFBP- binding domain, and a serine protease domain. The serine protease domain is most similar to certain bacterial serine proteases. By Northern blot analysis, Zumbrunn and Trueb (1996) showed that PRSS11 is expressed in a variety of human tissues, with strongest expression in placenta. Hu et al. (1998) also cloned PRSS11. The deduced 480- amino acid protein is 98% identical to the cow, guinea pig, and rabbit proteins. It contains an N terminus homologous to MAC25

(IGFBP7; 602867) with a conserved Kazal- type serine protease inhibitor motif, as well as a C- terminal PDZ domain. Semiquantitative RT- PCR and immunoblot analyses showed an approximately 7- fold increase of PRSS11 in osteoarthritis cartilage compared with controls. Functional and mutational analyses indicated that PRS11 is a serine protease dependent on the presence of a serine at position 328

[36494]

[36495] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[36496] Hu, S.- I.; Carozza, M.; Klein, M.; Nantermet, P.; Luk, D.; Crowl, R. M. : Human HtrA, an evolutionarily conserved serine protease identified as a differentially expressed gene product in osteoarthritic cartilage. J. Biol. Chem. 273: 34406- 34412, 1998. ; and

[36497] Zumbrunn, J.; Trueb, B. : Localization of the gene for a serine protease with IGF- binding domain (PRSS11) to human chromosome 10q25.3- q26.2. Genomics 45: 461- 462, 1997.

[36498] Further studies establishing the function and utilities of PRSS11 are found in John Hopkins OMIM database record

ID 602194, and in cited publications listed in Table 5, which are hereby incorporated by reference.Solute carrier family 15 (h+/peptide transporter), member 2 (SLC15A2, Accession NP_066568.2) is another GAM391 target gene, herein designated TARGET GENE. SLC15A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC15A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC15A2 BINDING SITE, designated SEQ ID:1490, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36499] Another function of GAM391 is therefore inhibition of Solute carrier family 15 (h+/peptide transporter), member 2 (SLC15A2, Accession NP_066568.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC15A2.

[36500] Solute carrier family 19 (folate transporter), member 1 (SLC19A1, Accession NP_003047.1) is another GAM391 target gene, herein designated TARGET GENE. SLC19A1 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by SLC19A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC19A1 BINDING SITE, designated SEQ ID:16419, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36501] Another function of GAM391 is therefore inhibition of Solute carrier family 19 (folate transporter), member 1 (SLC19A1, Accession NP_003047.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC19A1.

[36502] Solute carrier family 20 (phosphate transporter), member 1 (SLC20A1, Accession NP_005406.3) is another GAM391 target gene, herein designated TARGET GENE. SLC20A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC20A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC20A1 BINDING SITE, designated SEQ ID:9287, to the nucleotide sequence of GAM391 RNA, herein designated

GAM RNA, also designated SEQ ID:326.

[36503] Another function of GAM391 is therefore inhibition of Solute carrier family 20 (phosphate transporter), member 1 (SLC20A1, Accession NP_005406.3), a gene which could be a sodium- phosphate symporter. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC20A1.

[36504] The function of SLC20A1 has been established by previous studies. By expression in Xenopus oocytes and in mammalian cells, Kavanaugh et al. (1994) determined that GLVR1 is a sodium- dependent phosphate symporter. Voltage- clamp analysis indicated net cation influx, suggesting that phosphate is transported with excess sodium ions. Palmer et al. (1999) showed that the GLVR1 gene consists of 11 exons spanning approximately 18 kb of genomic DNA. Exon 1 is noncoding. Using a luciferase reporter gene assay in transiently transfected chondrocytes and osteoblasts, Palmer et al. (2001) determined that the activity of the promoter of SLC20A1, which they called PIT1, requires a TATA- like sequence and a single SP1 (OMIM Ref. No. 189906) site. They found that this SP1 site could bind SP1 and SP3 (OMIM Ref. No. 601804). Despite

the conservation of sequence between the human and mouse promoter, the promoter of mouse Pit1 depends on a combination of several cis- acting elements.

[36505]

[36506] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[36507] Kavanaugh, M. P.; Miller, D. G.; Zhang, W.; Law, W.; Kozak, S. L.; Kabat, D.; Miller, A. D. : Cell- surface receptors for gibbon ape leukemia virus and amphotropic murine retrovirus are inducible sodium- dependent phosphate symporters. Proc. Nat. Acad. Sci. 91: 7071- 7075, 1994. ; and

[36508] Palmer, G.; Manen, D.; Bonjour, J.- P.; Caverzasio, J. : Species- specific mechanisms control the activity of the Pit1/PIT1 phosphate transporter gene promoter in mouse and human. Gene 279.

[36509] Further studies establishing the function and utilities of SLC20A1 are found in John Hopkins OMIM database record ID 137570, and in cited publications listed in Table 5, which are hereby incorporated by reference.Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1, Accession NP_004718.1) is another GAM391 target gene, herein designated TARGET GENE.

SLC24A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC24A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC24A1 BINDING SITE, designated SEQ ID:17502, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36510] Another function of GAM391 is therefore inhibition of Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1, Accession NP_004718.1), a gene which is a critical component of the visual transduction cascade, controlling the calcium concentration of outer segments during light and darkness. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC24A1.

[36511] The function of SLC24A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Solute carrier family 39 (zinc transporter), member 3 (SLC39A3, Accession NP_653165.1) is another GAM391 target gene, herein designated TARGET GENE.

SLC39A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC39A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC39A3 BINDING SITE, designated SEQ ID:15092, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36512] Another function of GAM391 is therefore inhibition of Solute carrier family 39 (zinc transporter), member 3 (SLC39A3, Accession NP_653165.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC39A3.

[36513] SNRK (Accession NP_060189.2) is another GAM391 target gene, herein designated TARGET GENE. SNRK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNRK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNRK BINDING SITE, designated SEQ ID:12233, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA,

also designated SEQ ID:326.

[36514] Another function of GAM391 is therefore inhibition of SNRK (Accession NP_060189.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNRK.

[36515] Sry (sex determining region y)-box 11 (SOX11, Accession NP_003099.1) is another GAM391 target gene, herein designated TARGET GENE. SOX11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SOX11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SOX11 BINDING SITE, designated SEQ ID:14726, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36516] Another function of GAM391 is therefore inhibition of Sry (sex determining region y)-box 11 (SOX11, Accession NP_003099.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX11.

[36517] Sepiapterin reductase (7,8-dihydrobiopterin:nadp+ oxidoreductase) (SPR, Accession NP_003115.1) is another

GAM391 target gene, herein designated TARGET GENE. SPR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPR BINDING SITE, designated SEQ ID:6469, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36518] Another function of GAM391 is therefore inhibition of Sepiapterin reductase (7,8-dihydrobiopterin:nadp+ oxidoreductase) (SPR, Accession NP_003115.1), a gene which catalyzes the and therefore is associated with Sepiapterin reductase deficiency. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of Sepiapterin reductase deficiency, and of other diseases and clinical conditions associated with SPR.

[36519] The function of SPR has been established by previous studies. Bonafe et al. (2001) reported 2 patients with progressive psychomotor retardation, dystonia, severe dopamine and serotonin deficiencies (low levels of 5- hydroxyindoleacetic and homovanillic acids), and abnormal pterin pattern (high levels of biopterin and dihydro-

biopterin) in cerebrospinal fluid. They presented with normal urinary pterins and without hyperphenylalaninemia. Studies of skin fibroblasts revealed inactive sepiapterin reductase, the enzyme catalyzing the final 2- step reaction in the biosynthesis of tetrahydrobiopterin (BH4). Mutations in the SPR gene were detected in both patients: homozygous (182125.0001) in 1 and compound heterozygous (182125.0002) in the other. The authors suggested that autosomal recessive deficiency of sepiapterin reductase leads to BH4 and neurotransmitter deficiencies without hyperphenylalaninemia and may not be detected by neonatal screening for phenylketonuria.

[36520]

[36521] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[36522] Bonafe, L.; Thony, B.; Penzien, J. M.; Czarnecki, B.; Blau, N. : Mutations in the sepiapterin reductase gene cause a novel tetrahydrobiopterin- dependent monoamine- neurotransmitter deficiency without hyperphenylalaninemia. Am. J. Hum. Genet. 69: 269- 277, 2001. ; and

[36523] Blau, N.; Thony, B.; Renneberg, A.; Arnold, L. A.; Hyland, K. : Dihydropteridine reductase deficiency localized to the

central nervous system. J. Inherit. Metab. Dis. 21: 433-434, 1998.

[36524] Further studies establishing the function and utilities of SPR are found in John Hopkins OMIM database record ID 182125, and in cited publications listed in Table 5, which are hereby incorporated by reference.Sprouty homolog 4 (drosophila) (SPRY4, Accession NP_112226.2) is another GAM391 target gene, herein designated TARGET GENE. SPRY4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPRY4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPRY4 BINDING SITE, designated SEQ ID:1887, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36525] Another function of GAM391 is therefore inhibition of Sprouty homolog 4 (drosophila) (SPRY4, Accession NP_112226.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPRY4.

[36526] Signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3, Accession

NP_644805.1) is another GAM391 target gene, herein designated TARGET GENE. STAT3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by STAT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAT3 BINDING SITE, designated SEQ ID:10246, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36527] Another function of GAM391 is therefore inhibition of Signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3, Accession NP_644805.1), a gene which carries out a dual function: signal transduction and activation of transcription. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAT3.

[36528] The function of STAT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3, Accession

NP_003141.2) is another GAM391 target gene, herein designated TARGET GENE. STAT3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by STAT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAT3 BINDING SITE, designated SEQ ID:10246, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36529] Another function of GAM391 is therefore inhibition of Signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3, Accession NP_003141.2), a gene which carries out a dual function: signal transduction and activation of transcription. Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAT3.

[36530] The function of STAT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Surfeit 6 (SURF6, Accession NP_006744.2) is another GAM391 target gene, herein designated TARGET

GENE. SURF6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SURF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SURF6 BINDING SITE, designated SEQ ID:10519, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36531] Another function of GAM391 is therefore inhibition of Surfeit 6 (SURF6, Accession NP_006744.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURF6.

[36532] Synaptotagmin iii (SYT3, Accession NP_115674.1) is another GAM391 target gene, herein designated TARGET GENE. SYT3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SYT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYT3 BINDING SITE, designated SEQ ID:3513, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36533] Another function of GAM391 is therefore inhibition of Synaptotagmin iii (SYT3, Accession NP_115674.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT3.

[36534] TBC1D7 (Accession NP_057579.1) is another GAM391 target gene, herein designated TARGET GENE. TBC1D7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TBC1D7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TBC1D7 BINDING SITE, designated SEQ ID:17570, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36535] Another function of GAM391 is therefore inhibition of TBC1D7 (Accession NP_057579.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBC1D7.

[36536] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065578.2) is another GAM391 target gene, herein designated TARGET GENE. TCL6 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TCL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE, designated SEQ ID:4551, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36537] Another function of GAM391 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065578.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[36538] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065577.2) is another GAM391 target gene, herein designated TARGET GENE. TCL6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TCL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE, designated SEQ ID:4551, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA,

also designated SEQ ID:326.

[36539] Another function of GAM391 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065577.2) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[36540] Tumor necrosis factor receptor superfamily, member 19 (TNFRSF19, Accession NP_683760.1) is another GAM391 target gene, herein designated TARGET GENE. TNFRSF19 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF19 BINDING SITE, designated SEQ ID:14661, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36541] Another function of GAM391 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 19 (TNFRSF19, Accession NP_683760.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

TNFRSF19.

[36542] Testis-specific transcript, y-linked 14 (TTTY14, Accession NP_114138.1) is another GAM391 target gene, herein designated TARGET GENE. TTTY14 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TTTY14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TTTY14 BINDING SITE, designated SEQ ID:2750, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36543] Another function of GAM391 is therefore inhibition of Testis-specific transcript, y-linked 14 (TTTY14, Accession NP_114138.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTTY14.

[36544] Testis-specific transcript, y-linked 14 (TTTY14, Accession XP_291361.1) is another GAM391 target gene, herein designated TARGET GENE. TTTY14 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by TTTY14, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TTTY14 BINDING SITE, designated SEQ ID:2750, to the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, also designated SEQ ID:326.

[36545] Another function of GAM391 is therefore inhibition of Testis-specific transcript, y-linked 14 (TTTY14, Accession XP_291361.1) . Accordingly, utilities of GAM391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTTY14.

[36546]

[36547] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 633 (GAM633), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36548] GAM633 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM633 was detected is described hereinabove with reference to Figs. 8-15.

[36549] GAM633 gene, herein designated GAM GENE, and GAM633 target gene, herein designated TARGET GENE,

are human genes contained in the human genome.

[36550] GAM633 gene encodes a GAM633 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM633 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM633 precursor RNA is designated SEQ ID:68, and is provided hereinbelow with reference to the sequence listing part.

[36551] GAM633 precursor RNA folds onto itself, forming GAM633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36552] GAM633 precursor RNA folds onto itself, forming GAM633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is

due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[36553] Nucleotide sequence of GAM633 precursor RNA, designated SEQ-ID: 68, and a schematic representation of a predicted secondary folding of GAM633 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[36554] An enzyme complex designated DICER COMPLEX, `dices` the GAM633 folded precursor RNA into GAM633 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM633 RNA is designated SEQ ID:340, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[36555] GAM633 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM633 target

RNA, herein designated GAM TARGET RNA. GAM633 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[36556] GAM633 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM633 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM633 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM633 RNA may have a different number of target binding sites in untranslated regions of a GAM633 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[36557] The complementary binding of GAM633 RNA, herein designated GAM RNA, to target binding sites on GAM633 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM633 target RNA into GAM633 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36558] It is appreciated that GAM633 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM633 target genes. The mRNA of each one of this plurality of GAM633 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM633 RNA, herein designated GAM RNA, and which when bound by GAM633 RNA causes inhibition of translation of respective one or more GAM633 target proteins.

[36559] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM633 gene, herein designated GAM GENE, on one or more GAM633 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes.

As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36560] It is appreciated that specific functions and accordingly utilities of GAM633 correlate with, and may be deduced from, the identity of the target genes which GAM633 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36561]

[36562]

[36563] Adenylate cyclase 7 (ADCY7, Accession NM_001114.1) is a GAM633 target gene, herein designated TARGET GENE. ADCY7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADCY7, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY7 BINDING SITE, designated SEQ ID:8228, to the nucleotide sequence of GAM633 RNA, herein designated GAM RNA, also designated SEQ ID:340.

[36564] A function of GAM633 is therefore inhibition of Adenylate cyclase 7 (ADCY7, Accession NM_001114.1), a gene which this a membrane- bound, ca(2+)- inhibitable adenylyl cyclase. Accordingly, utilities of GAM633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY7.

[36565] The function of ADCY7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM75.1.KIAA1866 (Accession XM_027658.5) is another GAM633 target gene, herein designated TARGET GENE. KIAA1866 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1866, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1866 BINDING SITE, designated SEQ ID:3886, to the nucleotide sequence of GAM633 RNA,

herein designated GAM RNA, also designated SEQ ID:340.

[36566] Another function of GAM633 is therefore inhibition of KIAA1866 (Accession XM_027658.5) . Accordingly, utilities of GAM633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1866.

[36567] KIAA1879 (Accession XM_056635.4) is another GAM633 target gene, herein designated TARGET GENE. KIAA1879 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1879, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1879 BINDING SITE, designated SEQ ID:6010, to the nucleotide sequence of GAM633 RNA, herein designated GAM RNA, also designated SEQ ID:340.

[36568] Another function of GAM633 is therefore inhibition of KIAA1879 (Accession XM_056635.4) . Accordingly, utilities of GAM633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1879.

[36569] LOC147178 (Accession) is another GAM633 target gene, herein designated TARGET GENE. LOC147178 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147178, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147178 BINDING SITE, designated SEQ ID:2676, to the nucleotide sequence of GAM633 RNA, herein designated GAM RNA, also designated SEQ ID:340.

[36570] Another function of GAM633 is therefore inhibition of LOC147178 (Accession) . Accordingly, utilities of GAM633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147178.

[36571] LOC157697 (Accession XM_291282.2) is another GAM633 target gene, herein designated TARGET GENE. LOC157697 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC157697, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157697 BINDING SITE, designated SEQ ID:20176, to the nucleotide sequence of GAM633 RNA, herein designated GAM RNA, also designated SEQ ID:340.

[36572] Another function of GAM633 is therefore inhibition of LOC157697 (Accession XM_291282.2) . Accordingly, utilities of GAM633 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157697.

[36573]

[36574] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 895 (GAM895), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36575] GAM895 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM895 was detected is described hereinabove with reference to Figs. 8-15.

[36576] GAM895 gene, herein designated GAM GENE, and GAM895 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[36577] GAM895 gene encodes a GAM895 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM895 precursor RNA does not encode a protein. A nucleotide sequence

identical or highly similar to the nucleotide sequence of GAM895 precursor RNA is designated SEQ ID:93, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:93 is located at position 93949146 relative to chromosome 11.

[36578] GAM895 precursor RNA folds onto itself, forming GAM895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36579] GAM895 precursor RNA folds onto itself, forming GAM895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[36580] Nucleotide sequence of GAM895 precursor RNA, designated SEQ-ID: 93, and a schematic representation of a predicted secondary folding of GAM895 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[36581] An enzyme complex designated DICER COMPLEX, `dices` the GAM895 folded precursor RNA into GAM895 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM895 RNA is designated SEQ ID:379, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[36582] GAM895 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM895 target RNA, herein designated GAM TARGET RNA. GAM895 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[36583] GAM895 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM895 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM895 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM895 RNA may have a different number of target binding sites in untranslated regions of a GAM895 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[36584] The complementary binding of GAM895 RNA, herein designated GAM RNA, to target binding sites on GAM895 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM895 target RNA into GAM895 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36585] It is appreciated that GAM895 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM895 target genes. The mRNA of each one of this plurality of GAM895 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM895 RNA, herein designated GAM RNA, and which when bound by GAM895 RNA causes inhibition of translation of respective one or more GAM895 target proteins.

[36586] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM895 gene, herein designated GAM GENE, on one or more GAM895 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36587] It is appreciated that specific functions and accordingly utilities of GAM895 correlate with, and may be deduced from, the identity of the target genes which GAM895 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36588]

[36589]

[36590] Atp-binding cassette, sub-family a (abc1), member 1 (ABCA1, Accession NP_005493.2) is a GAM895 target gene, herein designated TARGET GENE. ABCA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCA1 BINDING SITE, designated SEQ ID:2647, to the nucleotide se-

quence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36591] A function of GAM895 is therefore inhibition of Atp-binding cassette, sub-family a (abc1), member 1 (ABCA1, Accession NP_005493.2), a gene which camp- dependent and sulfonylurea- sensitive anion transporter. and therefore is associated with Tangier disease (high density lipoprotein deficiency type i). Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of Tangier disease (high density lipoprotein deficiency type i), and of other diseases and clinical conditions associated with ABCA1.

[36592] The function of ABCA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.AD034 (Accession NP_113668.2) is another GAM895 target gene, herein designated TARGET GENE. AD034 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AD034, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AD034 BINDING SITE, designated

SEQ ID:5799, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36593] Another function of GAM895 is therefore inhibition of AD034 (Accession NP_113668.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AD034.

[36594] AD034 (Accession NP_694550.1) is another GAM895 target gene, herein designated TARGET GENE. AD034 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AD034, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AD034 BINDING SITE, designated SEQ ID:5799, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36595] Another function of GAM895 is therefore inhibition of AD034 (Accession NP_694550.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AD034.

[36596] Aprataxin (APTX, Accession NP_778242.1) is another GAM895 target gene, herein designated TARGET GENE. APTX BINDING SITE is a target binding site found in the 5`

untranslated region of multiple transcripts of mRNA encoded by APTX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated SEQ ID:11308, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36597] Another function of GAM895 is therefore inhibition of Aprataxin (APTX, Accession NP_778242.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APTX.

[36598] Cdc42 guanine nucleotide exchange factor (gef) 9 (ARHGEF9, Accession NP_056000.1) is another GAM895 target gene, herein designated TARGET GENE. ARHGEF9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGEF9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGEF9 BINDING SITE, designated SEQ ID:3229, to the nucleotide sequence of GAM895 RNA, herein designated

GAM RNA, also designated SEQ ID:379.

[36599] Another function of GAM895 is therefore inhibition of Cdc42 guanine nucleotide exchange factor (gef) 9 (ARHGEF9, Accession NP_056000.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF9.

[36600] Actin related protein 2/3 complex, subunit 5, 16kda (ARPC5, Accession NP_005708.1) is another GAM895 target gene, herein designated TARGET GENE. ARPC5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARPC5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARPC5 BINDING SITE, designated SEQ ID:3112, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36601] Another function of GAM895 is therefore inhibition of Actin related protein 2/3 complex, subunit 5, 16kda (ARPC5, Accession NP_005708.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARPC5.

[36602] b5+b5R (Accession NP_057314.1) is another GAM895 target gene, herein designated TARGET GENE. b5+b5R BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by b5+b5R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of b5+b5R BINDING SITE, designated SEQ ID:14738, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36603] Another function of GAM895 is therefore inhibition of b5+b5R (Accession NP_057314.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with b5+b5R.

[36604] Baculoviral iap repeat-containing 5 (survivin) (BIRC5, Accession NP_001159.1) is another GAM895 target gene, herein designated TARGET GENE. BIRC5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BIRC5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BIRC5 BINDING SITE,

designated SEQ ID:19223, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36605] Another function of GAM895 is therefore inhibition of Baculoviral iap repeat-containing 5 (survivin) (BIRC5, Accession NP_001159.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIRC5.

[36606] Basonuclin (BNC, Accession NP_001708.2) is another GAM895 target gene, herein designated TARGET GENE. BNC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BNC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BNC BINDING SITE, designated SEQ ID:19010, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36607] Another function of GAM895 is therefore inhibition of Basonuclin (BNC, Accession NP_001708.2), a gene which plays a role in the maintenance of proliferative capacity and prevention of terminal differentiation of keratinocytes. Accordingly, utilities of GAM895 include diag-

nosis, prevention and treatment of diseases and clinical conditions associated with BNC.

[36608] The function of BNC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM427.1.C13orf18 (Accession NP_079389.1) is another GAM895 target gene, herein designated TARGET GENE. C13orf18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C13orf18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C13orf18 BINDING SITE, designated SEQ ID:10373, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36609] Another function of GAM895 is therefore inhibition of C13orf18 (Accession NP_079389.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C13orf18.

[36610] Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_036321.2) is an-

other GAM895 target gene, herein designated TARGET GENE. CABYR BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CABYR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CABYR BINDING SITE, designated SEQ ID:16855, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36611] Another function of GAM895 is therefore inhibition of Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_036321.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CABYR.

[36612] Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_722453.1) is another GAM895 target gene, herein designated TARGET GENE. CABYR BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CABYR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CABYR BINDING SITE, designated SEQ ID:16855, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36613] Another function of GAM895 is therefore inhibition of Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_722453.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CABYR.

[36614] Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_722452.1) is another GAM895 target gene, herein designated TARGET GENE. CABYR BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CABYR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CABYR BINDING SITE, designated SEQ ID:16855, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36615] Another function of GAM895 is therefore inhibition of Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_722452.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CABYR.

[36616] Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_722454.1) is another GAM895 target gene, herein designated TARGET GENE. CABYR BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CABYR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CABYR BINDING SITE, designated SEQ ID:16855, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36617] Another function of GAM895 is therefore inhibition of Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_722454.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with CABYR.

[36618] Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_619585.1) is another GAM895 target gene, herein designated TARGET GENE. CABYR BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CABYR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CABYR BINDING SITE, designated SEQ ID:16855, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36619] Another function of GAM895 is therefore inhibition of Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_619585.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CABYR.

[36620] Calmodulin 1 (phosphorylase kinase, delta) (CALM1, Accession NP_008819.1) is another GAM895 target gene, herein designated TARGET GENE. CALM1 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by CALM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CALM1 BINDING SITE, designated SEQ ID:10029, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36621] Another function of GAM895 is therefore inhibition of Calmodulin 1 (phosphorylase kinase, delta) (CALM1, Accession NP_008819.1), a gene which plays roles in growth and the cell cycle as well as in signal transduction and the synthesis and release of neurotransmitters. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALM1.

[36622] The function of CALM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM180.1.Chromodomain protein, y chromosome-like (CDYL, Accession NP_004815.2) is another GAM895 target gene, herein designated TARGET GENE. CDYL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDYL,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDYL BINDING SITE, designated SEQ ID:11324, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36623] Another function of GAM895 is therefore inhibition of Chromodomain protein, y chromosome-like (CDYL, Accession NP_004815.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDYL.

[36624] Chromodomain protein, y chromosome-like (CDYL, Accession NP_736608.1) is another GAM895 target gene, herein designated TARGET GENE. CDYL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDYL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDYL BINDING SITE, designated SEQ ID:11324, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36625] Another function of GAM895 is therefore inhibition of

Chromodomain protein, y chromosome-like (CDYL, Accession NP_736608.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDYL.

[36626] Chromodomain protein, y chromosome-like (CDYL, Accession NP_736607.1) is another GAM895 target gene, herein designated TARGET GENE. CDYL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDYL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDYL BINDING SITE, designated SEQ ID:11324, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36627] Another function of GAM895 is therefore inhibition of Chromodomain protein, y chromosome-like (CDYL, Accession NP_736607.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDYL.

[36628] CGI-141 (Accession NP_057156.1) is another GAM895 target gene, herein designated TARGET GENE. CGI-141 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by CGI-141, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-141 BINDING SITE, designated SEQ ID:12491, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36629] Another function of GAM895 is therefore inhibition of CGI-141 (Accession NP_057156.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-141.

[36630] Contactin 3 (plasmacytoma associated) (CNTN3, Accession XP_039627.7) is another GAM895 target gene, herein designated TARGET GENE. CNTN3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTN3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNTN3 BINDING SITE, designated SEQ ID:19069, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36631] Another function of GAM895 is therefore inhibition of Contactin 3 (plasmacytoma associated) (CNTN3, Accession XP_039627.7), a gene which may play a role in the initial growth and guidance of axons. and therefore may be associated with Plasmacytomas. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of Plasmacytomas, and of other diseases and clinical conditions associated with CNTN3.

[36632] The function of CNTN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.2.CPR8 (Accession NP_065790.1) is another GAM895 target gene, herein designated TARGET GENE. CPR8 BINDING SITE1 and CPR8 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CPR8, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPR8 BINDING SITE1 and CPR8 BINDING SITE2, designated SEQ ID:9187 and SEQ ID:1778 respectively, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36633] Another function of GAM895 is therefore inhibition of CPR8 (Accession NP_065790.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPR8.

[36634] Camp responsive element binding protein-like 2 (CREBL2, Accession NP_001301.1) is another GAM895 target gene, herein designated TARGET GENE. CREBL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CREBL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CREBL2 BINDING SITE, designated SEQ ID:14613, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36635] Another function of GAM895 is therefore inhibition of Camp responsive element binding protein-like 2 (CREBL2, Accession NP_001301.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CREBL2.

[36636] DKFZp761B107 (Accession NP_775734.1) is another GAM895 target gene, herein designated TARGET GENE. DKFZp761B107 BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by DKFZp761B107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B107 BINDING SITE, designated SEQ ID:10303, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36637] Another function of GAM895 is therefore inhibition of DKFZp761B107 (Accession NP_775734.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B107.

[36638] Edar-associated death domain (EDARADD, Accession NP_542776.1) is another GAM895 target gene, herein designated TARGET GENE. EDARADD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EDARADD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDARADD BINDING SITE, designated SEQ ID:18853, to the nucleotide sequence of GAM895 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:379.

[36639] Another function of GAM895 is therefore inhibition of Edar-associated death domain (EDARADD, Accession NP_542776.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDARADD.

[36640] Edar-associated death domain (EDARADD, Accession NP_665860.1) is another GAM895 target gene, herein designated TARGET GENE. EDARADD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EDARADD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDARADD BINDING SITE, designated SEQ ID:18853, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36641] Another function of GAM895 is therefore inhibition of Edar-associated death domain (EDARADD, Accession NP_665860.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDARADD.

[36642] EEF2K (Accession NP_037434.1) is another GAM895 target

gene, herein designated TARGET GENE. EEF2K BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EEF2K, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EEF2K BINDING SITE, designated SEQ ID:3811, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36643] Another function of GAM895 is therefore inhibition of EEF2K (Accession NP_037434.1), a gene which phosphorylates serine or threonine on the eukaryotic elongation factor- 2 and therefore may be associated with Systemic lupus erythematosus and cancer. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of Systemic lupus erythematosus and cancer, and of other diseases and clinical conditions associated with EEF2K.

[36644] The function of EEF2K and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.EXO70 (Accession NP_056034.1) is another GAM895 target gene, herein designated TARGET GENE. EXO70 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by EXO70, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EXO70 BINDING SITE, designated SEQ ID:16998, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36645] Another function of GAM895 is therefore inhibition of EXO70 (Accession NP_056034.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EXO70.

[36646] Fatty acid binding protein 7, brain (FABP7, Accession NP_001437.1) is another GAM895 target gene, herein designated TARGET GENE. FABP7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FABP7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FABP7 BINDING SITE, designated SEQ ID:14375, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36647] Another function of GAM895 is therefore inhibition of

Fatty acid binding protein 7, brain (FABP7, Accession NP_001437.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FABP7.

[36648] Fc fragment of igg, low affinity iiib, receptor for (cd16) (FCGR3B, Accession NP_000561.1) is another GAM895 target gene, herein designated TARGET GENE. FCGR3B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FCGR3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCGR3B BINDING SITE, designated SEQ ID:12304, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36649] Another function of GAM895 is therefore inhibition of Fc fragment of igg, low affinity iiib, receptor for (cd16) (FCGR3B, Accession NP_000561.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCGR3B.

[36650] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial

dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075259.1) is another GAM895 target gene, herein designated TARGET GENE. FGFR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:7425, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36651] Another function of GAM895 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075259.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[36652] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jack-

son-weiss syndrome) (FGFR2, Accession NP_075418.1) is another GAM895 target gene, herein designated TARGET GENE. FGFR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:7425, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36653] Another function of GAM895 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075418.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[36654] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075264.2) is

another GAM895 target gene, herein designated TARGET GENE. FGFR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:7425, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36655] Another function of GAM895 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075264.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[36656] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075261.1) is another GAM895 target gene, herein designated TARGET

GENE. FGFR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:7425, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36657] Another function of GAM895 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075261.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[36658] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075258.1) is another GAM895 target gene, herein designated TARGET GENE. FGFR2 BINDING SITE is a target binding site found

in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:7425, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36659] Another function of GAM895 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075258.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[36660] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075420.1) is another GAM895 target gene, herein designated TARGET GENE. FGFR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of

mRNA encoded by FGFR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:7425, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36661] Another function of GAM895 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075420.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[36662] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075419.1) is another GAM895 target gene, herein designated TARGET GENE. FGFR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR2, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:7425, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36663] Another function of GAM895 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075419.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[36664] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075417.1) is another GAM895 target gene, herein designated TARGET GENE. FGFR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:7425, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36665] Another function of GAM895 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075417.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[36666] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_000132.1) is another GAM895 target gene, herein designated TARGET GENE. FGFR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:7425, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36667] Another function of GAM895 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_000132.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[36668] Formin homology 2 domain containing 2 (FHOD2, Accession XP_057927.2) is another GAM895 target gene, herein designated TARGET GENE. FHOD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FHOD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FHOD2 BINDING SITE, designated SEQ ID:19209, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36669] Another function of GAM895 is therefore inhibition of Formin homology 2 domain containing 2 (FHOD2, Accession XP_057927.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHOD2.

[36670] FLJ10298 (Accession NP_060520.2) is another GAM895 target gene, herein designated TARGET GENE. FLJ10298 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10298, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10298 BINDING SITE, designated SEQ ID:8638, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36671] Another function of GAM895 is therefore inhibition of FLJ10298 (Accession NP_060520.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10298.

[36672] FLJ12747 (Accession XP_290972.1) is another GAM895 target gene, herein designated TARGET GENE. FLJ12747 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ12747, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12747 BINDING SITE, designated SEQ ID:19622, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36673] Another function of GAM895 is therefore inhibition of FLJ12747 (Accession XP_290972.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12747.

[36674] FLJ20360 (Accession NP_060252.1) is another GAM895 target gene, herein designated TARGET GENE. FLJ20360 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20360, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20360 BINDING SITE, designated SEQ ID:6214, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36675] Another function of GAM895 is therefore inhibition of

FLJ20360 (Accession NP_060252.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20360.

[36676] FLJ20671 (Accession NP_060394.1) is another GAM895 target gene, herein designated TARGET GENE. FLJ20671 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20671, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20671 BINDING SITE, designated SEQ ID:14149, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36677] Another function of GAM895 is therefore inhibition of FLJ20671 (Accession NP_060394.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20671.

[36678] FLJ20719 (Accession NP_060410.1) is another GAM895 target gene, herein designated TARGET GENE. FLJ20719 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20719, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20719 BINDING SITE, designated SEQ ID:17227, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36679] Another function of GAM895 is therefore inhibition of FLJ20719 (Accession NP_060410.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20719.

[36680] FLJ23053 (Accession NP_075058.1) is another GAM895 target gene, herein designated TARGET GENE. FLJ23053 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23053, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23053 BINDING SITE, designated SEQ ID:3463, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36681] Another function of GAM895 is therefore inhibition of FLJ23053 (Accession NP_075058.1) . Accordingly, utilities

of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23053.

[36682] Fbj murine osteosarcoma viral oncogene homolog b (FOSB, Accession NP_006723.1) is another GAM895 target gene, herein designated TARGET GENE. FOSB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOSB BINDING SITE, designated SEQ ID:13889, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36683] Another function of GAM895 is therefore inhibition of Fbj murine osteosarcoma viral oncogene homolog b (FOSB, Accession NP_006723.1), a gene which interacts with jun proteins enhancing their dna binding activity. and therefore may be associated with Cocaine addiction. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of Cocaine addiction, and of other diseases and clinical conditions associated with FOSB.

[36684] The function of FOSB and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM53.1.Forkhead box a1 (FOXA1, Accession NP_004487.2) is another GAM895 target gene, herein designated TARGET GENE. FOXA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOXA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXA1 BINDING SITE, designated SEQ ID:19373, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36685] Another function of GAM895 is therefore inhibition of Forkhead box a1 (FOXA1, Accession NP_004487.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXA1.

[36686] Forkhead box d4 (FOXD4, Accession XP_095746.6) is another GAM895 target gene, herein designated TARGET GENE. FOXD4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FOXD4, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXD4 BINDING SITE, designated SEQ ID:5668, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36687] Another function of GAM895 is therefore inhibition of Forkhead box d4 (FOXD4, Accession XP_095746.6) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXD4.

[36688] Fucose-1-phosphate guanylyltransferase (FPGT, Accession NP_003829.1) is another GAM895 target gene, herein designated TARGET GENE. FPGT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FPGT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FPGT BINDING SITE, designated SEQ ID:17275, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36689] Another function of GAM895 is therefore inhibition of Fucose-1-phosphate guanylyltransferase (FPGT, Accession

NP_003829.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FPGT.

[36690] HIST2H2BE (Accession NP_003519.1) is another GAM895 target gene, herein designated TARGET GENE. HIST2H2BE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HIST2H2BE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIST2H2BE BINDING SITE, designated SEQ ID:7494, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36691] Another function of GAM895 is therefore inhibition of HIST2H2BE (Accession NP_003519.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIST2H2BE.

[36692] Hippocalcin like 4 (HPCAL4, Accession NP_057341.1) is another GAM895 target gene, herein designated TARGET GENE. HPCAL4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HPCAL4, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HPCAL4 BINDING SITE, designated SEQ ID:11696, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36693] Another function of GAM895 is therefore inhibition of Hippocalcin like 4 (HPCAL4, Accession NP_057341.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HPCAL4.

[36694] Interferon regulatory factor 5 (IRF5, Accession NP_002191.1) is another GAM895 target gene, herein designated TARGET GENE. IRF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IRF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRF5 BINDING SITE, designated SEQ ID:4930, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36695] Another function of GAM895 is therefore inhibition of In-

terferon regulatory factor 5 (IRF5, Accession NP_002191.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRF5.

[36696] Interferon regulatory factor 5 (IRF5, Accession NP_116032.1) is another GAM895 target gene, herein designated TARGET GENE. IRF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IRF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRF5 BINDING SITE, designated SEQ ID:4930, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36697] Another function of GAM895 is therefore inhibition of Interferon regulatory factor 5 (IRF5, Accession NP_116032.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRF5.

[36698] Potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1, Accession NP_003462.2) is another GAM895 target gene, herein designated TARGET

GENE. KCNAB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNAB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNAB1 BINDING SITE, designated SEQ ID:13233, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36699] Another function of GAM895 is therefore inhibition of Potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1, Accession NP_003462.2), a gene which is the regulatory beta subunit for a shaker-related voltage- gated potassium channel. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNAB1.

[36700] The function of KCNAB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM333.1.Potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1, Accession NP_751891.1) is another GAM895 target gene, herein

designated TARGET GENE. KCNAB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNAB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNAB1 BINDING SITE, designated SEQ ID:13233, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36701] Another function of GAM895 is therefore inhibition of Potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1, Accession NP_751891.1), a gene which is the regulatory beta subunit for a shaker-related voltage- gated potassium channel. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNAB1.

[36702] The function of KCNAB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM333.1.Potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1, Accession NP_751892.1) is another GAM895 target gene, herein

designated TARGET GENE. KCNAB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNAB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNAB1 BINDING SITE, designated SEQ ID:13233, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36703] Another function of GAM895 is therefore inhibition of Potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1, Accession NP_751892.1), a gene which is the regulatory beta subunit for a shaker-related voltage- gated potassium channel. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNAB1.

[36704] The function of KCNAB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM333.1.Kdel (lys-asp-glu-leu) endoplasmic reticulum protein retention receptor 3 (KDELR3, Accession NP_006846.1) is another GAM895 target gene, herein

designated TARGET GENE. KDELR3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KDELR3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KDELR3 BINDING SITE, designated SEQ ID:20033, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36705] Another function of GAM895 is therefore inhibition of Kdel (lys-asp-glu-leu) endoplasmic reticulum protein retention receptor 3 (KDELR3, Accession NP_006846.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KDELR3.

[36706] Kinase insert domain receptor (a type iii receptor tyrosine kinase) (KDR, Accession NP_002244.1) is another GAM895 target gene, herein designated TARGET GENE. KDR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KDR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KDR BINDING SITE, designated SEQ ID:5354, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36707] Another function of GAM895 is therefore inhibition of Kinase insert domain receptor (a type iii receptor tyrosine kinase) (KDR, Accession NP_002244.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KDR.

[36708] KIAA0237 (Accession NP_055562.1) is another GAM895 target gene, herein designated TARGET GENE. KIAA0237 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0237, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0237 BINDING SITE, designated SEQ ID:14809, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36709] Another function of GAM895 is therefore inhibition of KIAA0237 (Accession NP_055562.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0237.

[36710] KIAA1594 (Accession XP_050754.5) is another GAM895 target gene, herein designated TARGET GENE. KIAA1594 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1594, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1594 BINDING SITE, designated SEQ ID:13533, to the

nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36711] Another function of GAM895 is therefore inhibition of KIAA1594 (Accession XP_050754.5) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1594.

[36712] KIAA1805 (Accession NP_115810.1) is another GAM895 target gene, herein designated TARGET GENE. KIAA1805 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1805, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1805 BINDING SITE, designated SEQ ID:11408, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36713] Another function of GAM895 is therefore inhibition of KIAA1805 (Accession NP_115810.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1805.

[36714] KIAA1894 (Accession XP_058025.2) is another GAM895

target gene, herein designated TARGET GENE. KIAA1894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1894 BINDING SITE, designated SEQ ID:15021, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36715] Another function of GAM895 is therefore inhibition of KIAA1894 (Accession XP_058025.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1894.

[36716] KIAA1904 (Accession XP_056282.1) is another GAM895 target gene, herein designated TARGET GENE. KIAA1904 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1904, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1904 BINDING SITE, designated SEQ ID:17616, to the nucleotide sequence of GAM895 RNA, herein designated

GAM RNA, also designated SEQ ID:379.

[36717] Another function of GAM895 is therefore inhibition of KIAA1904 (Accession XP_056282.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1904.

[36718] LCHN (Accession XP_098615.2) is another GAM895 target gene, herein designated TARGET GENE. LCHN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCHN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCHN BINDING SITE, designated SEQ ID:13004, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36719] Another function of GAM895 is therefore inhibition of LCHN (Accession XP_098615.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCHN.

[36720] LGN (Accession NP_037428.2) is another GAM895 target gene, herein designated TARGET GENE. LGN BINDING SITE is a target binding site found in the 3` untranslated re-

gion of mRNA encoded by LGN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LGN BINDING SITE, designated SEQ ID:9501, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36721] Another function of GAM895 is therefore inhibition of LGN (Accession NP_037428.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGN.

[36722] LOC126755 (Accession XP_059074.1) is another GAM895 target gene, herein designated TARGET GENE. LOC126755 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC126755, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126755 BINDING SITE, designated SEQ ID:11812, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36723] Another function of GAM895 is therefore inhibition of LOC126755 (Accession XP_059074.1) . Accordingly, utili-

ties of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126755.

[36724] LOC134637 (Accession XP_059727.3) is another GAM895 target gene, herein designated TARGET GENE. LOC134637 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC134637, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC134637 BINDING SITE, designated SEQ ID:6440, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36725] Another function of GAM895 is therefore inhibition of LOC134637 (Accession XP_059727.3) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC134637.

[36726] LOC146520 (Accession XP_085492.1) is another GAM895 target gene, herein designated TARGET GENE. LOC146520 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146520, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146520 BINDING SITE, designated SEQ ID:4472, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36727] Another function of GAM895 is therefore inhibition of LOC146520 (Accession XP_085492.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146520.

[36728] LOC148696 (Accession XP_097505.1) is another GAM895 target gene, herein designated TARGET GENE. LOC148696 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148696, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148696 BINDING SITE, designated SEQ ID:12372, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36729] Another function of GAM895 is therefore inhibition of LOC148696 (Accession XP_097505.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC148696.

[36730] LOC151584 (Accession XP_098089.1) is another GAM895 target gene, herein designated TARGET GENE. LOC151584 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151584, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151584 BINDING SITE, designated SEQ ID:19877, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36731] Another function of GAM895 is therefore inhibition of LOC151584 (Accession XP_098089.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151584.

[36732] LOC154084 (Accession XP_098468.1) is another GAM895 target gene, herein designated TARGET GENE. LOC154084 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154084, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC154084 BINDING SITE, designated SEQ ID:10300, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36733] Another function of GAM895 is therefore inhibition of LOC154084 (Accession XP_098468.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154084.

[36734] LOC158427 (Accession NP_640339.3) is another GAM895 target gene, herein designated TARGET GENE. LOC158427 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158427, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158427 BINDING SITE, designated SEQ ID:1013, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36735] Another function of GAM895 is therefore inhibition of LOC158427 (Accession NP_640339.3) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC158427.

[36736] LOC199953 (Accession XP_114067.2) is another GAM895 target gene, herein designated TARGET GENE. LOC199953 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC199953, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199953 BINDING SITE, designated SEQ ID:13875, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36737] Another function of GAM895 is therefore inhibition of LOC199953 (Accession XP_114067.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199953.

[36738] LOC203107 (Accession XP_300975.1) is another GAM895 target gene, herein designated TARGET GENE. LOC203107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC203107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC203107 BINDING SITE, designated SEQ ID:1112, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36739] Another function of GAM895 is therefore inhibition of LOC203107 (Accession XP_300975.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203107.

[36740] LOC203504 (Accession XP_117550.1) is another GAM895 target gene, herein designated TARGET GENE. LOC203504 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC203504, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC203504 BINDING SITE, designated SEQ ID:15970, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36741] Another function of GAM895 is therefore inhibition of LOC203504 (Accession XP_117550.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203504.

[36742] LOC221424 (Accession XP_168060.2) is another GAM895 target gene, herein designated TARGET GENE. LOC221424 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221424, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221424 BINDING SITE, designated SEQ ID:9114, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36743] Another function of GAM895 is therefore inhibition of LOC221424 (Accession XP_168060.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221424.

[36744] LOC256861 (Accession XP_173004.1) is another GAM895 target gene, herein designated TARGET GENE. LOC256861 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC256861, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256861 BINDING SITE, designated SEQ ID:14032, to

the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36745] Another function of GAM895 is therefore inhibition of LOC256861 (Accession XP_173004.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256861.

[36746] LOC283104 (Accession XP_210888.1) is another GAM895 target gene, herein designated TARGET GENE. LOC283104 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283104, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283104 BINDING SITE, designated SEQ ID:10722, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36747] Another function of GAM895 is therefore inhibition of LOC283104 (Accession XP_210888.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283104.

[36748] LOC283241 (Accession NP_787089.1) is another GAM895

target gene, herein designated TARGET GENE. LOC283241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283241 BINDING SITE, designated SEQ ID:8821, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36749] Another function of GAM895 is therefore inhibition of LOC283241 (Accession NP_787089.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283241.

[36750] LOC283248 (Accession NP_775858.1) is another GAM895 target gene, herein designated TARGET GENE. LOC283248 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283248 BINDING SITE, designated SEQ ID:18722, to the nucleotide sequence of GAM895 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:379.

[36751] Another function of GAM895 is therefore inhibition of LOC283248 (Accession NP_775858.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283248.

[36752] LOC283425 (Accession XP_208665.1) is another GAM895 target gene, herein designated TARGET GENE. LOC283425 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283425, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283425 BINDING SITE, designated SEQ ID:2908, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36753] Another function of GAM895 is therefore inhibition of LOC283425 (Accession XP_208665.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283425.

[36754] LOC283578 (Accession XP_208746.1) is another GAM895 target gene, herein designated TARGET GENE. LOC283578

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283578, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283578 BINDING SITE, designated SEQ ID:14912, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36755] Another function of GAM895 is therefore inhibition of LOC283578 (Accession XP_208746.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283578.

[36756] LOC284018 (Accession XP_211303.1) is another GAM895 target gene, herein designated TARGET GENE. LOC284018 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284018, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284018 BINDING SITE, designated SEQ ID:12876, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36757] Another function of GAM895 is therefore inhibition of LOC284018 (Accession XP_211303.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284018.

[36758] LOC284433 (Accession XP_210787.1) is another GAM895 target gene, herein designated TARGET GENE. LOC284433 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284433, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284433 BINDING SITE, designated SEQ ID:6998, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36759] Another function of GAM895 is therefore inhibition of LOC284433 (Accession XP_210787.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284433.

[36760] LOC284440 (Accession XP_209210.1) is another GAM895 target gene, herein designated TARGET GENE. LOC284440 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC284440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284440 BINDING SITE, designated SEQ ID:14287, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36761] Another function of GAM895 is therefore inhibition of LOC284440 (Accession XP_209210.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284440.

[36762] LOC284530 (Accession XP_211512.1) is another GAM895 target gene, herein designated TARGET GENE. LOC284530 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284530, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284530 BINDING SITE, designated SEQ ID:11717, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36763] Another function of GAM895 is therefore inhibition of

LOC284530 (Accession XP_211512.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284530.

[36764] LOC284840 (Accession XP_211657.1) is another GAM895 target gene, herein designated TARGET GENE. LOC284840 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284840, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284840 BINDING SITE, designated SEQ ID:14102, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36765] Another function of GAM895 is therefore inhibition of LOC284840 (Accession XP_211657.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284840.

[36766] LOC284950 (Accession XP_211703.1) is another GAM895 target gene, herein designated TARGET GENE. LOC284950 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284950, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284950 BINDING SITE, designated SEQ ID:13512, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36767] Another function of GAM895 is therefore inhibition of LOC284950 (Accession XP_211703.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284950.

[36768] LOC285167 (Accession XP_211790.1) is another GAM895 target gene, herein designated TARGET GENE. LOC285167 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285167 BINDING SITE, designated SEQ ID:13845, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36769] Another function of GAM895 is therefore inhibition of LOC285167 (Accession XP_211790.1) . Accordingly, utili-

ties of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285167.

[36770] LOC285256 (Accession XP_211818.1) is another GAM895 target gene, herein designated TARGET GENE. LOC285256 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285256, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285256 BINDING SITE, designated SEQ ID:18929, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36771] Another function of GAM895 is therefore inhibition of LOC285256 (Accession XP_211818.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285256.

[36772] LOC285500 (Accession XP_209639.1) is another GAM895 target gene, herein designated TARGET GENE. LOC285500 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285500, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285500 BINDING SITE, designated SEQ ID:17122, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36773] Another function of GAM895 is therefore inhibition of LOC285500 (Accession XP_209639.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285500.

[36774] LOC285595 (Accession XP_211948.1) is another GAM895 target gene, herein designated TARGET GENE. LOC285595 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285595, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285595 BINDING SITE, designated SEQ ID:14073, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36775] Another function of GAM895 is therefore inhibition of LOC285595 (Accession XP_211948.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285595.

[36776] LOC285656 (Accession XP_211976.2) is another GAM895 target gene, herein designated TARGET GENE. LOC285656 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285656, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285656 BINDING SITE, designated SEQ ID:14073, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36777] Another function of GAM895 is therefore inhibition of LOC285656 (Accession XP_211976.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285656.

[36778] LOC285954 (Accession XP_212085.1) is another GAM895 target gene, herein designated TARGET GENE. LOC285954 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285954, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of LOC285954 BINDING SITE, designated SEQ ID:1096, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36779] Another function of GAM895 is therefore inhibition of LOC285954 (Accession XP_212085.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285954.

[36780] LOC286177 (Accession XP_212215.3) is another GAM895 target gene, herein designated TARGET GENE. LOC286177 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286177 BINDING SITE, designated SEQ ID:3170, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36781] Another function of GAM895 is therefore inhibition of LOC286177 (Accession XP_212215.3) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC286177.

[36782] LOC286401 (Accession XP_212310.1) is another GAM895 target gene, herein designated TARGET GENE. LOC286401 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286401, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286401 BINDING SITE, designated SEQ ID:5918, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36783] Another function of GAM895 is therefore inhibition of LOC286401 (Accession XP_212310.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286401.

[36784] LOC286437 (Accession XP_210050.1) is another GAM895 target gene, herein designated TARGET GENE. LOC286437 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286437, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of LOC286437 BINDING SITE, designated SEQ ID:17684, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36785] Another function of GAM895 is therefore inhibition of LOC286437 (Accession XP_210050.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286437.

[36786] LOC286532 (Accession XP_210093.1) is another GAM895 target gene, herein designated TARGET GENE. LOC286532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286532 BINDING SITE, designated SEQ ID:3346, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36787] Another function of GAM895 is therefore inhibition of LOC286532 (Accession XP_210093.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286532.

[36788] LOC339299 (Accession XP_294904.1) is another GAM895 target gene, herein designated TARGET GENE. LOC339299 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339299, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339299 BINDING SITE, designated SEQ ID:4240, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36789] Another function of GAM895 is therefore inhibition of LOC339299 (Accession XP_294904.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339299.

[36790] LOC339831 (Accession XP_295080.1) is another GAM895 target gene, herein designated TARGET GENE. LOC339831 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339831, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339831 BINDING SITE, designated SEQ ID:8112, to

the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36791] Another function of GAM895 is therefore inhibition of LOC339831 (Accession XP_295080.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339831.

[36792] LOC340327 (Accession XP_294325.1) is another GAM895 target gene, herein designated TARGET GENE. LOC340327 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340327, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340327 BINDING SITE, designated SEQ ID:3197, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36793] Another function of GAM895 is therefore inhibition of LOC340327 (Accession XP_294325.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340327.

[36794] LOC340527 (Accession XP_291321.1) is another GAM895

target gene, herein designated TARGET GENE. LOC340527 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340527, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340527 BINDING SITE, designated SEQ ID:13494, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36795] Another function of GAM895 is therefore inhibition of LOC340527 (Accession XP_291321.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340527.

[36796] LOC346259 (Accession XP_299387.1) is another GAM895 target gene, herein designated TARGET GENE. LOC346259 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC346259, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC346259 BINDING SITE, designated SEQ ID:8351, to the nucleotide sequence of GAM895 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:379.

[36797] Another function of GAM895 is therefore inhibition of LOC346259 (Accession XP_299387.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC346259.

[36798] LOC348393 (Accession XP_302741.1) is another GAM895 target gene, herein designated TARGET GENE. LOC348393 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348393 BINDING SITE, designated SEQ ID:9564, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36799] Another function of GAM895 is therefore inhibition of LOC348393 (Accession XP_302741.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348393.

[36800] LOC348475 (Accession XP_300748.1) is another GAM895 target gene, herein designated TARGET GENE. LOC348475

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348475 BINDING SITE, designated SEQ ID:18223, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36801] Another function of GAM895 is therefore inhibition of LOC348475 (Accession XP_300748.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348475.

[36802] LOC348532 (Accession XP_302818.1) is another GAM895 target gene, herein designated TARGET GENE. LOC348532 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348532 BINDING SITE, designated SEQ ID:9564, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36803] Another function of GAM895 is therefore inhibition of LOC348532 (Accession XP_302818.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348532.

[36804] LOC348989 (Accession XP_302935.1) is another GAM895 target gene, herein designated TARGET GENE. LOC348989 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348989, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348989 BINDING SITE, designated SEQ ID:14073, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36805] Another function of GAM895 is therefore inhibition of LOC348989 (Accession XP_302935.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348989.

[36806] LOC349254 (Accession XP_300471.1) is another GAM895 target gene, herein designated TARGET GENE. LOC349254 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC349254, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349254 BINDING SITE, designated SEQ ID:11021, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36807] Another function of GAM895 is therefore inhibition of LOC349254 (Accession XP_300471.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349254.

[36808] LOC349327 (Accession XP_300483.1) is another GAM895 target gene, herein designated TARGET GENE. LOC349327 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349327, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349327 BINDING SITE, designated SEQ ID:11021, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36809] Another function of GAM895 is therefore inhibition of

LOC349327 (Accession XP_300483.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349327.

[36810] LOC92973 (Accession XP_048529.2) is another GAM895 target gene, herein designated TARGET GENE. LOC92973 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92973, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92973 BINDING SITE, designated SEQ ID:1682, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36811] Another function of GAM895 is therefore inhibition of LOC92973 (Accession XP_048529.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92973.

[36812] LSM6 (Accession NP_009011.1) is another GAM895 target gene, herein designated TARGET GENE. LSM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LSM6, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LSM6 BINDING SITE, designated SEQ ID:8191, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36813] Another function of GAM895 is therefore inhibition of LSM6 (Accession NP_009011.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LSM6.

[36814] Melanoma antigen, family a, 12 (MAGEA12, Accession NP_005358.1) is another GAM895 target gene, herein designated TARGET GENE. MAGEA12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAGEA12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAGEA12 BINDING SITE, designated SEQ ID:14575, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36815] Another function of GAM895 is therefore inhibition of Melanoma antigen, family a, 12 (MAGEA12, Accession

NP_005358.1), a gene which may play a role in tumor transformation or aspects of tumor progression and therefore may be associated with Melanoma. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of Melanoma, and of other diseases and clinical conditions associated with MAGEA12.

[36816] The function of MAGEA12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM499.2.Melanoma antigen, family a, 3 (MAGEA3, Accession NP_005353.1) is another GAM895 target gene, herein designated TARGET GENE. MAGEA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAGEA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAGEA3 BINDING SITE, designated SEQ ID:14575, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36817] Another function of GAM895 is therefore inhibition of Melanoma antigen, family a, 3 (MAGEA3, Accession NP_005353.1), a gene which may play a role in embryonal

development and tumor transformation or aspects of tumor progression. antigen recognized on a melanoma by autologous cytolytic t lymphocytes. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGEA3.

[36818] The function of MAGEA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM842.2.Melanoma antigen, family a, 6 (MAGEA6, Accession NP_787064.1) is another GAM895 target gene, herein designated TARGET GENE. MAGEA6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAGEA6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAGEA6 BINDING SITE, designated SEQ ID:14575, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36819] Another function of GAM895 is therefore inhibition of Melanoma antigen, family a, 6 (MAGEA6, Accession NP_787064.1) . Accordingly, utilities of GAM895 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGEA6.

[36820] Melanoma antigen, family a, 6 (MAGEA6, Accession NP_005354.1) is another GAM895 target gene, herein designated TARGET GENE. MAGEA6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAGEA6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAGEA6 BINDING SITE, designated SEQ ID:14575, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36821] Another function of GAM895 is therefore inhibition of Melanoma antigen, family a, 6 (MAGEA6, Accession NP_005354.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGEA6.

[36822] Melanoma antigen, family a, 9 (MAGEA9, Accession NP_005356.1) is another GAM895 target gene, herein designated TARGET GENE. MAGEA9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAGEA9, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAGEA9 BINDING SITE, designated SEQ ID:7705, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36823] Another function of GAM895 is therefore inhibition of Melanoma antigen, family a, 9 (MAGEA9, Accession NP_005356.1), a gene which may play a role in embryonal development and tumor transformation or aspects of tumor progression. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGEA9.

[36824] The function of MAGEA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM207.2.MDC1 (Accession NP_055456.1) is another GAM895 target gene, herein designated TARGET GENE. MDC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MDC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of MDC1 BINDING SITE, designated SEQ ID:4580, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36825] Another function of GAM895 is therefore inhibition of MDC1 (Accession NP_055456.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDC1.

[36826] Methyl cpg binding protein 2 (rett syndrome) (MECP2, Accession NP_004983.1) is another GAM895 target gene, herein designated TARGET GENE. MECP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MECP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MECP2 BINDING SITE, designated SEQ ID:534, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36827] Another function of GAM895 is therefore inhibition of Methyl cpg binding protein 2 (rett syndrome) (MECP2, Accession NP_004983.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MECP2.

[36828] MGC15827 (Accession NP_116271.1) is another GAM895 target gene, herein designated TARGET GENE. MGC15827 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC15827, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15827 BINDING SITE, designated SEQ ID:14513, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36829] Another function of GAM895 is therefore inhibition of MGC15827 (Accession NP_116271.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15827.

[36830] MGC4562 (Accession NP_588616.1) is another GAM895 target gene, herein designated TARGET GENE. MGC4562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC4562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4562 BINDING SITE, designated SEQ ID:4552, to the

nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36831] Another function of GAM895 is therefore inhibition of MGC4562 (Accession NP_588616.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4562.

[36832] Myosin va (heavy polypeptide 12, myoxin) (MYO5A, Accession NP_000250.1) is another GAM895 target gene, herein designated TARGET GENE. MYO5A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYO5A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYO5A BINDING SITE, designated SEQ ID:18843, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36833] Another function of GAM895 is therefore inhibition of Myosin va (heavy polypeptide 12, myoxin) (MYO5A, Accession NP_000250.1), a gene which may have a role in intracellular transport. and therefore may be associated with Griscelli syndrome. Accordingly, utilities of GAM895

include diagnosis, prevention and treatment of Griscelli syndrome., and of other diseases and clinical conditions associated with MYO5A.

[36834] The function of MYO5A has been established by previous studies. Engle and Kennett (1994) cloned the human homolog of the 'dilute' gene and assigned it to human chromosome 15 by Southern blot analysis of a panel of human/rodent somatic cell hybrids. The 'dilute' gene maps to mouse chromosome 9, distal to a group of 3 loci of which the human homologs are located in the region 15q22- q26. Engle and Kennett (1994) suggested Griscelli syndrome (OMIM Ref. No. 214450) and neuroectodermal melanolysosomal disease (OMIM Ref. No. 256710) as candidates for mutations in the myoxin gene. By somatic cell hybrid analysis and in situ hybridization, Moore et al. (1995) mapped the MYH12 gene to 15q21, thus extending distally the region of chromosome 15 with homology of synteny to mouse chromosome 9.

[36835] Animal model experiments lend further support to the function of MYO5A. The 'flailer' (flr) mouse exhibits a phenotype consisting of frequent falling, convulsive limb movements (leg flailing), and ataxia persistent into adulthood. The phenotype is similar to that of homozygotes for

null alleles of Myo5a. Jones et al. (2000) determined that the flailer mouse expresses a novel gene combining the promoter and first 2 exons of guanine nucleotide- binding protein beta- 5 (GNB5; 604447) with the C- terminal exons of the closely linked myosin- 5A (MyoVA) gene (Myo5a). Biochemical and genetic studies indicated that the flailer protein, which is expressed predominantly in brain, competes with wildtype MyoVA in vivo, preventing the localization of smooth endoplasmic reticulum vesicles in the dendritic spines of cerebellar Purkinje cells. The flailer protein thus has a dominant- negative mechanism of action with a recessive mode of inheritance due to the dependence of competitive binding on the ratio between mutant and wildtype proteins. The chromosomal arrangement of Myo5a upstream of Gnb5 is consistent with non-homologous recombination as the mutational mechanism.

[36836] It is appreciated that the abovementioned animal model for MYO5A is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[36837] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[36838] Jones, J. M.; Huang, J.- D.; Mermall, V.; Hamilton, B. A.; Mooseker, M. S.; Escayg, A.; Copeland, N. G.; Jenkins, N. A.; Meisler, M. H. : The mouse neurological mutant flailer expresses a novel hybrid gene derived by exon shuffling between Gnb5 and Myo5a. Hum. Molec. Genet. 9: 821-828, 2000. ; and

[36839] Pastural, E.; Barrat, F. J.; Dufourcq- Lagelouse, R.; Certain, S.; Sanal, O.; Jabado, N.; Seger, R.; Griscelli, C.; Fischer, A.; de Saint Basile, G. : Griscelli disease maps to chromoso.

[36840] Further studies establishing the function and utilities of MYO5A are found in John Hopkins OMIM database record ID 160777, and in cited publications listed in Table 5, which are hereby incorporated by reference.Myozenin 3 (MYOZ3, Accession NP_588612.1) is another GAM895 target gene, herein designated TARGET GENE. MYOZ3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYOZ3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYOZ3 BINDING SITE, designated SEQ ID:11685, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36841] Another function of GAM895 is therefore inhibition of Myozenin 3 (MYOZ3, Accession NP_588612.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYOZ3.

[36842] MYST2 (Accession NP_008998.1) is another GAM895 target gene, herein designated TARGET GENE. MYST2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYST2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYST2 BINDING SITE, designated SEQ ID:3346, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36843] Another function of GAM895 is therefore inhibition of MYST2 (Accession NP_008998.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYST2.

[36844] Ndrg family member 4 (NDRG4, Accession NP_075061.1) is another GAM895 target gene, herein designated TARGET GENE. NDRG4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts

of mRNA encoded by NDRG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDRG4 BINDING SITE, designated SEQ ID:12095, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36845] Another function of GAM895 is therefore inhibition of Ndrg family member 4 (NDRG4, Accession NP_075061.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG4.

[36846] Ndrg family member 4 (NDRG4, Accession NP_065198.1) is another GAM895 target gene, herein designated TARGET GENE. NDRG4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NDRG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDRG4 BINDING SITE, designated SEQ ID:12095, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36847] Another function of GAM895 is therefore inhibition of Ndrg family member 4 (NDRG4, Accession NP_065198.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG4.

[36848] Niemann-pick disease, type c2 (NPC2, Accession NP_006423.1) is another GAM895 target gene, herein designated TARGET GENE. NPC2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NPC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPC2 BINDING SITE, designated SEQ ID:10948, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36849] Another function of GAM895 is therefore inhibition of Niemann-pick disease, type c2 (NPC2, Accession NP_006423.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPC2.

[36850] Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1) is another GAM895 target gene, herein

designated TARGET GENE. NQO1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NQO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NQO1 BINDING SITE, designated SEQ ID:13009, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36851] Another function of GAM895 is therefore inhibition of Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1), a gene which is cytochrome b5 reductase which reduces redox dyes and quinones. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NQO1.

[36852] The function of NQO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.5'-nucleotidase, ecto (cd73) (NT5E, Accession NP_002517.1) is another GAM895 target gene, herein designated TARGET GENE. NT5E BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by NT5E, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NT5E BINDING SITE, designated SEQ ID:17625, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36853] Another function of GAM895 is therefore inhibition of 5'-nucleotidase, ecto (cd73) (NT5E, Accession NP_002517.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NT5E.

[36854] P5 (Accession NP_005733.1) is another GAM895 target gene, herein designated TARGET GENE. P5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P5 BINDING SITE, designated SEQ ID:17994, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36855] Another function of GAM895 is therefore inhibition of P5

(Accession NP_005733.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P5.

[36856] Protein phosphatase 3 (formerly 2b), catalytic subunit, alpha isoform (calcineurin a alpha) (PPP3CA, Accession NP_000935.1) is another GAM895 target gene, herein designated TARGET GENE. PPP3CA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPP3CA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP3CA BINDING SITE, designated SEQ ID:4752, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36857] Another function of GAM895 is therefore inhibition of Protein phosphatase 3 (formerly 2b), catalytic subunit, alpha isoform (calcineurin a alpha) (PPP3CA, Accession NP_000935.1), a gene which is the catalytic subunit of calcium- dependent, calmodulin- stimulated protein phosphatase. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP3CA.

[36858] The function of PPP3CA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM451.1.Protein kinase, y-linked (PRKY, Accession NP_002751.1) is another GAM895 target gene, herein designated TARGET GENE. PRKY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKY BINDING SITE, designated SEQ ID:19311, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36859] Another function of GAM895 is therefore inhibition of Protein kinase, y-linked (PRKY, Accession NP_002751.1), a gene which is a putative protein kinase. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKY.

[36860] The function of PRKY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM72.1.Protein s (alpha) (PROS1, Accession NP_000304.1) is another GAM895 target gene, herein designated TARGET GENE. PROS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PROS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PROS1 BINDING SITE, designated SEQ ID:1078, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36861] Another function of GAM895 is therefore inhibition of Protein s (alpha) (PROS1, Accession NP_000304.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROS1.

[36862] Prostaglandin d2 receptor (dp) (PTGDR, Accession NP_000944.1) is another GAM895 target gene, herein designated TARGET GENE. PTGDR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGDR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGDR BINDING SITE, designated

SEQ ID:1012, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36863] Another function of GAM895 is therefore inhibition of Prostaglandin d2 receptor (dp) (PTGDR, Accession NP_000944.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGDR.

[36864] Peroxisomal farnesylated protein (PXF, Accession NP_002848.1) is another GAM895 target gene, herein designated TARGET GENE. PXF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PXF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PXF BINDING SITE, designated SEQ ID:17226, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36865] Another function of GAM895 is therefore inhibition of Peroxisomal farnesylated protein (PXF, Accession NP_002848.1), a gene which may function in peroxisomal biogenesis or assembly and therefore may be associated with Peroxisome biogenesis disorder (pbd). Accordingly,

utilities of GAM895 include diagnosis, prevention and treatment of Peroxisome biogenesis disorder (pbd), and of other diseases and clinical conditions associated with PXF.

[36866] The function of PXF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Rab5a, member ras oncogene family (RAB5A, Accession NP_004153.2) is another GAM895 target gene, herein designated TARGET GENE. RAB5A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB5A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB5A BINDING SITE, designated SEQ ID:3629, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36867] Another function of GAM895 is therefore inhibition of Rab5a, member ras oncogene family (RAB5A, Accession NP_004153.2), a gene which is a rate- limiting component of the machinery regulating the kinetics of membrane traffic. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with RAB5A.

[36868] The function of RAB5A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Rap2a, member of ras oncogene family (RAP2A, Accession NP_066361.1) is another GAM895 target gene, herein designated TARGET GENE. RAP2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAP2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAP2A BINDING SITE, designated SEQ ID:8623, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36869] Another function of GAM895 is therefore inhibition of Rap2a, member of ras oncogene family (RAP2A, Accession NP_066361.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP2A.

[36870] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739580.1) is another GAM895 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:16173, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36871] Another function of GAM895 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739580.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[36872] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739579.1) is another GAM895 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:16173, to the nucleotide sequence of GAM895 RNA, herein designated

GAM RNA, also designated SEQ ID:379.

[36873] Another function of GAM895 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739579.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[36874] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_055552.1) is another GAM895 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:16173, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36875] Another function of GAM895 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_055552.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[36876] Seryl-trna synthetase 2 (SARS2, Accession NP_060297.1)

is another GAM895 target gene, herein designated TARGET GENE. SARS2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SARS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SARS2 BINDING SITE, designated SEQ ID:3298, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36877] Another function of GAM895 is therefore inhibition of Seryl-trna synthetase 2 (SARS2, Accession NP_060297.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SARS2.

[36878] Sec23 homolog b (s. cerevisiae) (SEC23B, Accession NP_116781.1) is another GAM895 target gene, herein designated TARGET GENE. SEC23B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SEC23B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEC23B BINDING SITE, designated SEQ ID:505, to the nu-

cleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36879] Another function of GAM895 is therefore inhibition of Sec23 homolog b (s. cerevisiae) (SEC23B, Accession NP_116781.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC23B.

[36880] Sec23 homolog b (s. cerevisiae) (SEC23B, Accession NP_006354.2) is another GAM895 target gene, herein designated TARGET GENE. SEC23B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SEC23B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEC23B BINDING SITE, designated SEQ ID:505, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36881] Another function of GAM895 is therefore inhibition of Sec23 homolog b (s. cerevisiae) (SEC23B, Accession NP_006354.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC23B.

[36882] Sec23 homolog b (s. cerevisiae) (SEC23B, Accession NP_116780.1) is another GAM895 target gene, herein designated TARGET GENE. SEC23B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SEC23B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEC23B BINDING SITE, designated SEQ ID:505, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36883] Another function of GAM895 is therefore inhibition of Sec23 homolog b (s. cerevisiae) (SEC23B, Accession NP_116780.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC23B.

[36884] Sideroflexin 1 (SFXN1, Accession NP_073591.2) is another GAM895 target gene, herein designated TARGET GENE. SFXN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SFXN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of SFXN1 BINDING SITE, designated SEQ ID:4597, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36885] Another function of GAM895 is therefore inhibition of Sideroflexin 1 (SFXN1, Accession NP_073591.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN1.

[36886] Siat7c (Accession NP_694541.1) is another GAM895 target gene, herein designated TARGET GENE. Siat7c BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Siat7c, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Siat7c BINDING SITE, designated SEQ ID:3113, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36887] Another function of GAM895 is therefore inhibition of Siat7c (Accession NP_694541.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Siat7c.

[36888] S-phase kinase-associated protein 1a (p19a) (SKP1A, Ac-

cession NP_008861.2) is another GAM895 target gene, herein designated TARGET GENE. SKP1A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SKP1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SKP1A BINDING SITE, designated SEQ ID:19958, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36889] Another function of GAM895 is therefore inhibition of S-phase kinase-associated protein 1a (p19a) (SKP1A, Accession NP_008861.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SKP1A.

[36890] S-phase kinase-associated protein 1a (p19a) (SKP1A, Accession NP_733779.1) is another GAM895 target gene, herein designated TARGET GENE. SKP1A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SKP1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

SKP1A BINDING SITE, designated SEQ ID:19958, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36891] Another function of GAM895 is therefore inhibition of S-phase kinase-associated protein 1a (p19a) (SKP1A, Accession NP_733779.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SKP1A.

[36892] Spermatogenesis associated 2 (SPATA2, Accession NP_006029.1) is another GAM895 target gene, herein designated TARGET GENE. SPATA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPATA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPATA2 BINDING SITE, designated SEQ ID:17327, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36893] Another function of GAM895 is therefore inhibition of Spermatogenesis associated 2 (SPATA2, Accession NP_006029.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with SPATA2.

[36894] SRGAP1 (Accession XP_051143.3) is another GAM895 target gene, herein designated TARGET GENE. SRGAP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SRGAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRGAP1 BINDING SITE, designated SEQ ID:6087, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36895] Another function of GAM895 is therefore inhibition of SRGAP1 (Accession XP_051143.3) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRGAP1.

[36896] Signal transducer and activator of transcription 1, 91kda (STAT1, Accession NP_009330.1) is another GAM895 target gene, herein designated TARGET GENE. STAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by STAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of STAT1 BINDING SITE, designated SEQ ID:14937, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36897] Another function of GAM895 is therefore inhibition of Signal transducer and activator of transcription 1, 91kda (STAT1, Accession NP_009330.1), a gene which is involved in transcriptional regulation. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAT1.

[36898] The function of STAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.Synaptotagmin vi (SYT6, Accession XP_086135.1) is another GAM895 target gene, herein designated TARGET GENE. SYT6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYT6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYT6 BINDING SITE, designated SEQ ID:9597, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36899] Another function of GAM895 is therefore inhibition of Synaptotagmin vi (SYT6, Accession XP_086135.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT6.

[36900] Tbc1 domain family, member 4 (TBC1D4, Accession NP_055647.1) is another GAM895 target gene, herein designated TARGET GENE. TBC1D4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TBC1D4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TBC1D4 BINDING SITE, designated SEQ ID:14754, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36901] Another function of GAM895 is therefore inhibition of Tbc1 domain family, member 4 (TBC1D4, Accession NP_055647.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBC1D4.

[36902] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065575.1) is another GAM895 target gene, herein

designated TARGET GENE. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TCL6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:779 and SEQ ID:5137 respectively, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36903] Another function of GAM895 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065575.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[36904] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_055233.1) is another GAM895 target gene, herein designated TARGET GENE. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TCL6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:5137 and SEQ ID:779 respectively, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36905] Another function of GAM895 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_055233.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[36906] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065577.2) is another GAM895 target gene, herein designated TARGET GENE. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TCL6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:779 and SEQ ID:5137 respectively, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36907] Another function of GAM895 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession

NP_065577.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[36908] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_036600.2) is another GAM895 target gene, herein designated TARGET GENE. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TCL6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:5137 and SEQ ID:779 respectively, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36909] Another function of GAM895 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_036600.2) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[36910] TPT (Accession NP_055132.1) is another GAM895 target gene, herein designated TARGET GENE. TPT BINDING SITE is a target binding site found in the 3` untranslated re-

gion of mRNA encoded by TPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPT BINDING SITE, designated SEQ ID:17162, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36911] Another function of GAM895 is therefore inhibition of TPT (Accession NP_055132.1), a gene which Moderately similar to decaprenyl diphosphate synthase (S. pombe dps) and therefore may be associated with Triphalangeal thumb- polysyndactyly syndrome. Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of Triphalangeal thumb- polysyndactyly syndrome, and of other diseases and clinical conditions associated with TPT.

[36912] The function of TPT has been established by previous studies. Nicolai and Hamel (1988) described a large family in which multiple members exhibited a spectrum of pre- and postaxial anomalies of the limbs inherited as an autosomal dominant. In another study of this family, Tsukurov et al. (1994) found linkage of the malformation to a highly polymorphic locus containing a short tandem repeat sequence (STR), D7S550, located at 7q36; maximum lod

score = 6.85 at theta = 0.0. This region is homologous to a segment of mouse chromosome 5 where 2 nonallelic mutations, 'hammer- toe' (Hm) and 'hemimelic extra toes' (Hx), have been mapped. In the family reported by Tsukurov et al. (1994), hand malformations were typically bilateral but usually asymmetric. Both pre- and postaxial polydactyly and syndactyly were present. In all affected individuals the thumb was triphalangeal and the index finger was normal. Malformations of the feet were present in some affected persons but were usually less severe than those observed in the hands. Variable expression of the disease gene was demonstrated by asymmetries in limb deformities of affected individuals and the differences observed between monozygotic twins. Heus et al. (1999) constructed a detailed physical map of the candidate region for this form of preaxial polydactyly. They used a combination of methods to identify and position 11 transcripts within this map. By recombination analysis on families with preaxial polydactyly, they reduced the candidate region to approximately 450 kb. Mapping to the refined candidate region were the homeo box gene HLXB9 (OMIM Ref. No. 142994), a putative receptor (C7ORF2; 605522), and 2 transcripts of unknown function. All 4

transcripts were analyzed and sequenced in patients with preaxial polydactyly, but no pathogenic mutations were identified. Balci et al. (1999) described a Turkish family with triphalangeal thumb- polysyndactyly syndrome. Characteristic findings in this family were triphalangeal thumb, webbing between third, fourth, and fifth fingers associated with bony synostosis in the distal phalanges of the same fingers, and pre- and postaxial polysyndactyly of the feet. Some affected members of the family showed a more severe phenotype with complete syndactyly of all fingers giving a 'cup- like' appearance to the hands. Genetic linkage studies demonstrated linkage to 7q36. Kantaputra and Chalidapong (2000) reported a Thai man who had triphalangeal thumb- polysyndactyly syndrome and his daughter who had tibial hemimelia- polysyndactyly-triphalangeal thumb syndrome (OMIM Ref. No. 188770). The authors proposed that these conditions are actually the same disorder with wide variability. They suggested this condition be called 'tibial hemimelia- polysyndactyly-triphalangeal thumbs syndrome.'

[36913]

[36914] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[36915] Kantaputra, P. N.; Chalidapong, P. : Are triphalangeal thumb- polysyndactyly syndrome (TPTPS) and tibial hemimelia- polysyndactyly- triphalangeal thumb syndrome (THPTTS) identical?: A father with TPTPS and his daughter with THPTTS in a Thai family. Am. J. Med. Genet. 93: 126- 131, 2000. ; and

[36916] Nicolai, J.- P. A.; Hamel, B. C. J. : A family with complex bilateral polysyndactyly. J. Hand Surg. 13A: 405- 407, 1988.

[36917] Further studies establishing the function and utilities of TPT are found in John Hopkins OMIM database record ID 190605, and in cited publications listed in Table 5, which are hereby incorporated by reference.Unc-5 homolog d (c. elegans) (UNC5D, Accession NP_543148.1) is another GAM895 target gene, herein designated TARGET GENE. UNC5D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UNC5D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UNC5D BINDING SITE, designated SEQ ID:20188, to the nucleotide sequence of GAM895 RNA, herein designated

GAM RNA, also designated SEQ ID:379.

[36918] Another function of GAM895 is therefore inhibition of Unc-5 homolog d (c. elegans) (UNC5D, Accession NP_543148.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC5D.

[36919] Vent-like homeobox 2 (VENTX2, Accession NP_055283.1) is another GAM895 target gene, herein designated TARGET GENE. VENTX2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VENTX2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VENTX2 BINDING SITE, designated SEQ ID:6385, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36920] Another function of GAM895 is therefore inhibition of Vent-like homeobox 2 (VENTX2, Accession NP_055283.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VENTX2.

[36921] ZNF-kaiso (Accession NP_006768.1) is another GAM895 target gene, herein designated TARGET GENE. ZNF-kaiso

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF-kaiso, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF-kaiso BINDING SITE, designated SEQ ID:3272, to the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, also designated SEQ ID:379.

[36922] Another function of GAM895 is therefore inhibition of ZNF-kaiso (Accession NP_006768.1) . Accordingly, utilities of GAM895 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF-kaiso.

[36923]

[36924] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 1032 (GAM1032), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[36925] GAM1032 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1032 was detected is described hereinabove

with reference to Figs. 8-15.

[36926] GAM1032 gene, herein designated GAM GENE, and GAM1032 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[36927] GAM1032 gene encodes a GAM1032 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1032 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1032 precursor RNA is designated SEQ ID:169, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:169 is located at position 141427181 relative to chromosome 8.

[36928] GAM1032 precursor RNA folds onto itself, forming GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[36929] GAM1032 precursor RNA folds onto itself, forming

GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[36930] Nucleotide sequence of GAM1032 precursor RNA, designated SEQ-ID: 169, and a schematic representation of a predicted secondary folding of GAM1032 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[36931] An enzyme complex designated DICER COMPLEX, `dices` the GAM1032 folded precursor RNA into GAM1032 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM1032 RNA is designated SEQ ID:303, and is provided hereinbelow with refer-

ences to the sequence listing part and Table 3, hereby incorporated by reference.

[36932] GAM1032 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM1032 target RNA, herein designated GAM TARGET RNA. GAM1032 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[36933] GAM1032 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1032 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1032 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1032 RNA may have a different number of target binding sites in untranslated regions of a GAM1032 target

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[36934] The complementary binding of GAM1032 RNA, herein designated GAM RNA, to target binding sites on GAM1032 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1032 target RNA into GAM1032 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[36935] It is appreciated that GAM1032 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM1032 target genes. The mRNA of each one of this plurality of GAM1032 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1032 RNA, herein designated GAM RNA, and which when bound by GAM1032 RNA causes inhibition of translation of respective one or more GAM1032 target proteins.

[36936] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1032 gene, herein designated GAM GENE, on one or more GAM1032 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[36937] It is appreciated that specific functions and accordingly utilities of GAM1032 correlate with, and may be deduced from, the identity of the target genes which GAM1032 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[36938]

[36939]

[36940] Acid phosphatase 1, soluble (ACP1, Accession

NP_004291.1) is a GAM1032 target gene, herein designated TARGET GENE. ACP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACP1 BINDING SITE, designated SEQ ID:2659, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36941] A function of GAM1032 is therefore inhibition of Acid phosphatase 1, soluble (ACP1, Accession NP_004291.1), a gene which as demonstrated in starch- gel electrophoresis. and therefore may be associated with Acid phosphatase 1, soluble, a/b polymorphism of. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Acid phosphatase 1, soluble, a/b polymorphism of, and of other diseases and clinical conditions associated with ACP1.

[36942] The function of ACP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Acid phosphatase 1, soluble (ACP1, Accession

NP_009030.1) is another GAM1032 target gene, herein designated TARGET GENE. ACP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACP1 BINDING SITE, designated SEQ ID:2659, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36943] Another function of GAM1032 is therefore inhibition of Acid phosphatase 1, soluble (ACP1, Accession NP_009030.1), a gene which as demonstrated in starch-gel electrophoresis. and therefore may be associated with Acid phosphatase 1, soluble, a/b polymorphism of. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Acid phosphatase 1, soluble, a/b polymorphism of, and of other diseases and clinical conditions associated with ACP1.

[36944] The function of ACP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Acid phosphatase 1, soluble (ACP1, Accession

NP_808222.1) is another GAM1032 target gene, herein designated TARGET GENE. ACP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACP1 BINDING SITE, designated SEQ ID:2659, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36945] Another function of GAM1032 is therefore inhibition of Acid phosphatase 1, soluble (ACP1, Accession NP_808222.1), a gene which as demonstrated in starch-gel electrophoresis. and therefore may be associated with Acid phosphatase 1, soluble, a/b polymorphism of. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Acid phosphatase 1, soluble, a/b polymorphism of, and of other diseases and clinical conditions associated with ACP1.

[36946] The function of ACP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Adenylate cyclase 1 (brain) (ADCY1, Acces-

sion NP_066939.1) is another GAM1032 target gene, herein designated TARGET GENE. ADCY1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADCY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY1 BINDING SITE, designated SEQ ID:5742, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36947] Another function of GAM1032 is therefore inhibition of Adenylate cyclase 1 (brain) (ADCY1, Accession NP_066939.1), a gene which a calmodulin- sensitive adenylyl cyclase. it may play a role in memory acquisition and learning. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY1.

[36948] The function of ADCY1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.Amyotrophic lateral sclerosis 2 (juvenile) (ALS2, Accession NP_065970.1) is another GAM1032 target gene, herein designated TARGET GENE. ALS2 BINDING

SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ALS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALS2 BINDING SITE, designated SEQ ID:5747, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36949] Another function of GAM1032 is therefore inhibition of Amyotrophic lateral sclerosis 2 (juvenile) (ALS2, Accession NP_065970.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALS2.

[36950] Angiomotin (AMOT, Accession NP_573572.1) is another GAM1032 target gene, herein designated TARGET GENE. AMOT BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by AMOT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMOT BINDING SITE, designated SEQ ID:4436, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36951] Another function of GAM1032 is therefore inhibition of Angiomotin (AMOT, Accession NP_573572.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMOT.

[36952] ANKT (Accession NP_057443.1) is another GAM1032 target gene, herein designated TARGET GENE. ANKT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ANKT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANKT BINDING SITE, designated SEQ ID:15792, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36953] Another function of GAM1032 is therefore inhibition of ANKT (Accession NP_057443.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKT.

[36954] ANKT (Accession NP_060924.4) is another GAM1032 target gene, herein designated TARGET GENE. ANKT BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ANKT,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANKT BINDING SITE, designated SEQ ID:15792, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36955] Another function of GAM1032 is therefore inhibition of ANKT (Accession NP_060924.4) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKT.

[36956] Apolipoprotein l, 6 (APOL6, Accession NP_085144.1) is another GAM1032 target gene, herein designated TARGET GENE. APOL6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APOL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL6 BINDING SITE, designated SEQ ID:19543, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36957] Another function of GAM1032 is therefore inhibition of Apolipoprotein l, 6 (APOL6, Accession NP_085144.1) . Accordingly, utilities of GAM1032 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with APOL6.

[36958] Bardet-biedl syndrome 4 (BBS4, Accession NP_149017.2) is another GAM1032 target gene, herein designated TARGET GENE. BBS4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BBS4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BBS4 BINDING SITE, designated SEQ ID:12747, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36959] Another function of GAM1032 is therefore inhibition of Bardet-biedl syndrome 4 (BBS4, Accession NP_149017.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BBS4.

[36960] BG1 (Accession NP_055977.3) is another GAM1032 target gene, herein designated TARGET GENE. BG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of BG1 BINDING SITE, designated SEQ ID:19594, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36961] Another function of GAM1032 is therefore inhibition of BG1 (Accession NP_055977.3) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BG1.

[36962] Biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen) (BPHL, Accession NP_004323.1) is another GAM1032 target gene, herein designated TARGET GENE. BPHL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BPHL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BPHL BINDING SITE, designated SEQ ID:4510, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36963] Another function of GAM1032 is therefore inhibition of Biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen) (BPHL, Accession

NP_004323.1), a gene which involves in detoxification processes. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BPHL.

[36964] The function of BPHL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Chromosome 15 open reading frame 12 (C15orf12, Accession NP_060755.1) is another GAM1032 target gene, herein designated TARGET GENE. C15orf12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C15orf12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C15orf12 BINDING SITE, designated SEQ ID:10592, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36965] Another function of GAM1032 is therefore inhibition of Chromosome 15 open reading frame 12 (C15orf12, Accession NP_060755.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C15orf12.

[36966] Chromosome 17 open reading frame 28 (C17orf28, Accession NP_085133.1) is another GAM1032 target gene, herein designated TARGET GENE. C17orf28 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C17orf28, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C17orf28 BINDING SITE, designated SEQ ID:6729, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36967] Another function of GAM1032 is therefore inhibition of Chromosome 17 open reading frame 28 (C17orf28, Accession NP_085133.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C17orf28.

[36968] Chromosome 1 open reading frame 21 (C1orf21, Accession NP_110433.1) is another GAM1032 target gene, herein designated TARGET GENE. C1orf21 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1orf21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of C1orf21 BINDING SITE, designated SEQ ID:17052, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36969] Another function of GAM1032 is therefore inhibition of Chromosome 1 open reading frame 21 (C1orf21, Accession NP_110433.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf21.

[36970] Chromosome 20 open reading frame 129 (C20orf129, Accession NP_112181.1) is another GAM1032 target gene, herein designated TARGET GENE. C20orf129 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf129, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf129 BINDING SITE, designated SEQ ID:11258, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36971] Another function of GAM1032 is therefore inhibition of Chromosome 20 open reading frame 129 (C20orf129, Accession NP_112181.1) . Accordingly, utilities of GAM1032

include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf129.

[36972] Chromosome 20 open reading frame 161 (C20orf161, Accession NP_219489.1) is another GAM1032 target gene, herein designated TARGET GENE. C20orf161 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C20orf161, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf161 BINDING SITE, designated SEQ ID:10164, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36973] Another function of GAM1032 is therefore inhibition of Chromosome 20 open reading frame 161 (C20orf161, Accession NP_219489.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf161.

[36974] Chromosome 21 open reading frame 97 (C21orf97, Accession NP_068760.1) is another GAM1032 target gene, herein designated TARGET GENE. C21orf97 BINDING SITE is a target binding site found in the 3` untranslated re-

gion of mRNA encoded by C21orf97, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C21orf97 BINDING SITE, designated SEQ ID:5545, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36975] Another function of GAM1032 is therefore inhibition of Chromosome 21 open reading frame 97 (C21orf97, Accession NP_068760.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf97.

[36976] Calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2, Accession NP_705720.1) is another GAM1032 target gene, herein designated TARGET GENE. CAMKK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CAMKK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMKK2 BINDING SITE, designated SEQ ID:7725, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:303.

[36977] Another function of GAM1032 is therefore inhibition of Calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2, Accession NP_705720.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMKK2.

[36978] Calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2, Accession NP_757380.1) is another GAM1032 target gene, herein designated TARGET GENE. CAMKK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CAMKK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMKK2 BINDING SITE, designated SEQ ID:7725, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36979] Another function of GAM1032 is therefore inhibition of Calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2, Accession NP_757380.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with CAMKK2.

[36980] Calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2, Accession NP_705719.2) is another GAM1032 target gene, herein designated TARGET GENE. CAMKK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CAMKK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMKK2 BINDING SITE, designated SEQ ID:7725, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36981] Another function of GAM1032 is therefore inhibition of Calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2, Accession NP_705719.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMKK2.

[36982] Calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2, Accession NP_757365.1) is another GAM1032 target gene, herein designated TARGET GENE.

CAMKK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CAMKK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMKK2 BINDING SITE, designated SEQ ID:7725, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36983] Another function of GAM1032 is therefore inhibition of Calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2, Accession NP_757365.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMKK2.

[36984] Calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2, Accession NP_006540.3) is another GAM1032 target gene, herein designated TARGET GENE. CAMKK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CAMKK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of CAMKK2 BINDING SITE, designated SEQ ID:7725, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36985] Another function of GAM1032 is therefore inhibition of Calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2, Accession NP_006540.3) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMKK2.

[36986] Caspase 4, apoptosis-related cysteine protease (CASP4, Accession NP_001216.1) is another GAM1032 target gene, herein designated TARGET GENE. CASP4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP4 BINDING SITE, designated SEQ ID:3772, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36987] Another function of GAM1032 is therefore inhibition of Caspase 4, apoptosis-related cysteine protease (CASP4,

Accession NP_001216.1), a gene which is an apoptosis-related caspase and involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP4.

[36988] The function of CASP4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM810.2.Caspase 4, apoptosis-related cysteine protease (CASP4, Accession NP_150650.1) is another GAM1032 target gene, herein designated TARGET GENE. CASP4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP4 BINDING SITE, designated SEQ ID:3772, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36989] Another function of GAM1032 is therefore inhibition of Caspase 4, apoptosis-related cysteine protease (CASP4,

Accession NP_150650.1), a gene which is an apoptosis-related caspase and involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP4.

[36990] The function of CASP4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM810.2.Caspase 4, apoptosis-related cysteine protease (CASP4, Accession NP_150649.1) is another GAM1032 target gene, herein designated TARGET GENE. CASP4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP4 BINDING SITE, designated SEQ ID:3772, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36991] Another function of GAM1032 is therefore inhibition of Caspase 4, apoptosis-related cysteine protease (CASP4,

Accession NP_150649.1), a gene which is an apoptosis-related caspase and involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP4.

[36992] The function of CASP4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM810.2.Cd1d antigen, d polypeptide (CD1D, Accession NP_001757.1) is another GAM1032 target gene, herein designated TARGET GENE. CD1D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD1D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD1D BINDING SITE, designated SEQ ID:16191, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36993] Another function of GAM1032 is therefore inhibition of Cd1d antigen, d polypeptide (CD1D, Accession NP_001757.1), a gene which is a member D of the CD1

family; involved in antigen presentation . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD1D.

[36994] The function of CD1D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.1.Cell division cycle 25b (CDC25B, Accession NP_068658.1) is another GAM1032 target gene, herein designated TARGET GENE. CDC25B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDC25B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC25B BINDING SITE, designated SEQ ID:11047, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36995] Another function of GAM1032 is therefore inhibition of Cell division cycle 25b (CDC25B, Accession NP_068658.1), a gene which is positively activated by dephosphorylation. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with CDC25B.

[36996] The function of CDC25B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM504.2.Cell division cycle 25b (CDC25B, Accession NP_068660.1) is another GAM1032 target gene, herein designated TARGET GENE. CDC25B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDC25B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC25B BINDING SITE, designated SEQ ID:11047, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36997] Another function of GAM1032 is therefore inhibition of Cell division cycle 25b (CDC25B, Accession NP_068660.1), a gene which is positively activated by dephosphorylation. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC25B.

[36998] The function of CDC25B and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM504.2.Cell division cycle 25b (CDC25B, Accession NP_004349.1) is another GAM1032 target gene, herein designated TARGET GENE. CDC25B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDC25B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC25B BINDING SITE, designated SEQ ID:11047, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[36999] Another function of GAM1032 is therefore inhibition of Cell division cycle 25b (CDC25B, Accession NP_004349.1), a gene which is positively activated by dephosphorylation. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC25B.

[37000] The function of CDC25B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM504.2.Cell division cycle 25b (CDC25B, Accession NP_068659.1) is another GAM1032 target gene, herein

designated TARGET GENE. CDC25B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDC25B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC25B BINDING SITE, designated SEQ ID:11047, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37001] Another function of GAM1032 is therefore inhibition of Cell division cycle 25b (CDC25B, Accession NP_068659.1), a gene which is positively activated by dephosphorylation. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC25B.

[37002] The function of CDC25B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM504.2.Cofilin 2 (muscle) (CFL2, Accession NP_068733.1) is another GAM1032 target gene, herein designated TARGET GENE. CFL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CFL2, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CFL2 BINDING SITE, designated SEQ ID:16082, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37003] Another function of GAM1032 is therefore inhibition of Cofilin 2 (muscle) (CFL2, Accession NP_068733.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CFL2.

[37004] Chloride channel 1, skeletal muscle (thomsen disease, autosomal dominant) (CLCN1, Accession NP_000074.1) is another GAM1032 target gene, herein designated TARGET GENE. CLCN1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CLCN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLCN1 BINDING SITE, designated SEQ ID:7487, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37005] Another function of GAM1032 is therefore inhibition of Chloride channel 1, skeletal muscle (thomsen disease, autosomal dominant) (CLCN1, Accession NP_000074.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN1.

[37006] Ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) (CLN8, Accession NP_061764.2) is another GAM1032 target gene, herein designated TARGET GENE. CLN8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLN8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLN8 BINDING SITE, designated SEQ ID:17822, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37007] Another function of GAM1032 is therefore inhibition of Ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) (CLN8, Accession NP_061764.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLN8.

[37008] CLONE24945 (Accession NP_056498.1) is another GAM1032 target gene, herein designated TARGET GENE. CLONE24945 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLONE24945, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLONE24945 BINDING SITE, designated SEQ ID:7108, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37009] Another function of GAM1032 is therefore inhibition of CLONE24945 (Accession NP_056498.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLONE24945.

[37010] Citrate lyase beta like (CLYBL, Accession NP_612124.2) is another GAM1032 target gene, herein designated TARGET GENE. CLYBL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLYBL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of CLYBL BINDING SITE, designated SEQ ID:6231, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37011] Another function of GAM1032 is therefore inhibition of Citrate lyase beta like (CLYBL, Accession NP_612124.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLYBL.

[37012] Collagen, type xix, alpha 1 (COL19A1, Accession NP_001849.1) is another GAM1032 target gene, herein designated TARGET GENE. COL19A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by COL19A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL19A1 BINDING SITE, designated SEQ ID:3270, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37013] Another function of GAM1032 is therefore inhibition of Collagen, type xix, alpha 1 (COL19A1, Accession NP_001849.1), a gene which may act as a cross- bridge between fibrils and other extracellular matrix molecules.

Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL19A1.

[37014] The function of COL19A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Collagen, type iv, alpha 6 (COL4A6, Accession NP_378667.1) is another GAM1032 target gene, herein designated TARGET GENE. COL4A6 BINDING SITE1 and COL4A6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by COL4A6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL4A6 BINDING SITE1 and COL4A6 BINDING SITE2, designated SEQ ID:13214 and SEQ ID:15255 respectively, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37015] Another function of GAM1032 is therefore inhibition of Collagen, type iv, alpha 6 (COL4A6, Accession NP_378667.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with COL4A6.

[37016] CXYorf1 (Accession XP_088704.2) is another GAM1032 target gene, herein designated TARGET GENE. CXYorf1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CXYorf1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CXYorf1 BINDING SITE, designated SEQ ID:8588, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37017] Another function of GAM1032 is therefore inhibition of CXYorf1 (Accession XP_088704.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXYorf1.

[37018] CYB5-M (Accession NP_085056.1) is another GAM1032 target gene, herein designated TARGET GENE. CYB5-M BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYB5-M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

CYB5-M BINDING SITE, designated SEQ ID:17320, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37019] Another function of GAM1032 is therefore inhibition of CYB5-M (Accession NP_085056.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYB5-M.

[37020] DEPP (Accession NP_008952.1) is another GAM1032 target gene, herein designated TARGET GENE. DEPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DEPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DEPP BINDING SITE, designated SEQ ID:10673, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37021] Another function of GAM1032 is therefore inhibition of DEPP (Accession NP_008952.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DEPP.

[37022] DIS3 (Accession NP_055768.2) is another GAM1032 target

gene, herein designated TARGET GENE. DIS3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DIS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DIS3 BINDING SITE, designated SEQ ID:16408, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37023] Another function of GAM1032 is therefore inhibition of DIS3 (Accession NP_055768.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIS3.

[37024] DISPB (Accession NP_277045.1) is another GAM1032 target gene, herein designated TARGET GENE. DISPB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DISPB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DISPB BINDING SITE, designated SEQ ID:17823, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37025] Another function of GAM1032 is therefore inhibition of DISPB (Accession NP_277045.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DISPB.

[37026] dJ383J4.3 (Accession XP_294938.1) is another GAM1032 target gene, herein designated TARGET GENE. dJ383J4.3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by dJ383J4.3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of dJ383J4.3 BINDING SITE, designated SEQ ID:9430, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37027] Another function of GAM1032 is therefore inhibition of dJ383J4.3 (Accession XP_294938.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with dJ383J4.3.

[37028] DKFZP434C171 (Accession NP_056436.1) is another GAM1032 target gene, herein designated TARGET GENE. DKFZP434C171 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

DKFZP434C171, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434C171 BINDING SITE, designated SEQ ID:3164, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37029] Another function of GAM1032 is therefore inhibition of DKFZP434C171 (Accession NP_056436.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C171.

[37030] DKFZp434O0320 (Accession XP_097012.2) is another GAM1032 target gene, herein designated TARGET GENE. DKFZp434O0320 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434O0320, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434O0320 BINDING SITE, designated SEQ ID:12853, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37031] Another function of GAM1032 is therefore inhibition of DKFZp434O0320 (Accession XP_097012.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434O0320.

[37032] DKFZp547B1713 (Accession NP_689592.1) is another GAM1032 target gene, herein designated TARGET GENE. DKFZp547B1713 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547B1713, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547B1713 BINDING SITE, designated SEQ ID:8359, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37033] Another function of GAM1032 is therefore inhibition of DKFZp547B1713 (Accession NP_689592.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547B1713.

[37034] DKFZP566I1024 (Accession NP_056226.1) is another GAM1032 target gene, herein designated TARGET GENE.

DKFZP566I1024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP566I1024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566I1024 BINDING SITE, designated SEQ ID:7803, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37035] Another function of GAM1032 is therefore inhibition of DKFZP566I1024 (Accession NP_056226.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566I1024.

[37036] DKFZp586F1019 (Accession NP_112159.1) is another GAM1032 target gene, herein designated TARGET GENE. DKFZp586F1019 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp586F1019, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp586F1019 BINDING SITE, designated SEQ ID:5132, to the nucleotide sequence of

GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37037] Another function of GAM1032 is therefore inhibition of DKFZp586F1019 (Accession NP_112159.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp586F1019.

[37038] DKFZp686G052 (Accession XP_300559.1) is another GAM1032 target gene, herein designated TARGET GENE. DKFZp686G052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp686G052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp686G052 BINDING SITE, designated SEQ ID:11872, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37039] Another function of GAM1032 is therefore inhibition of DKFZp686G052 (Accession XP_300559.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp686G052.

[37040] Doublesex and mab-3 related transcription factor 2 (DMRT2, Accession NP_006548.1) is another GAM1032 target gene, herein designated TARGET GENE. DMRT2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DMRT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DMRT2 BINDING SITE, designated SEQ ID:5107, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37041] Another function of GAM1032 is therefore inhibition of Doublesex and mab-3 related transcription factor 2 (DMRT2, Accession NP_006548.1), a gene which May be involved in male sexual development. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMRT2.

[37042] The function of DMRT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM439.1.Dmrt-like family c2 (DMRTC2, Accession NP_149041.1) is another GAM1032 target gene, herein designated TARGET GENE. DMRTC2 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by DMRTC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DMRTC2 BINDING SITE, designated SEQ ID:9542, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37043] Another function of GAM1032 is therefore inhibition of Dmrt-like family c2 (DMRTC2, Accession NP_149041.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMRTC2.

[37044] Dynamin 2 (DNM2, Accession NP_004936.1) is another GAM1032 target gene, herein designated TARGET GENE. DNM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DNM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DNM2 BINDING SITE, designated SEQ ID:19535, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37045] Another function of GAM1032 is therefore inhibition of Dynamin 2 (DNM2, Accession NP_004936.1), a gene which regulates budding of endocytic vesicles . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNM2.

[37046] The function of DNM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Deltex homolog 2 (drosophila) (DTX2, Accession NP_065943.1) is another GAM1032 target gene, herein designated TARGET GENE. DTX2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DTX2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DTX2 BINDING SITE, designated SEQ ID:19806, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37047] Another function of GAM1032 is therefore inhibition of Deltex homolog 2 (drosophila) (DTX2, Accession NP_065943.1) . Accordingly, utilities of GAM1032 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with DTX2.

[37048] E2f transcription factor 3 (E2F3, Accession NP_001940.1) is another GAM1032 target gene, herein designated TARGET GENE. E2F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by E2F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of E2F3 BINDING SITE, designated SEQ ID:16241, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37049] Another function of GAM1032 is therefore inhibition of E2f transcription factor 3 (E2F3, Accession NP_001940.1), a gene which binds dna and controls cell- cycle progression from g1 to s phase. and therefore may be associated with Hereditary autosomal dominant myoclonus dystonia. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Hereditary autosomal dominant myoclonus dystonia, and of other diseases and clinical conditions associated with E2F3.

[37050] The function of E2F3 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM44.1.EDRF1 (Accession NP_056423.2) is another GAM1032 target gene, herein designated TARGET GENE. EDRF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EDRF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDRF1 BINDING SITE, designated SEQ ID:5132, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37051] Another function of GAM1032 is therefore inhibition of EDRF1 (Accession NP_056423.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDRF1.

[37052] Estrogen receptor 1 (ESR1, Accession NP_000116.1) is another GAM1032 target gene, herein designated TARGET GENE. ESR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ESR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ESR1 BINDING SITE, designated SEQ ID:11698,

to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37053] Another function of GAM1032 is therefore inhibition of Estrogen receptor 1 (ESR1, Accession NP_000116.1), a gene which involved in hormone- mediated inhibition of gene expression. and therefore may be associated with Estrogen receptor mutant. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Estrogen receptor mutant, and of other diseases and clinical conditions associated with ESR1.

[37054] The function of ESR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM289.1.F-box only protein 10 (FBXO10, Accession XP_291314.1) is another GAM1032 target gene, herein designated TARGET GENE. FBXO10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FBXO10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXO10 BINDING SITE, designated SEQ ID:1583, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also des-

ignated SEQ ID:303.

[37055] Another function of GAM1032 is therefore inhibition of F-box only protein 10 (FBXO10, Accession XP_291314.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO10.

[37056] FLJ10496 (Accession NP_060584.2) is another GAM1032 target gene, herein designated TARGET GENE. FLJ10496 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10496, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10496 BINDING SITE, designated SEQ ID:6405, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37057] Another function of GAM1032 is therefore inhibition of FLJ10496 (Accession NP_060584.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10496.

[37058] FLJ10648 (Accession NP_060637.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ10648

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10648, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10648 BINDING SITE, designated SEQ ID:13957, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37059] Another function of GAM1032 is therefore inhibition of FLJ10648 (Accession NP_060637.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10648.

[37060] FLJ10932 (Accession NP_060747.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ10932 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10932, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10932 BINDING SITE, designated SEQ ID:2710, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37061] Another function of GAM1032 is therefore inhibition of FLJ10932 (Accession NP_060747.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10932.

[37062] FLJ11506 (Accession NP_078942.2) is another GAM1032 target gene, herein designated TARGET GENE. FLJ11506 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11506, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11506 BINDING SITE, designated SEQ ID:1155, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37063] Another function of GAM1032 is therefore inhibition of FLJ11506 (Accession NP_078942.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11506.

[37064] FLJ12439 (Accession NP_075565.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ12439 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ12439, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12439 BINDING SITE, designated SEQ ID:14060, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37065] Another function of GAM1032 is therefore inhibition of FLJ12439 (Accession NP_075565.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12439.

[37066] FLJ13204 (Accession NP_079037.2) is another GAM1032 target gene, herein designated TARGET GENE. FLJ13204 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13204, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13204 BINDING SITE, designated SEQ ID:4441, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37067] Another function of GAM1032 is therefore inhibition of

FLJ13204 (Accession NP_079037.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13204.

[37068] FLJ13769 (Accession NP_079288.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ13769 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13769, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13769 BINDING SITE, designated SEQ ID:2505, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37069] Another function of GAM1032 is therefore inhibition of FLJ13769 (Accession NP_079288.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13769.

[37070] FLJ14154 (Accession NP_079121.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ14154 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14154, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14154 BINDING SITE, designated SEQ ID:5645, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37071] Another function of GAM1032 is therefore inhibition of FLJ14154 (Accession NP_079121.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14154.

[37072] FLJ14166 (Accession NP_078841.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ14166 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ14166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14166 BINDING SITE, designated SEQ ID:2917, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37073] Another function of GAM1032 is therefore inhibition of FLJ14166 (Accession NP_078841.1) . Accordingly, utilities

of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14166.

[37074] FLJ20014 (Accession NP_060092.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ20014 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20014, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20014 BINDING SITE, designated SEQ ID:2766, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37075] Another function of GAM1032 is therefore inhibition of FLJ20014 (Accession NP_060092.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20014.

[37076] FLJ20401 (Accession NP_060275.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ20401 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20401, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20401 BINDING SITE, designated SEQ ID:4190, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37077] Another function of GAM1032 is therefore inhibition of FLJ20401 (Accession NP_060275.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20401.

[37078] FLJ20445 (Accession NP_060294.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ20445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20445 BINDING SITE, designated SEQ ID:12035, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37079] Another function of GAM1032 is therefore inhibition of FLJ20445 (Accession NP_060294.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20445.

[37080] FLJ20584 (Accession NP_060361.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ20584 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20584, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20584 BINDING SITE, designated SEQ ID:8842, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37081] Another function of GAM1032 is therefore inhibition of FLJ20584 (Accession NP_060361.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20584.

[37082] FLJ21148 (Accession NP_079136.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ21148 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21148, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ21148 BINDING SITE, designated SEQ ID:11110, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37083] Another function of GAM1032 is therefore inhibition of FLJ21148 (Accession NP_079136.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21148.

[37084] FLJ21240 (Accession NP_079123.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ21240 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21240, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21240 BINDING SITE, designated SEQ ID:6131, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37085] Another function of GAM1032 is therefore inhibition of FLJ21240 (Accession NP_079123.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ21240.

[37086] FLJ21802 (Accession NP_078920.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ21802 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21802, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21802 BINDING SITE, designated SEQ ID:7802, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37087] Another function of GAM1032 is therefore inhibition of FLJ21802 (Accession NP_078920.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21802.

[37088] FLJ22639 (Accession NP_079072.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ22639 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22639, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ22639 BINDING SITE, designated SEQ ID:2390, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37089] Another function of GAM1032 is therefore inhibition of FLJ22639 (Accession NP_079072.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22639.

[37090] FLJ25954 (Accession NP_775843.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ25954 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ25954, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25954 BINDING SITE, designated SEQ ID:3762, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37091] Another function of GAM1032 is therefore inhibition of FLJ25954 (Accession NP_775843.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25954.

[37092] FLJ30567 (Accession NP_659459.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ30567 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30567, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30567 BINDING SITE, designated SEQ ID:12412, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37093] Another function of GAM1032 is therefore inhibition of FLJ30567 (Accession NP_659459.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30567.

[37094] FLJ30655 (Accession NP_653244.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ30655 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30655, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30655 BINDING SITE, designated SEQ ID:1102, to the

nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37095] Another function of GAM1032 is therefore inhibition of FLJ30655 (Accession NP_653244.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30655.

[37096] FLJ32112 (Accession NP_694580.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ32112 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32112, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32112 BINDING SITE, designated SEQ ID:13700, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37097] Another function of GAM1032 is therefore inhibition of FLJ32112 (Accession NP_694580.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32112.

[37098] FLJ35721 (Accession NP_775955.1) is another GAM1032

target gene, herein designated TARGET GENE. FLJ35721 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35721, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35721 BINDING SITE, designated SEQ ID:9904, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37099] Another function of GAM1032 is therefore inhibition of FLJ35721 (Accession NP_775955.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35721.

[37100] FLJ39249 (Accession NP_775935.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ39249 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39249, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39249 BINDING SITE, designated SEQ ID:6728, to the nucleotide sequence of GAM1032 RNA, herein designated

GAM RNA, also designated SEQ ID:303.

[37101] Another function of GAM1032 is therefore inhibition of FLJ39249 (Accession NP_775935.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39249.

[37102] FLJ39639 (Accession XP_290687.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ39639 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39639, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39639 BINDING SITE, designated SEQ ID:8387, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37103] Another function of GAM1032 is therefore inhibition of FLJ39639 (Accession XP_290687.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39639.

[37104] FLJ90013 (Accession NP_699196.1) is another GAM1032 target gene, herein designated TARGET GENE. FLJ90013

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90013, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90013 BINDING SITE, designated SEQ ID:4414, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37105] Another function of GAM1032 is therefore inhibition of FLJ90013 (Accession NP_699196.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90013.

[37106] GAF1 (Accession NP_056285.1) is another GAM1032 target gene, herein designated TARGET GENE. GAF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAF1 BINDING SITE, designated SEQ ID:6004, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37107] Another function of GAM1032 is therefore inhibition of GAF1 (Accession NP_056285.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAF1.

[37108] Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) is another GAM1032 target gene, herein designated TARGET GENE. GGA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE, designated SEQ ID:3682, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37109] Another function of GAM1032 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[37110] Golgi associated, gamma adaptin ear containing, arf bind-

ing protein 2 (GGA2, Accession NP_619581.1) is another GAM1032 target gene, herein designated TARGET GENE. GGA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE, designated SEQ ID:3682, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37111] Another function of GAM1032 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[37112] Glucocorticoid induced transcript 1 (GLCCI1, Accession XP_166529.2) is another GAM1032 target gene, herein designated TARGET GENE. GLCCI1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLCCI1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GLCCI1 BINDING SITE, designated SEQ ID:15598, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37113] Another function of GAM1032 is therefore inhibition of Glucocorticoid induced transcript 1 (GLCCI1, Accession XP_166529.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLCCI1.

[37114] Glucocorticoid modulatory element binding protein 2 (GMEB2, Accession NP_036516.1) is another GAM1032 target gene, herein designated TARGET GENE. GMEB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GMEB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GMEB2 BINDING SITE, designated SEQ ID:1427, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37115] Another function of GAM1032 is therefore inhibition of Glucocorticoid modulatory element binding protein 2

(GMEB2, Accession NP_036516.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GMEB2.

[37116] Guanine nucleotide binding protein (g protein), alpha 11 (gq class) (GNA11, Accession NP_002058.1) is another GAM1032 target gene, herein designated TARGET GENE. GNA11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNA11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNA11 BINDING SITE, designated SEQ ID:10253, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37117] Another function of GAM1032 is therefore inhibition of Guanine nucleotide binding protein (g protein), alpha 11 (gq class) (GNA11, Accession NP_002058.1), a gene which acts as an activator of phospholipase c. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNA11.

[37118] The function of GNA11 has been established by previous studies. Strathmann and Simon (1991) described the

Gna11 gene in the mouse. The human gene was cloned by Jiang et al. (1991) and found to be 359 amino acids long. Mouse Gna11 and Gna15 (OMIM Ref. No. 139314) are tandemly duplicated in a head- to- tail array. Davignon et al. (1996) showed that the upstream gene, Gna11, is ubiquitously expressed, whereas expression of the downstream gene, Gna15, is restricted to hematopoietic cells. There was no evidence for alternative splicing within the coding sequence of either gene.

[37119] Animal model experiments lend further support to the function of GNA11. Using gene targeting, Offermanns et al. (1998) generated Gna11- deficient mice that were viable and fertile with no apparent behavioral or morphologic defects. They bred Gnaq (OMIM Ref. No. 600998)-deficient mice with Gna11- deficient mice and observed gene dosage effects between Gnaq and Gna11. Embryos completely lacking both genes died in utero with heart malformations. Mice inheriting a single copy of either gene died within hours of birth with craniofacial and/or cardiac defects. Offermanns et al. (1998) concluded that at least 2 active alleles of these genes are required for extrauterine life. Genetic, morphologic, and pharmacologic analyses of intercross offspring inheriting different com-

binations of these 2 mutations indicated that Gnaq and Gna11 have overlapping functions in embryonic cardiomyocyte proliferation and craniofacial development.

[37120] It is appreciated that the abovementioned animal model for GNA11 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[37121] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[37122] Offermanns, S.; Zhao, L.- P.; Gohla, A.; Sarosi, I.; Simon, M. I.; Wilkie, T. M. : Embryonic cardiomyocyte hypoplasia and craniofacial defects in G- alpha- q/G- alpha- 11- mutant mice. EMBO J. 17: 4304- 4312, 1998. ; and

[37123] Strathmann, M. P.; Simon, M. I. : G- alpha- 12 and G- alpha- 13 subunits define a fourth class of G protein alpha subunits. Proc. Nat. Acad. Sci. 88: 5582- 5586, 1991.

[37124] Further studies establishing the function and utilities of GNA11 are found in John Hopkins OMIM database record ID 139313, and in cited publications listed in Table 5, which are hereby incorporated by reference.Guanine nucleotide binding protein (g protein), alpha transducing activity polypeptide 1 (GNAT1, Accession NP_000163.2) is

another GAM1032 target gene, herein designated TARGET GENE. GNAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GNAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNAT1 BINDING SITE, designated SEQ ID:13082, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37125] Another function of GAM1032 is therefore inhibition of Guanine nucleotide binding protein (g protein), alpha transducing activity polypeptide 1 (GNAT1, Accession NP_000163.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNAT1.

[37126] Guanine nucleotide binding protein (g protein), alpha transducing activity polypeptide 1 (GNAT1, Accession NP_653082.1) is another GAM1032 target gene, herein designated TARGET GENE. GNAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GNAT1, corresponding to a target binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNAT1 BINDING SITE, designated SEQ ID:13082, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37127] Another function of GAM1032 is therefore inhibition of Guanine nucleotide binding protein (g protein), alpha transducing activity polypeptide 1 (GNAT1, Accession NP_653082.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNAT1.

[37128] Guanylate cyclase 2c (heat stable enterotoxin receptor) (GUCY2C, Accession NP_004954.1) is another GAM1032 target gene, herein designated TARGET GENE. GUCY2C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GUCY2C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GUCY2C BINDING SITE, designated SEQ ID:9622, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37129] Another function of GAM1032 is therefore inhibition of

Guanylate cyclase 2c (heat stable enterotoxin receptor) (GUCY2C, Accession NP_004954.1), a gene which is a receptor for the e.coli heat- stable enterotoxin and guanylate cyclase activated by the endogenous peptide guanylin. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GUCY2C.

[37130] The function of GUCY2C has been established by previous studies. Mann et al. (1996) described guanylyl cyclase C (called GC- C by them) as a transmembrane receptor expressed primarily in the intestine that regulates chloride secretion via the cystic fibrosis transmembrane conductance regulator (OMIM Ref. No. 602421). Binding of GC- C to either the endogenous peptide guanylin (OMIM Ref. No. 139392) or the bacterially derived heat- stable enterotoxin STa, results in increased levels of cGMP and the stimulation of water and chloride secretion. In the case of exposure to STa, this leads to debilitating secretory diarrhea. From a human colonic cell line, Singh et al. (1991) isolated a cDNA whose predicted amino acid sequence is 81% homologous to the GC- C intestinal enterotoxin STa receptor in rat. After transient transfection of COS- 7 cells with the human cDNA, the investigators observed a con-

centration- dependent response to STa in transfected cells as measured by intracellular cGMP accumulation. They referred to this human STa receptor as STaR. Similarly, de Sauvage et al. (1991) identified a human cDNA encoding an STa receptor. The receptor has an extracellular ligand-binding domain and a cytoplasmic guanylyl cyclase domain, as do members of the natriuretic peptide receptor family. They showed that stable mammalian cell lines overexpressing the STa receptor bind radioiodinated STa (with a K(d) in the nanomolar range) and exhibit a ligand-induced increase in the cellular cGMP level

[37131]

[37132] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[37133] Mann, E. A.; Swenson, E. S.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Taguchi, T.; Testa, J. R.; Giannella, R. A. : Localization of the guanylyl cyclase C gene to mouse chromosome 6 and human chromosome 12p12. Genomics 34: 265- 267, 1996. ; and

[37134] de Sauvage, F. J.; Camerato, T. R.; Goeddel, D. V. : Primary structure and functional expression of the human receptor for Escherichia coli heat- stable enterotoxin. J. Biol. Chem.

266: 1.

[37135] Further studies establishing the function and utilities of GUCY2C are found in John Hopkins OMIM database record ID 601330, and in cited publications listed in Table 5, which are hereby incorporated by reference.H63 (Accession NP_816929.1) is another GAM1032 target gene, herein designated TARGET GENE. H63 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H63, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H63 BINDING SITE, designated SEQ ID:3048, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37136] Another function of GAM1032 is therefore inhibition of H63 (Accession NP_816929.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H63.

[37137] H63 (Accession NP_612432.2) is another GAM1032 target gene, herein designated TARGET GENE. H63 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H63,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H63 BINDING SITE, designated SEQ ID:3048, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37138] Another function of GAM1032 is therefore inhibition of H63 (Accession NP_612432.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H63.

[37139] Hyaluronan synthase 1 (HAS1, Accession NP_001514.1) is another GAM1032 target gene, herein designated TARGET GENE. HAS1 BINDING SITE1 and HAS1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HAS1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HAS1 BINDING SITE1 and HAS1 BINDING SITE2, designated SEQ ID:16698 and SEQ ID:3709 respectively, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37140] Another function of GAM1032 is therefore inhibition of

Hyaluronan synthase 1 (HAS1, Accession NP_001514.1), a gene which plays a role in hyaluronan/hyaluronic acid (ha) synthesis. also able to catalyze the synthesis of chito-oligosaccharide depending on the substrate. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAS1.

[37141] The function of HAS1 has been established by previous studies. Hyaluronan or hyaluronic acid (HA) is a high molecular weight unbranched polysaccharide, synthesized by a wide variety of organisms from bacteria to mammals, and found in the extracellular matrix. It consists of alter-nating glucuronic acid and N- acetylglucosamine residues that are linked by beta- 1- 3 and beta- 1- 4 glycosidic bonds. Watanabe and Yamaguchi (1996) noted that unlike other glycosaminoglycans, HA synthesis occurs at the in-ner surface of the plasma membrane and the chains are extruded through pore- like structures into the extracel-lular space. Hyaluronan serves a variety of functions, in-cluding space filling, lubrication of joints, and provision of a matrix through which cells can migrate. The interaction of HA with the leukocyte receptor CD44 (OMIM Ref. No. 107269) is important in tissue- specific homing by leuko-

cytes and overexpression of HA receptors has been correlated with tumor metastasis (Hall et al., 1995). Itano and Kimata (1996) used a transient expression system in a mouse mammary carcinoma cell line that lacks HA expression to isolate cDNA clones capable of restoring HA synthesis activity. The mouse cDNA sequence identified predicted a 583- amino acid protein with similarity to the Xenopus DG42 protein and a bacterial HA synthase.

[37142]

[37143] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[37144] Watanabe, K.; Yamaguchi, Y. : Molecular identification of a putative human hyaluronan synthase. J. Biol. Chem. 271: 22945- 22948, 1996. ; and

[37145] Itano, N.; Kimata, K. : Expression cloning and molecular characterization of HAS protein, a eukaryotic hyaluronan synthase. J. Biol. Chem. 271: 9875- 9878, 1996.

[37146] Further studies establishing the function and utilities of HAS1 are found in John Hopkins OMIM database record ID 601463, and in cited publications listed in Table 5, which are hereby incorporated by reference.HCNGP (Accession NP_037392.1) is another GAM1032 target gene, herein

designated TARGET GENE. HCNGP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HCNGP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HCNGP BINDING SITE, designated SEQ ID:18142, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37147] Another function of GAM1032 is therefore inhibition of HCNGP (Accession NP_037392.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCNGP.

[37148] HES2 (Accession XP_290879.1) is another GAM1032 target gene, herein designated TARGET GENE. HES2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HES2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HES2 BINDING SITE, designated SEQ ID:16768, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37149] Another function of GAM1032 is therefore inhibition of HES2 (Accession XP_290879.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HES2.

[37150] Human immunodeficiency virus type i enhancer binding protein 1 (HIVEP1, Accession NP_002105.1) is another GAM1032 target gene, herein designated TARGET GENE. HIVEP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HIVEP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIVEP1 BINDING SITE, designated SEQ ID:6005, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37151] Another function of GAM1032 is therefore inhibition of Human immunodeficiency virus type i enhancer binding protein 1 (HIVEP1, Accession NP_002105.1), a gene which specifically binds to the dna sequence 5'- gggactttcc- 3' which is found in the enhancer elements of numerous viral promoters such as those of sv40, cmv, or hiv1. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with HIVEP1.

[37152] The function of HIVEP1 has been established by previous studies. The sequence GGGACTTTCC is found in the enhancer elements of numerous viral promoters, including those of simian virus 40 (SV40), cytomegalovirus (CMV), and the human immunodeficiency virus (HIV). In addition, related sequences are found in the enhancer elements of a number of cellular promoters, including those of the class I major histocompatibility gene complex (OMIM Ref. No. 142800), the kappa immunoglobulin gene (OMIM Ref. No. 147200), the interleukin- 2 receptor gene (OMIM Ref. No. 147730), and the interferon- beta gene (OMIM Ref. No. 147640). Mutagenesis of these enhancer elements has indicated their role in the transcriptional regulation of both viral and cellular genes. Zinc finger protein- 40, a protein that binds to these sequences, has a molecular mass of 298 kD and contains 2 widely separated zinc finger binding domains, each of which binds to the same DNA sequence. This protein has variously been known as HIVEP1 (human immunodeficiency virus type 1 enhancer-binding protein- 1), MBP- 1 (major histocompatibility complex- binding protein- 1), and PRDII- BF1 (positive regulatory domain II- binding factor 1). (See HIVEP2,

143054.) By Southern analysis of a panel of mouse/human somatic cell hybrid DNAs and by in situ hybridization, Gaynor et al. (1991) mapped the HIVEP1 gene to 6p24-p22.3. In the course of fine mapping of 39 ESTs on 6p24-p23, Olavesen et al. (1997) confirmed the assignment of ZNF40 to this region.

[37153]

[37154] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[37155] Gaynor, R. B.; Muchardt, C.; Diep, A.; Mohandas, T. K.; Sparkes, R. S.; Lusis, A. J. : Localization of the zinc finger DNA- binding protein HIV- EP1/MBP- 1/PRDII- BF1 to human chromosome 6p22.3- p24. Genomics 9: 758- 761, 1991. ; and

[37156] Olavesen, M. G.; Bentley, E.; Mason, R. V. F.; Stephens, R. J.; Ragoussis, J. : Fine mapping of 39 ESTs on human chromosome 6p23- p25. Genomics 46: 303- 306, 1997.

[37157] Further studies establishing the function and utilities of HIVEP1 are found in John Hopkins OMIM database record ID 194540, and in cited publications listed in Table 5, which are hereby incorporated by reference.Holocarboxylase synthetase

(biotin-[proprionyl-coenzyme a-carboxylase (atp-hydrolysing)] ligase) (HLCS, Accession NP_000402.2) is another GAM1032 target gene, herein designated TARGET GENE. HLCS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HLCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:4592, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37158] Another function of GAM1032 is therefore inhibition of Holocarboxylase synthetase (biotin-[proprionyl-coenzyme a-carboxylase (atp-hydrolysing)] ligase) (HLCS, Accession NP_000402.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLCS.

[37159] Heat shock 90kda protein 1, alpha-like 3 (HSPCAL3, Accession XP_084514.3) is another GAM1032 target gene, herein designated TARGET GENE. HSPCAL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSPCAL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPCAL3 BINDING SITE, designated SEQ ID:1703, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37160] Another function of GAM1032 is therefore inhibition of Heat shock 90kda protein 1, alpha-like 3 (HSPCAL3, Accession XP_084514.3) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPCAL3.

[37161] Interleukin 18 receptor 1 (IL18R1, Accession NP_003846.1) is another GAM1032 target gene, herein designated TARGET GENE. IL18R1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL18R1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL18R1 BINDING SITE, designated SEQ ID:17153, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37162] Another function of GAM1032 is therefore inhibition of Interleukin 18 receptor 1 (IL18R1, Accession

NP_003846.1), a gene which is required for dorsal- ventral embryonic polarity and promotes heterophilic cellular adhesion. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL18R1.

[37163] The function of IL18R1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM190.1.Internexin neuronal intermediate filament protein, alpha (INA, Accession NP_116116.1) is another GAM1032 target gene, herein designated TARGET GENE. INA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INA BINDING SITE, designated SEQ ID:2428, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37164] Another function of GAM1032 is therefore inhibition of Internexin neuronal intermediate filament protein, alpha (INA, Accession NP_116116.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with INA.

[37165] Inositol polyphosphate-5-phosphatase, 145kda (INPP5D, Accession NP_005532.1) is another GAM1032 target gene, herein designated TARGET GENE. INPP5D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INPP5D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INPP5D BINDING SITE, designated SEQ ID:8687, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37166] Another function of GAM1032 is therefore inhibition of Inositol polyphosphate-5-phosphatase, 145kda (INPP5D, Accession NP_005532.1), a gene which hydrolyzes Ins(1,3,4,5)P4 and PtdIns(3,4,5)P3; contains an SH2- domain and therefore may be associated with Severe osteoporosis. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Severe osteoporosis, and of other diseases and clinical conditions associated with INPP5D.

[37167] The function of INPP5D and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM347.1.Il2-inducible t-cell kinase (ITK, Accession NP_005537.3) is another GAM1032 target gene, herein designated TARGET GENE. ITK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITK BINDING SITE, designated SEQ ID:978, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37168] Another function of GAM1032 is therefore inhibition of Il2-inducible t-cell kinase (ITK, Accession NP_005537.3), a gene which plays a role in t cell proliferation and differentiation. and therefore may be associated with Myelodysplastic syndrome. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Myelodysplastic syndrome, and of other diseases and clinical conditions associated with ITK.

[37169] The function of ITK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.Kv channel interacting protein 2 (KCNIP2, Ac-

cession NP_775464.1) is another GAM1032 target gene, herein designated TARGET GENE. KCNIP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNIP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNIP2 BINDING SITE, designated SEQ ID:16093, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37170] Another function of GAM1032 is therefore inhibition of Kv channel interacting protein 2 (KCNIP2, Accession NP_775464.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNIP2.

[37171] KIAA0329 (Accession NP_055659.1) is another GAM1032 target gene, herein designated TARGET GENE. KIAA0329 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0329 BINDING SITE, designated SEQ ID:5874, to the

nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37172] Another function of GAM1032 is therefore inhibition of KIAA0329 (Accession NP_055659.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0329.

[37173] KIAA0377 (Accession NP_055474.1) is another GAM1032 target gene, herein designated TARGET GENE. KIAA0377 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0377, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0377 BINDING SITE, designated SEQ ID:17827, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37174] Another function of GAM1032 is therefore inhibition of KIAA0377 (Accession NP_055474.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0377.

[37175] KIAA0459 (Accession XP_027862.1) is another GAM1032

target gene, herein designated TARGET GENE. KIAA0459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:8436, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37176] Another function of GAM1032 is therefore inhibition of KIAA0459 (Accession XP_027862.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459.

[37177] KIAA0694 (Accession XP_051970.2) is another GAM1032 target gene, herein designated TARGET GENE. KIAA0694 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0694, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0694 BINDING SITE, designated SEQ ID:10714, to the nucleotide sequence of GAM1032 RNA, herein designated

GAM RNA, also designated SEQ ID:303.

[37178] Another function of GAM1032 is therefore inhibition of KIAA0694 (Accession XP_051970.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0694.

[37179] KIAA1271 (Accession XP_045472.1) is another GAM1032 target gene, herein designated TARGET GENE. KIAA1271 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1271, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1271 BINDING SITE, designated SEQ ID:12182, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37180] Another function of GAM1032 is therefore inhibition of KIAA1271 (Accession XP_045472.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1271.

[37181] KIAA1465 (Accession XP_027396.4) is another GAM1032 target gene, herein designated TARGET GENE. KIAA1465

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1465, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1465 BINDING SITE, designated SEQ ID:18401, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37182] Another function of GAM1032 is therefore inhibition of KIAA1465 (Accession XP_027396.4) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1465.

[37183] KIAA1718 (Accession XP_034823.5) is another GAM1032 target gene, herein designated TARGET GENE. KIAA1718 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1718, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1718 BINDING SITE, designated SEQ ID:8259, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37184] Another function of GAM1032 is therefore inhibition of KIAA1718 (Accession XP_034823.5) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1718.

[37185] KIAA1879 (Accession XP_056635.1) is another GAM1032 target gene, herein designated TARGET GENE. KIAA1879 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1879, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1879 BINDING SITE, designated SEQ ID:16159, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37186] Another function of GAM1032 is therefore inhibition of KIAA1879 (Accession XP_056635.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1879.

[37187] KIF25 (Accession NP_085118.1) is another GAM1032 target gene, herein designated TARGET GENE. KIF25 BINDING SITE is a target binding site found in the 5` untranslated

region of multiple transcripts of mRNA encoded by KIF25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIF25 BINDING SITE, designated SEQ ID:4138, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37188] Another function of GAM1032 is therefore inhibition of KIF25 (Accession NP_085118.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF25.

[37189] KIF25 (Accession NP_005346.2) is another GAM1032 target gene, herein designated TARGET GENE. KIF25 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by KIF25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIF25 BINDING SITE, designated SEQ ID:4138, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37190] Another function of GAM1032 is therefore inhibition of KIF25 (Accession NP_005346.2) . Accordingly, utilities of

GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF25.

[37191] Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1 (KIR2DL1, Accession NP_055033.1) is another GAM1032 target gene, herein designated TARGET GENE. KIR2DL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIR2DL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIR2DL1 BINDING SITE, designated SEQ ID:7645, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37192] Another function of GAM1032 is therefore inhibition of Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1 (KIR2DL1, Accession NP_055033.1), a gene which inhibits the activity of nk cells thus preventing cell lysis. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIR2DL1.

[37193] The function of KIR2DL1 has been established by previous studies. The existence of human inhibitory natural killer

(NK) cell receptors for MHC class I molecules (now designated killer cell Ig- like receptors, or KIRs), was inferred from the observation that NK cells killed HLA class I- deficient cell lines (Ljunggren and Karre, 1990). The inhibition could be disrupted by antibodies against membrane glycoproteins on NK cells that recognized HLA- A and HLA-C (OMIM Ref. No. 142840). Complementary DNA cloning of the receptors revealed a family of genes, designated the killer cell inhibitory receptors. Inhibitory KIRs are found in 3 distinct isoforms. KIRs that recognize HLA- C are usually monomeric glycoproteins of about 58 kD with 2 immunoglobulin- like domains (KIR2D). KIRs that are reactive with HLA- B are approximately 70- kD monomeric glycoproteins with 3 Ig- like domains (KIR3D). KIRs that are reactive with HLA- A also possess 3 extracellular Ig- like domains but are expressed as 2, approximately 70- kD disulfide- linked homodimer subunits. Molecular analysis of KIRs and other inhibitory receptors (e.g., LILRB1, 604811) has revealed a common cytoplasmic sequence (I/VxYxxL/V) called an ITIM (immunoreceptor tyrosine- based inhibitory motif). KIRs with a long cytoplasmic tail have 2 ITIMs (OMIM Ref. No. KIR2DL). Upon MHC I engagement and tyrosine phospho-

rylation of the ITIM, intracellular protein tyrosine phosphatases such as SHP1 (PTPN6; 176883) are recruited, and an inhibitory signal cascade ensues. Other receptors, of about 50 kD (p50s), with short cytoplasmic regions (KIR2DS and KIR3DS) without ITIMs have transmembrane regions containing a charged amino acid and initiate stimulatory cascades by association with DAP12 (TYROBP; 604142), a membrane receptor expressing ITAM (immunoreceptor tyrosine- based activation motif). For reviews of KIRs and other NK receptors, see Lanier (1997, 1998, 2000 KIR2D receptors are divided into 2 families based on their specificities for different HLA- C allotypes. KIR2DL1 has specificity for HLA- C alleles with asn77 and lys80, while KIR2DL2 (OMIM Ref. No. 604937) has specificity for HLA- C alleles with ser77 and asn80. Fan et al. (2001) described the crystal structure of KIR2DL1 and HLA- Cw4 at a resolution of 2.8 angstroms. They determined that met44 of KIR2DL1 is in a pocket that hosts, through both polar and hydrophobic interactions, lys80 of HLA- Cw4

[37194]

[37195] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[37196] Andre, P.; Biassoni, R.; Colonna, M.; Cosman, D.; Lanier, L. L.; Long, E. O.; Lopez- Botet, M.; Moretta, A.; Moretta, L.; Parham, P.; Trowsdale, J.; Vivier, E.; Wagtmann, N.; Wilson, M. J. : New nomenclature for MHC receptors. Nature Immun. 2: 661 only, 2001. ; and

[37197] Colonna, M.; Samaridis, J. : Cloning of immunoglobulin-superfamily members associated with HLA- C and HLA- B recognition by human natural killer cells. Science 268: 405- 408, 1995.

[37198] Further studies establishing the function and utilities of KIR2DL1 are found in John Hopkins OMIM database record ID 604936, and in cited publications listed in Table 5, which are hereby incorporated by reference.Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2 (KIR2DL2, Accession NP_055034.1) is another GAM1032 target gene, herein designated TARGET GENE. KIR2DL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIR2DL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIR2DL2 BINDING SITE, designated SEQ

ID:7645, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37199] Another function of GAM1032 is therefore inhibition of Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2 (KIR2DL2, Accession NP_055034.1), a gene which is a receptor on natural killer cells and inhibits the activity of nk cells thus preventing cell lysis. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIR2DL2.

[37200] The function of KIR2DL2 has been established by previous studies. background information on the KIR family of natural killer (NK) cell Ig- like receptors, see KIR2DL1 (OMIM Ref. No. 604936). By screening NK cells with a KIR2DL3 cDNA probe, Wagtmann et al. (1995) isolated a KIR2DL2 cDNA, which they called clone 43 (CL43), encoding a deduced 348- amino acid type I transmembrane protein. Sequence analysis revealed a structure similar to that described for KIR2DL1, with 2 extracellular C2- type Ig- like domains, a transmembrane domain, and a long cytoplasmic tail with 2 ITIMs (immunoreceptor tyrosine- based inhibitory motifs). Dohring et al. (1996) also identified KIR2DL2, which they termed NKAT6. By analysis of so-

matic cell hybrids, Colonna and Samaridis (1995) and Wagtmann et al. (1995) mapped the KIR gene family to chromosome 19

[37201]

[37202] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[37203] Dohring, C.; Samaridis, J.; Colonna, M. : Alternatively spliced forms of human killer inhibitory receptors. Immunogenetics 44: 227- 230, 1996. ; and

[37204] Wagtmann, N.; Biassoni, R.; Cantoni, C.; Verdiani, S.; Malnati, M. S.; Vitale, M.; Bottino, C.; Moretta, L.; Moretta, A.; Long, E. O. : Molecular clones of the p58 NK cell receptor reve.

[37205] Further studies establishing the function and utilities of KIR2DL2 are found in John Hopkins OMIM database record ID 604937, and in cited publications listed in Table 5, which are hereby incorporated by reference.LKAP (Accession NP_061954.1) is another GAM1032 target gene, herein designated TARGET GENE. LKAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LKAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LKAP BINDING SITE, designated SEQ ID:13514, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37206] Another function of GAM1032 is therefore inhibition of LKAP (Accession NP_061954.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LKAP.

[37207] Ligand of numb-protein x (LNX, Accession NP_116011.1) is another GAM1032 target gene, herein designated TARGET GENE. LNX BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LNX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LNX BINDING SITE, designated SEQ ID:3987, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37208] Another function of GAM1032 is therefore inhibition of Ligand of numb-protein x (LNX, Accession NP_116011.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with LNX.

[37209] LOC121498 (Accession XP_062669.7) is another GAM1032 target gene, herein designated TARGET GENE. LOC121498 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC121498, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC121498 BINDING SITE, designated SEQ ID:10999, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37210] Another function of GAM1032 is therefore inhibition of LOC121498 (Accession XP_062669.7) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121498.

[37211] LOC132870 (Accession XP_059608.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC132870 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC132870, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC132870 BINDING SITE, designated SEQ ID:17125, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37212] Another function of GAM1032 is therefore inhibition of LOC132870 (Accession XP_059608.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132870.

[37213] LOC143188 (Accession XP_096387.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC143188 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC143188, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143188 BINDING SITE, designated SEQ ID:11783, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37214] Another function of GAM1032 is therefore inhibition of LOC143188 (Accession XP_096387.1) . Accordingly, utili-

ties of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143188.

[37215] LOC146542 (Accession NP_660314.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC146542 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146542, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146542 BINDING SITE, designated SEQ ID:16407, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37216] Another function of GAM1032 is therefore inhibition of LOC146542 (Accession NP_660314.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146542.

[37217] LOC147622 (Accession XP_097255.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC147622 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC147622, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147622 BINDING SITE, designated SEQ ID:4440, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37218] Another function of GAM1032 is therefore inhibition of LOC147622 (Accession XP_097255.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147622.

[37219] LOC147791 (Accession XP_097293.2) is another GAM1032 target gene, herein designated TARGET GENE. LOC147791 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147791, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147791 BINDING SITE, designated SEQ ID:4967, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37220] Another function of GAM1032 is therefore inhibition of LOC147791 (Accession XP_097293.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147791.

[37221] LOC149271 (Accession XP_086475.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC149271 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149271, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149271 BINDING SITE, designated SEQ ID:5890, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37222] Another function of GAM1032 is therefore inhibition of LOC149271 (Accession XP_086475.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149271.

[37223] LOC149372 (Accession XP_086509.1) is another GAM1032 target gene, herein designated TARGET GENE.

LOC149372 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149372, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149372 BINDING SITE, designated SEQ ID:19078, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37224] Another function of GAM1032 is therefore inhibition of LOC149372 (Accession XP_086509.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149372.

[37225] LOC149386 (Accession XP_097631.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC149386 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149386, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149386 BINDING SITE, designated SEQ ID:6026, to the nucleotide sequence of

GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37226] Another function of GAM1032 is therefore inhibition of LOC149386 (Accession XP_097631.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149386.

[37227] LOC150166 (Accession XP_097824.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC150166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150166 BINDING SITE, designated SEQ ID:11388, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37228] Another function of GAM1032 is therefore inhibition of LOC150166 (Accession XP_097824.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150166.

[37229] LOC150225 (Accession XP_097870.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC150225 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150225, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150225 BINDING SITE, designated SEQ ID:18349, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37230] Another function of GAM1032 is therefore inhibition of LOC150225 (Accession XP_097870.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150225.

[37231] LOC150946 (Accession XP_097977.2) is another GAM1032 target gene, herein designated TARGET GENE. LOC150946 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150946, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC150946 BINDING SITE, designated SEQ ID:3747, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37232] Another function of GAM1032 is therefore inhibition of LOC150946 (Accession XP_097977.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150946.

[37233] LOC151162 (Accession XP_098012.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC151162 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151162, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151162 BINDING SITE, designated SEQ ID:17135, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37234] Another function of GAM1032 is therefore inhibition of LOC151162 (Accession XP_098012.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC151162.

[37235] LOC151647 (Accession XP_087261.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC151647 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151647, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151647 BINDING SITE, designated SEQ ID:13917, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37236] Another function of GAM1032 is therefore inhibition of LOC151647 (Accession XP_087261.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151647.

[37237] LOC152920 (Accession XP_087561.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC152920 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152920, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152920 BINDING SITE, designated SEQ ID:10090, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37238] Another function of GAM1032 is therefore inhibition of LOC152920 (Accession XP_087561.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152920.

[37239] LOC154184 (Accession XP_098488.2) is another GAM1032 target gene, herein designated TARGET GENE. LOC154184 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC154184, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154184 BINDING SITE, designated SEQ ID:3687, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37240] Another function of GAM1032 is therefore inhibition of

LOC154184 (Accession XP_098488.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154184.

[37241] LOC157273 (Accession XP_098743.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC157273 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC157273, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157273 BINDING SITE, designated SEQ ID:626, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37242] Another function of GAM1032 is therefore inhibition of LOC157273 (Accession XP_098743.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157273.

[37243] LOC157381 (Accession XP_098754.5) is another GAM1032 target gene, herein designated TARGET GENE. LOC157381 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC157381, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157381 BINDING SITE, designated SEQ ID:15936, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37244] Another function of GAM1032 is therefore inhibition of LOC157381 (Accession XP_098754.5) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157381.

[37245] LOC157627 (Accession XP_088347.2) is another GAM1032 target gene, herein designated TARGET GENE. LOC157627 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC157627, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157627 BINDING SITE, designated SEQ ID:17425, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:303.

[37246] Another function of GAM1032 is therefore inhibition of LOC157627 (Accession XP_088347.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157627.

[37247] LOC157653 (Accession XP_088353.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC157653 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC157653, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157653 BINDING SITE, designated SEQ ID:3788, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37248] Another function of GAM1032 is therefore inhibition of LOC157653 (Accession XP_088353.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157653.

[37249] LOC163182 (Accession XP_092058.1) is another

GAM1032 target gene, herein designated TARGET GENE. LOC163182 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC163182, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163182 BINDING SITE, designated SEQ ID:3542, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37250] Another function of GAM1032 is therefore inhibition of LOC163182 (Accession XP_092058.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163182.

[37251] LOC163223 (Accession XP_092087.3) is another GAM1032 target gene, herein designated TARGET GENE. LOC163223 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC163223, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163223 BINDING SITE, desig-

nated SEQ ID:12269, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37252] Another function of GAM1032 is therefore inhibition of LOC163223 (Accession XP_092087.3) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163223.

[37253] LOC170106 (Accession XP_093106.2) is another GAM1032 target gene, herein designated TARGET GENE. LOC170106 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC170106, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC170106 BINDING SITE, designated SEQ ID:17459, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37254] Another function of GAM1032 is therefore inhibition of LOC170106 (Accession XP_093106.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC170106.

[37255] LOC200230 (Accession XP_114166.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC200230 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200230, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200230 BINDING SITE, designated SEQ ID:18830, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37256] Another function of GAM1032 is therefore inhibition of LOC200230 (Accession XP_114166.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200230.

[37257] LOC201292 (Accession NP_775818.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC201292 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201292, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201292 BINDING SITE, designated SEQ ID:8558, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37258] Another function of GAM1032 is therefore inhibition of LOC201292 (Accession NP_775818.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201292.

[37259] LOC201868 (Accession XP_114393.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC201868 BINDING SITE1 and LOC201868 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC201868, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201868 BINDING SITE1 and LOC201868 BINDING SITE2, designated SEQ ID:5434 and SEQ ID:13599 respectively, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37260] Another function of GAM1032 is therefore inhibition of

LOC201868 (Accession XP_114393.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201868.

[37261] LOC221922 (Accession XP_166555.2) is another GAM1032 target gene, herein designated TARGET GENE. LOC221922 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221922 BINDING SITE, designated SEQ ID:15583, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37262] Another function of GAM1032 is therefore inhibition of LOC221922 (Accession XP_166555.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221922.

[37263] LOC253805 (Accession XP_172854.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC253805 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC253805, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253805 BINDING SITE, designated SEQ ID:4330, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37264] Another function of GAM1032 is therefore inhibition of LOC253805 (Accession XP_172854.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253805.

[37265] LOC283442 (Accession XP_211037.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC283442 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283442 BINDING SITE, designated SEQ ID:5721, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:303.

[37266] Another function of GAM1032 is therefore inhibition of LOC283442 (Accession XP_211037.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283442.

[37267] LOC283624 (Accession XP_211126.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC283624 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283624, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283624 BINDING SITE, designated SEQ ID:953, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37268] Another function of GAM1032 is therefore inhibition of LOC283624 (Accession XP_211126.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283624.

[37269] LOC283741 (Accession XP_208115.1) is another

GAM1032 target gene, herein designated TARGET GENE. LOC283741 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283741, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283741 BINDING SITE, designated SEQ ID:12978, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37270] Another function of GAM1032 is therefore inhibition of LOC283741 (Accession XP_208115.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283741.

[37271] LOC283753 (Accession XP_208821.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC283753 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283753, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283753 BINDING SITE, desig-

nated SEQ ID:8981, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37272] Another function of GAM1032 is therefore inhibition of LOC283753 (Accession XP_208821.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283753.

[37273] LOC283801 (Accession XP_208122.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC283801 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283801, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283801 BINDING SITE, designated SEQ ID:15824, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37274] Another function of GAM1032 is therefore inhibition of LOC283801 (Accession XP_208122.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283801.

[37275] LOC284173 (Accession XP_211362.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC284173 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284173, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284173 BINDING SITE, designated SEQ ID:19059, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37276] Another function of GAM1032 is therefore inhibition of LOC284173 (Accession XP_211362.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284173.

[37277] LOC284196 (Accession XP_209067.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC284196 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284196, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284196 BINDING SITE, designated SEQ ID:15363, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37278] Another function of GAM1032 is therefore inhibition of LOC284196 (Accession XP_209067.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284196.

[37279] LOC284266 (Accession XP_211403.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC284266 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284266, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284266 BINDING SITE, designated SEQ ID:17603, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37280] Another function of GAM1032 is therefore inhibition of LOC284266 (Accession XP_211403.1) . Accordingly, utili-

ties of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284266.

[37281] LOC284280 (Accession XP_211416.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC284280 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284280, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284280 BINDING SITE, designated SEQ ID:6856, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37282] Another function of GAM1032 is therefore inhibition of LOC284280 (Accession XP_211416.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284280.

[37283] LOC284542 (Accession XP_209254.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC284542 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC284542, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284542 BINDING SITE, designated SEQ ID:843, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37284] Another function of GAM1032 is therefore inhibition of LOC284542 (Accession XP_209254.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284542.

[37285] LOC284595 (Accession XP_209280.3) is another GAM1032 target gene, herein designated TARGET GENE. LOC284595 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284595, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284595 BINDING SITE, designated SEQ ID:8588, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37286] Another function of GAM1032 is therefore inhibition of LOC284595 (Accession XP_209280.3) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284595.

[37287] LOC284751 (Accession XP_211622.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC284751 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284751, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284751 BINDING SITE, designated SEQ ID:10782, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37288] Another function of GAM1032 is therefore inhibition of LOC284751 (Accession XP_211622.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284751.

[37289] LOC284829 (Accession XP_211645.1) is another GAM1032 target gene, herein designated TARGET GENE.

LOC284829 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284829, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284829 BINDING SITE, designated SEQ ID:12531, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37290] Another function of GAM1032 is therefore inhibition of LOC284829 (Accession XP_211645.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284829.

[37291] LOC284865 (Accession XP_211672.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC284865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284865 BINDING SITE, designated SEQ ID:7677, to the nucleotide sequence of

GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37292] Another function of GAM1032 is therefore inhibition of LOC284865 (Accession XP_211672.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284865.

[37293] LOC284965 (Accession XP_209425.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC284965 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284965, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284965 BINDING SITE, designated SEQ ID:8588, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37294] Another function of GAM1032 is therefore inhibition of LOC284965 (Accession XP_209425.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284965.

[37295] LOC284975 (Accession XP_211711.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC284975 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284975 BINDING SITE, designated SEQ ID:7383, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37296] Another function of GAM1032 is therefore inhibition of LOC284975 (Accession XP_211711.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284975.

[37297] LOC285123 (Accession XP_211773.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC285123 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC285123 BINDING SITE, designated SEQ ID:5205, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37298] Another function of GAM1032 is therefore inhibition of LOC285123 (Accession XP_211773.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285123.

[37299] LOC285409 (Accession XP_209600.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC285409 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285409, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285409 BINDING SITE, designated SEQ ID:5936, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37300] Another function of GAM1032 is therefore inhibition of LOC285409 (Accession XP_209600.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285409.

[37301] LOC285442 (Accession XP_208320.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC285442 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285442 BINDING SITE, designated SEQ ID:16068, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37302] Another function of GAM1032 is therefore inhibition of LOC285442 (Accession XP_208320.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285442.

[37303] LOC285692 (Accession XP_211984.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC285692 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285692, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285692 BINDING SITE, designated SEQ ID:4966, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37304] Another function of GAM1032 is therefore inhibition of LOC285692 (Accession XP_211984.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285692.

[37305] LOC285735 (Accession XP_212002.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC285735 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285735 BINDING SITE, designated SEQ ID:4051, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37306] Another function of GAM1032 is therefore inhibition of

LOC285735 (Accession XP_212002.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285735.

[37307] LOC285819 (Accession XP_212053.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC285819 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285819, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285819 BINDING SITE, designated SEQ ID:16977, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37308] Another function of GAM1032 is therefore inhibition of LOC285819 (Accession XP_212053.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285819.

[37309] LOC285936 (Accession XP_209834.2) is another GAM1032 target gene, herein designated TARGET GENE. LOC285936 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC285936, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285936 BINDING SITE, designated SEQ ID:3314, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37310] Another function of GAM1032 is therefore inhibition of LOC285936 (Accession XP_209834.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285936.

[37311] LOC286101 (Accession XP_209902.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC286101 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286101 BINDING SITE, designated SEQ ID:7174, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:303.

[37312] Another function of GAM1032 is therefore inhibition of LOC286101 (Accession XP_209902.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286101.

[37313] LOC286135 (Accession XP_212196.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC286135 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286135 BINDING SITE, designated SEQ ID:5795, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37314] Another function of GAM1032 is therefore inhibition of LOC286135 (Accession XP_212196.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286135.

[37315] LOC286221 (Accession XP_212233.1) is another

GAM1032 target gene, herein designated TARGET GENE. LOC286221 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286221, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286221 BINDING SITE, designated SEQ ID:5769, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37316] Another function of GAM1032 is therefore inhibition of LOC286221 (Accession XP_212233.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286221.

[37317] LOC286374 (Accession XP_212293.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC286374 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286374, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286374 BINDING SITE, desig-

nated SEQ ID:14940, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37318] Another function of GAM1032 is therefore inhibition of LOC286374 (Accession XP_212293.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286374.

[37319] LOC286545 (Accession XP_208450.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC286545 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286545, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286545 BINDING SITE, designated SEQ ID:2448, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37320] Another function of GAM1032 is therefore inhibition of LOC286545 (Accession XP_208450.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC286545.

[37321] LOC338609 (Accession XP_294664.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC338609 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338609, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338609 BINDING SITE, designated SEQ ID:15446, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37322] Another function of GAM1032 is therefore inhibition of LOC338609 (Accession XP_294664.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338609.

[37323] LOC338862 (Accession XP_290601.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC338862 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338862, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338862 BINDING SITE, designated SEQ ID:3752, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37324] Another function of GAM1032 is therefore inhibition of LOC338862 (Accession XP_290601.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338862.

[37325] LOC339025 (Accession XP_294778.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC339025 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339025, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339025 BINDING SITE, designated SEQ ID:10038, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37326] Another function of GAM1032 is therefore inhibition of LOC339025 (Accession XP_294778.1) . Accordingly, utili-

ties of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339025.

[37327] LOC339062 (Accession XP_294795.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC339062 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339062, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339062 BINDING SITE, designated SEQ ID:17771, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37328] Another function of GAM1032 is therefore inhibition of LOC339062 (Accession XP_294795.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339062.

[37329] LOC339502 (Accession XP_294983.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC339502 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC339502, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339502 BINDING SITE, designated SEQ ID:20113, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37330] Another function of GAM1032 is therefore inhibition of LOC339502 (Accession XP_294983.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339502.

[37331] LOC339581 (Accession XP_293116.2) is another GAM1032 target gene, herein designated TARGET GENE. LOC339581 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339581, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339581 BINDING SITE, designated SEQ ID:9113, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37332] Another function of GAM1032 is therefore inhibition of LOC339581 (Accession XP_293116.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339581.

[37333] LOC339663 (Accession XP_295028.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC339663 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339663 BINDING SITE, designated SEQ ID:14951, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37334] Another function of GAM1032 is therefore inhibition of LOC339663 (Accession XP_295028.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339663.

[37335] LOC340064 (Accession XP_295144.1) is another GAM1032 target gene, herein designated TARGET GENE.

LOC340064 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340064, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340064 BINDING SITE, designated SEQ ID:3820, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37336] Another function of GAM1032 is therefore inhibition of LOC340064 (Accession XP_295144.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340064.

[37337] LOC340323 (Accession XP_291236.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC340323 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340323 BINDING SITE, designated SEQ ID:5378, to the nucleotide sequence of

GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37338] Another function of GAM1032 is therefore inhibition of LOC340323 (Accession XP_291236.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340323.

[37339] LOC340428 (Accession XP_290420.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC340428 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340428, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340428 BINDING SITE, designated SEQ ID:6280, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37340] Another function of GAM1032 is therefore inhibition of LOC340428 (Accession XP_290420.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340428.

[37341] LOC344360 (Accession XP_297561.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC344360 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC344360, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC344360 BINDING SITE, designated SEQ ID:15185, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37342] Another function of GAM1032 is therefore inhibition of LOC344360 (Accession XP_297561.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC344360.

[37343] LOC344563 (Accession XP_297716.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC344563 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC344563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC344563 BINDING SITE, designated SEQ ID:676, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37344] Another function of GAM1032 is therefore inhibition of LOC344563 (Accession XP_297716.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC344563.

[37345] LOC347240 (Accession XP_294563.2) is another GAM1032 target gene, herein designated TARGET GENE. LOC347240 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC347240, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347240 BINDING SITE, designated SEQ ID:17210, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37346] Another function of GAM1032 is therefore inhibition of LOC347240 (Accession XP_294563.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC347240.

[37347] LOC347853 (Accession XP_300546.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC347853 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC347853, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347853 BINDING SITE, designated SEQ ID:8070, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37348] Another function of GAM1032 is therefore inhibition of LOC347853 (Accession XP_300546.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347853.

[37349] LOC347905 (Accession XP_302624.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC347905 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347905, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347905 BINDING SITE, designated SEQ ID:2888, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37350] Another function of GAM1032 is therefore inhibition of LOC347905 (Accession XP_302624.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347905.

[37351] LOC347921 (Accession XP_300275.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC347921 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347921, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347921 BINDING SITE, designated SEQ ID:10678, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37352] Another function of GAM1032 is therefore inhibition of

LOC347921 (Accession XP_300275.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347921.

[37353] LOC348378 (Accession XP_300723.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC348378 BINDING SITE1 and LOC348378 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348378, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348378 BINDING SITE1 and LOC348378 BINDING SITE2, designated SEQ ID:10330 and SEQ ID:6570 respectively, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37354] Another function of GAM1032 is therefore inhibition of LOC348378 (Accession XP_300723.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348378.

[37355] LOC348454 (Accession XP_290909.1) is another GAM1032 target gene, herein designated TARGET GENE.

LOC348454 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348454, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348454 BINDING SITE, designated SEQ ID:14041, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37356] Another function of GAM1032 is therefore inhibition of LOC348454 (Accession XP_290909.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348454.

[37357] LOC348504 (Accession XP_300769.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC348504 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348504, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348504 BINDING SITE, designated SEQ ID:5434, to the nucleotide sequence of

GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37358] Another function of GAM1032 is therefore inhibition of LOC348504 (Accession XP_300769.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348504.

[37359] LOC348529 (Accession XP_302813.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC348529 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348529, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348529 BINDING SITE, designated SEQ ID:3393, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37360] Another function of GAM1032 is therefore inhibition of LOC348529 (Accession XP_302813.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348529.

[37361] LOC348701 (Accession XP_300810.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC348701 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348701, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348701 BINDING SITE, designated SEQ ID:5909, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37362] Another function of GAM1032 is therefore inhibition of LOC348701 (Accession XP_300810.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348701.

[37363] LOC348704 (Accession XP_302859.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC348704 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348704, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC348704 BINDING SITE, designated SEQ ID:1119, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37364] Another function of GAM1032 is therefore inhibition of LOC348704 (Accession XP_302859.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348704.

[37365] LOC348843 (Accession XP_302903.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC348843 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348843, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348843 BINDING SITE, designated SEQ ID:13599, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37366] Another function of GAM1032 is therefore inhibition of LOC348843 (Accession XP_302903.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348843.

[37367] LOC348929 (Accession XP_300881.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC348929 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348929, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348929 BINDING SITE, designated SEQ ID:3253, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37368] Another function of GAM1032 is therefore inhibition of LOC348929 (Accession XP_300881.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348929.

[37369] LOC349098 (Accession XP_300943.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC349098 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349098, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349098 BINDING SITE, designated SEQ ID:5378, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37370] Another function of GAM1032 is therefore inhibition of LOC349098 (Accession XP_300943.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349098.

[37371] LOC349303 (Accession XP_301018.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC349303 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349303, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349303 BINDING SITE, designated SEQ ID:9235, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37372] Another function of GAM1032 is therefore inhibition of

LOC349303 (Accession XP_301018.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349303.

[37373] LOC349315 (Accession XP_301025.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC349315 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349315, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349315 BINDING SITE, designated SEQ ID:9235, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37374] Another function of GAM1032 is therefore inhibition of LOC349315 (Accession XP_301025.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349315.

[37375] LOC349317 (Accession XP_301026.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC349317 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC349317, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349317 BINDING SITE, designated SEQ ID:15717, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37376] Another function of GAM1032 is therefore inhibition of LOC349317 (Accession XP_301026.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349317.

[37377] LOC349333 (Accession XP_301035.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC349333 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349333, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349333 BINDING SITE, designated SEQ ID:15717, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:303.

[37378] Another function of GAM1032 is therefore inhibition of LOC349333 (Accession XP_301035.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349333.

[37379] LOC349338 (Accession XP_301040.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC349338 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349338, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349338 BINDING SITE, designated SEQ ID:8588, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37380] Another function of GAM1032 is therefore inhibition of LOC349338 (Accession XP_301040.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349338.

[37381] LOC350448 (Accession XP_304096.1) is another

GAM1032 target gene, herein designated TARGET GENE. LOC350448 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC350448, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC350448 BINDING SITE, designated SEQ ID:10058, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37382] Another function of GAM1032 is therefore inhibition of LOC350448 (Accession XP_304096.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC350448.

[37383] LOC352386 (Accession XP_305612.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC352386 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC352386, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC352386 BINDING SITE, desig-

nated SEQ ID:4515, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37384] Another function of GAM1032 is therefore inhibition of LOC352386 (Accession XP_305612.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC352386.

[37385] LOC352691 (Accession XP_302538.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC352691 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC352691, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC352691 BINDING SITE, designated SEQ ID:17140, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37386] Another function of GAM1032 is therefore inhibition of LOC352691 (Accession XP_302538.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC352691.

[37387] LOC51333 (Accession NP_057727.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC51333 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51333, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51333 BINDING SITE, designated SEQ ID:8816, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37388] Another function of GAM1032 is therefore inhibition of LOC51333 (Accession NP_057727.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51333.

[37389] LOC90246 (Accession XP_030283.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC90246 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC90246, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

LOC90246 BINDING SITE, designated SEQ ID:4074, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37390] Another function of GAM1032 is therefore inhibition of LOC90246 (Accession XP_030283.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90246.

[37391] LOC90785 (Accession XP_034110.1) is another GAM1032 target gene, herein designated TARGET GENE. LOC90785 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90785, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90785 BINDING SITE, designated SEQ ID:13538, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37392] Another function of GAM1032 is therefore inhibition of LOC90785 (Accession XP_034110.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90785.

[37393] LOC91974 (Accession XP_041974.2) is another GAM1032 target gene, herein designated TARGET GENE. LOC91974 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91974, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91974 BINDING SITE, designated SEQ ID:16067, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37394] Another function of GAM1032 is therefore inhibition of LOC91974 (Accession XP_041974.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91974.

[37395] Lipin 2 (LPIN2, Accession NP_055461.1) is another GAM1032 target gene, herein designated TARGET GENE. LPIN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LPIN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LPIN2 BINDING SITE, designated SEQ ID:1006, to the nu-

cleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37396] Another function of GAM1032 is therefore inhibition of Lipin 2 (LPIN2, Accession NP_055461.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPIN2.

[37397] Leucine-rich repeats and immunoglobulin-like domains 1 (LRIG1, Accession NP_056356.1) is another GAM1032 target gene, herein designated TARGET GENE. LRIG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRIG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LRIG1 BINDING SITE, designated SEQ ID:2045, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37398] Another function of GAM1032 is therefore inhibition of Leucine-rich repeats and immunoglobulin-like domains 1 (LRIG1, Accession NP_056356.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRIG1.

[37399] Lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS, Accession NP_002331.2) is another GAM1032 target gene, herein designated TARGET GENE. LSS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LSS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LSS BINDING SITE, designated SEQ ID:18091, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37400] Another function of GAM1032 is therefore inhibition of Lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS, Accession NP_002331.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LSS.

[37401] Methyl-cpg binding domain protein 2 (MBD2, Accession NP_056647.1) is another GAM1032 target gene, herein designated TARGET GENE. MBD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MBD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of MBD2 BINDING SITE, designated SEQ ID:13083, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37402] Another function of GAM1032 is therefore inhibition of Methyl-cpg binding domain protein 2 (MBD2, Accession NP_056647.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBD2.

[37403] Melanoma cell adhesion molecule (MCAM, Accession NP_006491.1) is another GAM1032 target gene, herein designated TARGET GENE. MCAM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MCAM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCAM BINDING SITE, designated SEQ ID:16374, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37404] Another function of GAM1032 is therefore inhibition of Melanoma cell adhesion molecule (MCAM, Accession NP_006491.1) . Accordingly, utilities of GAM1032 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with MCAM.

[37405] MGC10200 (Accession NP_659497.1) is another GAM1032 target gene, herein designated TARGET GENE. MGC10200 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10200, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10200 BINDING SITE, designated SEQ ID:18523, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37406] Another function of GAM1032 is therefore inhibition of MGC10200 (Accession NP_659497.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10200.

[37407] MGC2574 (Accession NP_077003.1) is another GAM1032 target gene, herein designated TARGET GENE. MGC2574 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2574, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC2574 BINDING SITE, designated SEQ ID:16697, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37408] Another function of GAM1032 is therefore inhibition of MGC2574 (Accession NP_077003.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2574.

[37409] MGC34648 (Accession NP_689873.1) is another GAM1032 target gene, herein designated TARGET GENE. MGC34648 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC34648, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34648 BINDING SITE, designated SEQ ID:14517, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37410] Another function of GAM1032 is therefore inhibition of MGC34648 (Accession NP_689873.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC34648.

[37411] MGC45441 (Accession NP_689712.1) is another GAM1032 target gene, herein designated TARGET GENE. MGC45441 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC45441, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC45441 BINDING SITE, designated SEQ ID:11172, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37412] Another function of GAM1032 is therefore inhibition of MGC45441 (Accession NP_689712.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC45441.

[37413] Antigen identified by monoclonal antibody ki-67 (MKI67, Accession NP_002408.2) is another GAM1032 target gene, herein designated TARGET GENE. MKI67 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MKI67, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of MKI67 BINDING SITE, designated SEQ ID:7829, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37414] Another function of GAM1032 is therefore inhibition of Antigen identified by monoclonal antibody ki-67 (MKI67, Accession NP_002408.2), a gene which thought to be required for maintaining cell proliferation. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKI67.

[37415] The function of MKI67 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM330.2.Myeloperoxidase (MPO, Accession NP_000241.1) is another GAM1032 target gene, herein designated TARGET GENE. MPO BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MPO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPO BINDING SITE, designated SEQ ID:14549, to the nucleotide sequence of GAM1032

RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37416] Another function of GAM1032 is therefore inhibition of Myeloperoxidase (MPO, Accession NP_000241.1), a gene which is present in primary granules of neutrophilic granulocytes. and therefore is associated with Acute promyelocytic leukemia, alzheimer disease. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Acute promyelocytic leukemia, alzheimer disease., and of other diseases and clinical conditions associated with MPO.

[37417] The function of MPO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM374.1.Membrane-spanning 4-domains, subfamily a, member 8b (MS4A8B, Accession NP_113645.1) is another GAM1032 target gene, herein designated TARGET GENE. MS4A8B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MS4A8B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MS4A8B BINDING SITE, designated

SEQ ID:7880, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37418] Another function of GAM1032 is therefore inhibition of Membrane-spanning 4-domains, subfamily a, member 8b (MS4A8B, Accession NP_113645.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MS4A8B.

[37419] 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR, Accession NP_000245.1) is another GAM1032 target gene, herein designated TARGET GENE. MTR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTR BINDING SITE, designated SEQ ID:12733, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37420] Another function of GAM1032 is therefore inhibition of 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR, Accession NP_000245.1) . Accordingly, utili-

ties of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTR.

[37421] MTRF1L (Accession NP_061914.2) is another GAM1032 target gene, herein designated TARGET GENE. MTRF1L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTRF1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTRF1L BINDING SITE, designated SEQ ID:16068, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37422] Another function of GAM1032 is therefore inhibition of MTRF1L (Accession NP_061914.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTRF1L.

[37423] Nanog (Accession NP_079141.1) is another GAM1032 target gene, herein designated TARGET GENE. Nanog BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Nanog, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Nanog BINDING SITE, designated SEQ ID:12978, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37424] Another function of GAM1032 is therefore inhibition of Nanog (Accession NP_079141.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Nanog.

[37425] Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1) is another GAM1032 target gene, herein designated TARGET GENE. NCOA6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCOA6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE, designated SEQ ID:10389, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37426] Another function of GAM1032 is therefore inhibition of Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1), a gene which activates gene transcription

through ligand- dependent association with coactivators. and therefore may be associated with Breast cancer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Breast cancer., and of other diseases and clinical conditions associated with NCOA6.

[37427] The function of NCOA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Neural precursor cell expressed, developmentally down-regulated 4 (NEDD4, Accession XP_046129.4) is another GAM1032 target gene, herein designated TARGET GENE. NEDD4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NEDD4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEDD4 BINDING SITE, designated SEQ ID:6062, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37428] Another function of GAM1032 is therefore inhibition of Neural precursor cell expressed, developmentally down-regulated 4 (NEDD4, Accession XP_046129.4), a gene

which ubiquitinates regulatory proteins involved in transcription. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEDD4.

[37429] The function of NEDD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM48.2.Sialidase 3 (membrane sialidase) (NEU3, Accession NP_006647.2) is another GAM1032 target gene, herein designated TARGET GENE. NEU3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NEU3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEU3 BINDING SITE, designated SEQ ID:12441, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37430] Another function of GAM1032 is therefore inhibition of Sialidase 3 (membrane sialidase) (NEU3, Accession NP_006647.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEU3.

[37431] Notch homolog 3 (drosophila) (NOTCH3, Accession NP_000426.1) is another GAM1032 target gene, herein designated TARGET GENE. NOTCH3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOTCH3 BINDING SITE, designated SEQ ID:8237, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37432] Another function of GAM1032 is therefore inhibition of Notch homolog 3 (drosophila) (NOTCH3, Accession NP_000426.1), a gene which may function in cell fate specification during development. and therefore may be associated with Cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (cadasil). Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (cadasil), and of other diseases and clinical conditions associated with NOTCH3.

[37433] The function of NOTCH3 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM195.2.Olfactory receptor, family 2, subfamily h, member 1 (OR2H1, Accession NP_112145.1) is another GAM1032 target gene, herein designated TARGET GENE. OR2H1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OR2H1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OR2H1 BINDING SITE, designated SEQ ID:19602, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37434] Another function of GAM1032 is therefore inhibition of Olfactory receptor, family 2, subfamily h, member 1 (OR2H1, Accession NP_112145.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OR2H1.

[37435] Phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG, Accession NP_002640.2) is another GAM1032 target gene, herein designated TARGET GENE. PIK3CG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3CG, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3CG BINDING SITE, designated SEQ ID:6205, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37436] Another function of GAM1032 is therefore inhibition of Phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG, Accession NP_002640.2), a gene which regulating cell growth. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3CG.

[37437] The function of PIK3CG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.1.Proteolipid protein 1 (pelizaeus-merzbacher disease, spastic paraplegia 2, uncomplicated) (PLP1, Accession NP_000524.2) is another GAM1032 target gene, herein designated TARGET GENE. PLP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of PLP1 BINDING SITE, designated SEQ ID:17932, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37438] Another function of GAM1032 is therefore inhibition of Proteolipid protein 1 (pelizaeus-merzbacher disease, spastic paraplegia 2, uncomplicated) (PLP1, Accession NP_000524.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLP1.

[37439] Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) is another GAM1032 target gene, herein designated TARGET GENE. PNMA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PNMA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PNMA2 BINDING SITE, designated SEQ ID:15213, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37440] Another function of GAM1032 is therefore inhibition of Paraneoplastic antigen ma2 (PNMA2, Accession

NP_009188.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNMA2.

[37441] Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) is another GAM1032 target gene, herein designated TARGET GENE. POFUT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by POFUT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POFUT1 BINDING SITE, designated SEQ ID:3733, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37442] Another function of GAM1032 is therefore inhibition of Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POFUT1.

[37443] Polymerase (dna directed), gamma (POLG, Accession NP_002684.1) is another GAM1032 target gene, herein designated TARGET GENE. POLG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by POLG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLG BINDING SITE, designated SEQ ID:10516, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37444] Another function of GAM1032 is therefore inhibition of Polymerase (dna directed), gamma (POLG, Accession NP_002684.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLG.

[37445] Polymerase (dna directed), mu (POLM, Accession NP_037416.1) is another GAM1032 target gene, herein designated TARGET GENE. POLM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLM BINDING SITE, designated SEQ ID:6542, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37446] Another function of GAM1032 is therefore inhibition of Polymerase (dna directed), mu (POLM, Accession NP_037416.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLM.

[37447] Peroxisome proliferative activated receptor, gamma, coactivator 1 (PPARGC1, Accession NP_037393.1) is another GAM1032 target gene, herein designated TARGET GENE. PPARGC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPARGC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPARGC1 BINDING SITE, designated SEQ ID:9562, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37448] Another function of GAM1032 is therefore inhibition of Peroxisome proliferative activated receptor, gamma, coactivator 1 (PPARGC1, Accession NP_037393.1), a gene which may play a role in insulin sensitivity and thermogenesis and therefore may be associated with Familial partial lipodystrophy and type ii diabetes. Accordingly, utilities of

GAM1032 include diagnosis, prevention and treatment of Familial partial lipodystrophy and type ii diabetes, and of other diseases and clinical conditions associated with PPARGC1.

[37449] The function of PPARGC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM169.1.Protein phosphatase 1, regulatory (inhibitor) subunit 13b (PPP1R13B, Accession NP_056131.1) is another GAM1032 target gene, herein designated TARGET GENE. PPP1R13B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPP1R13B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R13B BINDING SITE, designated SEQ ID:10316, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37450] Another function of GAM1032 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 13b (PPP1R13B, Accession NP_056131.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with PPP1R13B.

[37451] Protein kinase c, mu (PRKCM, Accession NP_002733.1) is another GAM1032 target gene, herein designated TARGET GENE. PRKCM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKCM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKCM BINDING SITE, designated SEQ ID:3896, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37452] Another function of GAM1032 is therefore inhibition of Protein kinase c, mu (PRKCM, Accession NP_002733.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKCM.

[37453] PRO0659 (Accession NP_054857.2) is another GAM1032 target gene, herein designated TARGET GENE. PRO0659 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0659, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0659 BINDING SITE, designated SEQ ID:18366, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37454] Another function of GAM1032 is therefore inhibition of PRO0659 (Accession NP_054857.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0659.

[37455] Prostein (Accession NP_149093.1) is another GAM1032 target gene, herein designated TARGET GENE. Prostein BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Prostein, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Prostein BINDING SITE, designated SEQ ID:12567, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37456] Another function of GAM1032 is therefore inhibition of Prostein (Accession NP_149093.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with Prostein.

[37457] Psoriasis susceptibility 1 candidate 1 (PSORS1C1, Accession NP_054787.1) is another GAM1032 target gene, herein designated TARGET GENE. PSORS1C1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSORS1C1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSORS1C1 BINDING SITE, designated SEQ ID:11955, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37458] Another function of GAM1032 is therefore inhibition of Psoriasis susceptibility 1 candidate 1 (PSORS1C1, Accession NP_054787.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSORS1C1.

[37459] PTP9Q22 (Accession NP_818931.1) is another GAM1032 target gene, herein designated TARGET GENE. PTP9Q22 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTP9Q22, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTP9Q22 BINDING SITE, designated SEQ ID:4253, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37460] Another function of GAM1032 is therefore inhibition of PTP9Q22 (Accession NP_818931.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTP9Q22.

[37461] PTP9Q22 (Accession NP_689635.3) is another GAM1032 target gene, herein designated TARGET GENE. PTP9Q22 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTP9Q22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTP9Q22 BINDING SITE, designated SEQ ID:4253, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37462] Another function of GAM1032 is therefore inhibition of

PTP9Q22 (Accession NP_689635.3) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTP9Q22.

[37463] Protein tyrosine phosphatase, receptor type, o (PTPRO, Accession NP_109595.1) is another GAM1032 target gene, herein designated TARGET GENE. PTPRO BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTPRO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPRO BINDING SITE, designated SEQ ID:1369, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37464] Another function of GAM1032 is therefore inhibition of Protein tyrosine phosphatase, receptor type, o (PTPRO, Accession NP_109595.1), a gene which may function as a cell contact receptor that mediates and controls cell- cell signals and therefore may be associated with Pancreatic carcinoma. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Pancreatic carcinoma, and of other diseases and clinical conditions asso-

ciated with PTPRO.

[37465] The function of PTPRO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM207.2.Protein tyrosine phosphatase, receptor type, o (PTPRO, Accession NP_109596.1) is another GAM1032 target gene, herein designated TARGET GENE. PTPRO BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTPRO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPRO BINDING SITE, designated SEQ ID:1369, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37466] Another function of GAM1032 is therefore inhibition of Protein tyrosine phosphatase, receptor type, o (PTPRO, Accession NP_109596.1), a gene which may function as a cell contact receptor that mediates and controls cell- cell signals and therefore may be associated with Pancreatic carcinoma. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Pancreatic carci-

noma, and of other diseases and clinical conditions associated with PTPRO.

[37467] The function of PTPRO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM207.2.Paxillin (PXN, Accession NP_002850.1) is another GAM1032 target gene, herein designated TARGET GENE. PXN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PXN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PXN BINDING SITE, designated SEQ ID:16601, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37468] Another function of GAM1032 is therefore inhibition of Paxillin (PXN, Accession NP_002850.1), a gene which may be involved in p53- dependent apoptosis and therefore may be associated with Cancer. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with PXN.

[37469] The function of PXN and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Ran binding protein 17 (RANBP17, Accession NP_075048.1) is another GAM1032 target gene, herein designated TARGET GENE. RANBP17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RANBP17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RANBP17 BINDING SITE, designated SEQ ID:3335, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37470] Another function of GAM1032 is therefore inhibition of Ran binding protein 17 (RANBP17, Accession NP_075048.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RANBP17.

[37471] Retinoblastoma 1 (including osteosarcoma) (RB1, Accession NP_000312.1) is another GAM1032 target gene, herein designated TARGET GENE. RB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RB1, corresponding to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RB1 BINDING SITE, designated SEQ ID:12895, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37472] Another function of GAM1032 is therefore inhibition of Retinoblastoma 1 (including osteosarcoma) (RB1, Accession NP_000312.1), a gene which probably acts as a regulator of other genes and therefore is associated with Retinoblastoma. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Retinoblastoma, and of other diseases and clinical conditions associated with RB1.

[37473] The function of RB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM519.1.Regulatory factor x, 5 (influences hla class ii expression) (RFX5, Accession NP_000440.1) is another GAM1032 target gene, herein designated TARGET GENE. RFX5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RFX5, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RFX5 BINDING SITE, designated SEQ ID:16892, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37474] Another function of GAM1032 is therefore inhibition of Regulatory factor x, 5 (influences hla class ii expression) (RFX5, Accession NP_000440.1), a gene which activates transcription from class ii mhc promoters. and therefore may be associated with Bare lymphocyte syndrome type ii complementation group c (or hla class ii- deficient combined immunodeficiency); a form of severe combined immunodeficiency disease (scid). Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Bare lymphocyte syndrome type ii complementation group c (or hla class ii- deficient combined immunodeficiency); a form of severe combined immunodeficiency disease (scid)., and of other diseases and clinical conditions associated with RFX5.

[37475] The function of RFX5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM329.1.Regulator of g-protein signalling 11 (RGS11,

Accession NP_003825.1) is another GAM1032 target gene, herein designated TARGET GENE. RGS11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RGS11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RGS11 BINDING SITE, designated SEQ ID:1065, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37476] Another function of GAM1032 is therefore inhibition of Regulator of g-protein signalling 11 (RGS11, Accession NP_003825.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS11.

[37477] RINZF (Accession NP_076418.2) is another GAM1032 target gene, herein designated TARGET GENE. RINZF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RINZF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RINZF BINDING SITE, designated SEQ ID:7593, to the nucleotide se-

quence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37478] Another function of GAM1032 is therefore inhibition of RINZF (Accession NP_076418.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RINZF.

[37479] RNASE3L (Accession NP_037367.2) is another GAM1032 target gene, herein designated TARGET GENE. RNASE3L BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RNASE3L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNASE3L BINDING SITE, designated SEQ ID:16650, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37480] Another function of GAM1032 is therefore inhibition of RNASE3L (Accession NP_037367.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNASE3L.

[37481] Ring finger protein (c3h2c3 type) 6 (RNF6, Accession NP_005968.1) is another GAM1032 target gene, herein

designated TARGET GENE. RNF6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RNF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF6 BINDING SITE, designated SEQ ID:3285, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37482] Another function of GAM1032 is therefore inhibition of Ring finger protein (c3h2c3 type) 6 (RNF6, Accession NP_005968.1), a gene which is a RING finger protein, may be a tumor suppressor and therefore may be associated with Esophageal squamous cell carcinoma, somatic. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Esophageal squamous cell carcinoma, somatic, and of other diseases and clinical conditions associated with RNF6.

[37483] The function of RNF6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM515.1.Retinoid x receptor, alpha (RXRA, Accession NP_002948.1) is another GAM1032 target gene, herein

designated TARGET GENE. RXRA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RXRA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RXRA BINDING SITE, designated SEQ ID:11932, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37484] Another function of GAM1032 is therefore inhibition of Retinoid x receptor, alpha (RXRA, Accession NP_002948.1), a gene which activates genes required for vitamin A metabolism, binds 9- cis retinoic acid. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RXRA.

[37485] The function of RXRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM146.1.SBLF (Accession NP_006864.2) is another GAM1032 target gene, herein designated TARGET GENE. SBLF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SBLF, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SBLF BINDING SITE, designated SEQ ID:8023, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37486] Another function of GAM1032 is therefore inhibition of SBLF (Accession NP_006864.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SBLF.

[37487] Sodium channel, voltage-gated, type ii, beta polypeptide (SCN2B, Accession NP_004579.1) is another GAM1032 target gene, herein designated TARGET GENE. SCN2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCN2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCN2B BINDING SITE, designated SEQ ID:635, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37488] Another function of GAM1032 is therefore inhibition of Sodium channel, voltage-gated, type ii, beta polypeptide

(SCN2B, Accession NP_004579.1), a gene which modulates channel properties. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN2B.

[37489] The function of SCN2B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Serine (or cysteine) proteinase inhibitor, clade a (alpha-1 antiproteinase, antitrypsin), member 3 (SERPINA3, Accession NP_001076.1) is another GAM1032 target gene, herein designated TARGET GENE. SERPINA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERPINA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERPINA3 BINDING SITE, designated SEQ ID:2046, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37490] Another function of GAM1032 is therefore inhibition of Serine (or cysteine) proteinase inhibitor, clade a (alpha-1 antiproteinase, antitrypsin), member 3 (SERPINA3, Accession NP_001076.1), a gene which is a member of the ser-

pin family of serine protease inhibitors. and therefore may be associated with Chronic obstructive pulmonary disease (copd) or of occlusive cerebrovascular disease. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Chronic obstructive pulmonary disease (copd) or of occlusive cerebrovascular disease, and of other diseases and clinical conditions associated with SERPINA3.

[37491] The function of SERPINA3 has been established by previous studies. Alpha- 1- antichymotrypsin is a plasma protease inhibitor synthesized in the liver. It is a single glycopeptide chain of about 68,000 daltons and belongs to the class of serine protease inhibitors. In man, the normal serum level is about one- tenth that of alpha- 1- antitrypsin (PI; 107400), with which it shares nucleic acid and protein sequence homology (Chandra et al., 1983). Both are major acute phase reactants; their concentrations in plasma increase in response to trauma, surgery, and infection. Antithrombin III, which also is structurally similar to alpha- 1- antitrypsin, shows less sequence homology to antichymotrypsin and is not an acute phase reactant. Kelsey et al. (1988) cloned and analyzed the AACT gene, partly because of the possibility that genetic variation in

other protease inhibitors may influence the prognosis in AAT deficiency. They isolated the AACT gene on a series of cosmid clones, with restriction mapping of about 70 kb around the gene.

[37492]

[37493] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[37494] Chandra, T.; Stackhouse, R.; Kidd, V. J.; Robson, K. J. H.; Woo, S. L. C. : Sequence homology between human alpha- 1- antichymotrypsin, alpha- 1- antitrypsin, and antithrombin III. Biochemistry 22: 5055- 5061, 1983. ; and

[37495] Kelsey, G. D.; Abeliovich, D.; McMahon, C. J.; Whitehouse, D.; Corney, G.; Povey, S.; Hopkinson, D. A.; Wolfe, J.; Mieli- Vergani, G.; Mowat, A. P. : Cloning of the human alpha- 1 antichym.

[37496] Further studies establishing the function and utilities of SERPINA3 are found in John Hopkins OMIM database record ID 107280, and in cited publications listed in Table 5, which are hereby incorporated by reference.SF4 (Accession NP_066987.1) is another GAM1032 target gene, herein designated TARGET GENE. SF4 BINDING SITE is a target binding site found in the 3` untranslated re-

gion of mRNA encoded by SF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SF4 BINDING SITE, designated SEQ ID:860, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37497] Another function of GAM1032 is therefore inhibition of SF4 (Accession NP_066987.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SF4.

[37498] Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_775323.1) is another GAM1032 target gene, herein designated TARGET GENE. SIAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SIAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIAT1 BINDING SITE, designated SEQ ID:11766, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37499] Another function of GAM1032 is therefore inhibition of Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_775323.1), a gene which transfers sialic acid from the donor of substrate cmp- sialic acid to galactose containing acceptor substrates. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIAT1.

[37500] The function of SIAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.2.Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_775324.1) is another GAM1032 target gene, herein designated TARGET GENE. SIAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SIAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIAT1 BINDING SITE, designated SEQ ID:11766, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37501] Another function of GAM1032 is therefore inhibition of Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_775324.1), a gene which transfers sialic acid from the donor of substrate cmp- sialic acid to galactose containing acceptor substrates. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIAT1.

[37502] The function of SIAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.2.Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_003023.1) is another GAM1032 target gene, herein designated TARGET GENE. SIAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SIAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIAT1 BINDING SITE, designated SEQ ID:11766, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37503] Another function of GAM1032 is therefore inhibition of Sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) (SIAT1, Accession NP_003023.1), a gene which transfers sialic acid from the donor of substrate cmp- sialic acid to galactose containing acceptor substrates. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIAT1.

[37504] The function of SIAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.2.Solute carrier family 12 (potassium/chloride transporters), member 7 (SLC12A7, Accession NP_006589.1) is another GAM1032 target gene, herein designated TARGET GENE. SLC12A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC12A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC12A7 BINDING SITE, designated SEQ ID:17066, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37505] Another function of GAM1032 is therefore inhibition of Solute carrier family 12 (potassium/chloride transporters), member 7 (SLC12A7, Accession NP_006589.1), a gene which is a potassium/chloride- cotransporter. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC12A7.

[37506] The function of SLC12A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM105.1.SLC35A4 (Accession NP_542401.1) is another GAM1032 target gene, herein designated TARGET GENE. SLC35A4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC35A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC35A4 BINDING SITE, designated SEQ ID:5796, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37507] Another function of GAM1032 is therefore inhibition of SLC35A4 (Accession NP_542401.1) . Accordingly, utilities

of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35A4.

[37508] SLC35E2 (Accession XP_049733.6) is another GAM1032 target gene, herein designated TARGET GENE. SLC35E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC35E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC35E2 BINDING SITE, designated SEQ ID:14041, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37509] Another function of GAM1032 is therefore inhibition of SLC35E2 (Accession XP_049733.6) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35E2.

[37510] Smith-magenis syndrome chromosome region, candidate 5 (SMCR5, Accession NP_658987.1) is another GAM1032 target gene, herein designated TARGET GENE. SMCR5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SMCR5, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMCR5 BINDING SITE, designated SEQ ID:10482, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37511] Another function of GAM1032 is therefore inhibition of Smith-magenis syndrome chromosome region, candidate 5 (SMCR5, Accession NP_658987.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMCR5.

[37512] SORCS2 (Accession NP_065828.1) is another GAM1032 target gene, herein designated TARGET GENE. SORCS2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SORCS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SORCS2 BINDING SITE, designated SEQ ID:6379, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37513] Another function of GAM1032 is therefore inhibition of SORCS2 (Accession NP_065828.1) . Accordingly, utilities

of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SORCS2.

[37514] Sp7 transcription factor (SP7, Accession NP_690599.1) is another GAM1032 target gene, herein designated TARGET GENE. SP7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SP7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SP7 BINDING SITE, designated SEQ ID:20063, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37515] Another function of GAM1032 is therefore inhibition of Sp7 transcription factor (SP7, Accession NP_690599.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SP7.

[37516] Spondin 1, (f-spondin) extracellular matrix protein (SPON1, Accession NP_006099.1) is another GAM1032 target gene, herein designated TARGET GENE. SPON1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPON1, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPON1 BINDING SITE, designated SEQ ID:14025, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37517] Another function of GAM1032 is therefore inhibition of Spondin 1, (f-spondin) extracellular matrix protein (SPON1, Accession NP_006099.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPON1.

[37518] Sulfite oxidase (SUOX, Accession NP_000447.1) is another GAM1032 target gene, herein designated TARGET GENE. SUOX BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SUOX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SUOX BINDING SITE, designated SEQ ID:15310, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37519] Another function of GAM1032 is therefore inhibition of Sulfite oxidase (SUOX, Accession NP_000447.1), a gene

which sulfite oxidase deficiency and therefore is associated with Sulfite oxidase deficiency. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Sulfite oxidase deficiency, and of other diseases and clinical conditions associated with SUOX.

[37520] The function of SUOX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM206.1.Tachykinin receptor 3 (TACR3, Accession NP_001050.1) is another GAM1032 target gene, herein designated TARGET GENE. TACR3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TACR3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TACR3 BINDING SITE, designated SEQ ID:15957, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37521] Another function of GAM1032 is therefore inhibition of Tachykinin receptor 3 (TACR3, Accession NP_001050.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with TACR3.

[37522] T-box 18 (TBX18, Accession XP_291165.1) is another GAM1032 target gene, herein designated TARGET GENE. TBX18 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TBX18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TBX18 BINDING SITE, designated SEQ ID:550, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37523] Another function of GAM1032 is therefore inhibition of T-box 18 (TBX18, Accession XP_291165.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBX18.

[37524] Thymidine kinase 2, mitochondrial (TK2, Accession NP_004605.1) is another GAM1032 target gene, herein designated TARGET GENE. TK2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of TK2 BINDING SITE, designated SEQ ID:17771, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37525] Another function of GAM1032 is therefore inhibition of Thymidine kinase 2, mitochondrial (TK2, Accession NP_004605.1), a gene which phosphorylates thymidine, deoxycytidine, deoxyuridine, and also anti- viral and anti-cancer nucleoside analogs and therefore may be associated with Mitochondrial dna depletion myopathy. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of Mitochondrial dna depletion myopathy, and of other diseases and clinical conditions associated with TK2.

[37526] The function of TK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.1.Toll-like receptor 4 (TLR4, Accession NP_612566.1) is another GAM1032 target gene, herein designated TARGET GENE. TLR4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TLR4, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLR4 BINDING SITE, designated SEQ ID:10745, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37527] Another function of GAM1032 is therefore inhibition of Toll-like receptor 4 (TLR4, Accession NP_612566.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLR4.

[37528] Toll-like receptor 4 (TLR4, Accession NP_612564.1) is another GAM1032 target gene, herein designated TARGET GENE. TLR4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TLR4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLR4 BINDING SITE, designated SEQ ID:10745, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37529] Another function of GAM1032 is therefore inhibition of Toll-like receptor 4 (TLR4, Accession NP_612564.1) . Ac-

cordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLR4.

[37530] Toll-like receptor 4 (TLR4, Accession NP_003257.1) is another GAM1032 target gene, herein designated TARGET GENE. TLR4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TLR4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLR4 BINDING SITE, designated SEQ ID:10745, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37531] Another function of GAM1032 is therefore inhibition of Toll-like receptor 4 (TLR4, Accession NP_003257.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLR4.

[37532] Toll-like receptor 4 (TLR4, Accession NP_612567.1) is another GAM1032 target gene, herein designated TARGET GENE. TLR4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of

mRNA encoded by TLR4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLR4 BINDING SITE, designated SEQ ID:10745, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37533] Another function of GAM1032 is therefore inhibition of Toll-like receptor 4 (TLR4, Accession NP_612567.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLR4.

[37534] Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690616.1) is another GAM1032 target gene, herein designated TARGET GENE. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF6 BINDING SITE, designated SEQ ID:3084, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ

ID:303.

[37535] Another function of GAM1032 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690616.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF6.

[37536] Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690612.1) is another GAM1032 target gene, herein designated TARGET GENE. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF6 BINDING SITE, designated SEQ ID:3084, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37537] Another function of GAM1032 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690612.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with TNFRSF6.

[37538] Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690615.1) is another GAM1032 target gene, herein designated TARGET GENE. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF6 BINDING SITE, designated SEQ ID:3084, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37539] Another function of GAM1032 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690615.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF6.

[37540] Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690614.1) is another GAM1032 target gene, herein designated TARGET GENE. TNFRSF6

BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF6 BINDING SITE, designated SEQ ID:3084, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37541] Another function of GAM1032 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690614.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF6.

[37542] Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690611.1) is another GAM1032 target gene, herein designated TARGET GENE. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of TNFRSF6 BINDING SITE, designated SEQ ID:3084, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37543] Another function of GAM1032 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690611.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF6.

[37544] Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690613.1) is another GAM1032 target gene, herein designated TARGET GENE. TNFRSF6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF6 BINDING SITE, designated SEQ ID:3084, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37545] Another function of GAM1032 is therefore inhibition of

Tumor necrosis factor receptor superfamily, member 6 (TNFRSF6, Accession NP_690613.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF6.

[37546] TOLLIP (Accession NP_061882.2) is another GAM1032 target gene, herein designated TARGET GENE. TOLLIP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TOLLIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOLLIP BINDING SITE, designated SEQ ID:13742, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37547] Another function of GAM1032 is therefore inhibition of TOLLIP (Accession NP_061882.2) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOLLIP.

[37548] Tyrosinase-related protein 1 (TYRP1, Accession NP_000541.1) is another GAM1032 target gene, herein designated TARGET GENE. TYRP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA

encoded by TYRP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TYRP1 BINDING SITE, designated SEQ ID:11984, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37549] Another function of GAM1032 is therefore inhibition of Tyrosinase-related protein 1 (TYRP1, Accession NP_000541.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TYRP1.

[37550] USP12L1 (Accession XP_167944.1) is another GAM1032 target gene, herein designated TARGET GENE. USP12L1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by USP12L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of USP12L1 BINDING SITE, designated SEQ ID:8209, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37551] Another function of GAM1032 is therefore inhibition of

USP12L1 (Accession XP_167944.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP12L1.

[37552] VIPL (Accession NP_110432.1) is another GAM1032 target gene, herein designated TARGET GENE. VIPL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VIPL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VIPL BINDING SITE, designated SEQ ID:9897, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37553] Another function of GAM1032 is therefore inhibition of VIPL (Accession NP_110432.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIPL.

[37554] Ww domain binding protein 2 (WBP2, Accession NP_036610.2) is another GAM1032 target gene, herein designated TARGET GENE. WBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WBP2, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBP2 BINDING SITE, designated SEQ ID:17972, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37555] Another function of GAM1032 is therefore inhibition of Ww domain binding protein 2 (WBP2, Accession NP_036610.2), a gene which binds with high affinity to the WW domain contained in YAP;. Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBP2.

[37556] The function of WBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM342.2.ZAK (Accession NP_598407.1) is another GAM1032 target gene, herein designated TARGET GENE. ZAK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZAK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAK BINDING SITE, designated SEQ

ID:5951, to the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, also designated SEQ ID:303.

[37557] Another function of GAM1032 is therefore inhibition of ZAK (Accession NP_598407.1) . Accordingly, utilities of GAM1032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAK.

[37558]

[37559] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 1338 (GAM1338), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[37560] GAM1338 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1338 was detected is described hereinabove with reference to Figs. 8-15.

[37561] GAM1338 gene, herein designated GAM GENE, and GAM1338 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[37562] GAM1338 gene encodes a GAM1338 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1338

precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1338 precursor RNA is designated SEQ ID:36, and is provided hereinbelow with reference to the sequence listing part.

[37563] GAM1338 precursor RNA folds onto itself, forming GAM1338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[37564] GAM1338 precursor RNA folds onto itself, forming GAM1338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[37565] Nucleotide sequence of GAM1338 precursor RNA, designated SEQ-ID: 36, and a schematic representation of a predicted secondary folding of GAM1338 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[37566] An enzyme complex designated DICER COMPLEX, `dices` the GAM1338 folded precursor RNA into GAM1338 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM1338 RNA is designated SEQ ID:360, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[37567] GAM1338 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM1338 target RNA, herein designated GAM TARGET RNA. GAM1338 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, desig-

nated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[37568] GAM1338 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1338 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1338 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1338 RNA may have a different number of target binding sites in untranslated regions of a GAM1338 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[37569] The complementary binding of GAM1338 RNA, herein designated GAM RNA, to target binding sites on GAM1338 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1338 target RNA into GAM1338 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[37570] It is appreciated that GAM1338 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM1338 target genes. The mRNA of each one of this plurality of GAM1338 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1338 RNA, herein designated GAM RNA, and which when bound by GAM1338 RNA causes inhibition of translation of respective one or more GAM1338 target proteins.

[37571] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1338 gene, herein designated GAM GENE, on one or more GAM1338 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[37572] It is appreciated that specific functions and accordingly utilities of GAM1338 correlate with, and may be deduced from, the identity of the target genes which GAM1338 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[37573]

[37574]

[37575] 15E1.2 (Accession XP_290596.1) is a GAM1338 target gene, herein designated TARGET GENE. 15E1.2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by 15E1.2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of 15E1.2 BINDING SITE, designated SEQ ID:13885, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA,

also designated SEQ ID:360.

[37576] A function of GAM1338 is therefore inhibition of 15E1.2 (Accession XP_290596.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 15E1.2.

[37577] 7h3 (Accession NP_149014.2) is another GAM1338 target gene, herein designated TARGET GENE. 7h3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by 7h3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of 7h3 BINDING SITE, designated SEQ ID:16813, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37578] Another function of GAM1338 is therefore inhibition of 7h3 (Accession NP_149014.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 7h3.

[37579] Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2) is another GAM1338 target gene, herein designated TARGET GENE. A1BG BINDING SITE1 and A1BG BINDING SITE2 are target binding sites found in untranslated regions of

mRNA encoded by A1BG, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A1BG BINDING SITE1 and A1BG BINDING SITE2, designated SEQ ID:10791 and SEQ ID:19693 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37580] Another function of GAM1338 is therefore inhibition of Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2), a gene which a plasma protein of unknown function. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A1BG.

[37581] The function of A1BG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.A2BP1 (Accession NP_061193.2) is another GAM1338 target gene, herein designated TARGET GENE. A2BP1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by A2BP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A2BP1 BINDING SITE, designated SEQ ID:1212, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37582] Another function of GAM1338 is therefore inhibition of A2BP1 (Accession NP_061193.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A2BP1.

[37583] Aminoadipate-semialdehyde synthase (AASS, Accession NP_005754.2) is another GAM1338 target gene, herein designated TARGET GENE. AASS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AASS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AASS BINDING SITE, designated SEQ ID:18163, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37584] Another function of GAM1338 is therefore inhibition of Aminoadipate-semialdehyde synthase (AASS, Accession NP_005754.2) . Accordingly, utilities of GAM1338 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with AASS.

[37585] ABCA13 (Accession NP_689914.2) is another GAM1338 target gene, herein designated TARGET GENE. ABCA13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCA13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCA13 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37586] Another function of GAM1338 is therefore inhibition of ABCA13 (Accession NP_689914.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCA13.

[37587] Atp-binding cassette, sub-family c (cftr/mrp), member 11 (ABCC11, Accession NP_149163.2) is another GAM1338 target gene, herein designated TARGET GENE. ABCC11 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ABCC11, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCC11 BINDING SITE, designated SEQ ID:18047, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37588] Another function of GAM1338 is therefore inhibition of Atp-binding cassette, sub-family c (cftr/mrp), member 11 (ABCC11, Accession NP_149163.2), a gene which acts as a multispecific organic anion pump which can transport nucleotide analogs (by similarity). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC11.

[37589] The function of ABCC11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Acyl-coenzyme a dehydrogenase, short/branched chain (ACADSB, Accession NP_001600.1) is another GAM1338 target gene, herein designated TARGET GENE. ACADSB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACADSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACADSB BINDING SITE, designated SEQ ID:14907, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37590] Another function of GAM1338 is therefore inhibition of Acyl-coenzyme a dehydrogenase, short/branched chain (ACADSB, Accession NP_001600.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACADSB.

[37591] AGO4 (Accession NP_060099.2) is another GAM1338 target gene, herein designated TARGET GENE. AGO4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AGO4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGO4 BINDING SITE, designated SEQ ID:13702, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37592] Another function of GAM1338 is therefore inhibition of AGO4 (Accession NP_060099.2) . Accordingly, utilities of

GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGO4.

[37593] Aryl hydrocarbon receptor (AHR, Accession NP_001612.1) is another GAM1338 target gene, herein designated TARGET GENE. AHR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AHR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AHR BINDING SITE, designated SEQ ID:9011, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37594] Another function of GAM1338 is therefore inhibition of Aryl hydrocarbon receptor (AHR, Accession NP_001612.1), a gene which plays a role in modulating carcinogenesis through the induction of xenobiotic- metabolizing enzymes and therefore may be associated with Stomach tumors. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Stomach tumors, and of other diseases and clinical conditions associated with AHR.

[37595] The function of AHR and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM30.1.Absent in melanoma 1 (AIM1, Accession XP_166300.1) is another GAM1338 target gene, herein designated TARGET GENE. AIM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AIM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AIM1 BINDING SITE, designated SEQ ID:1383, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37596] Another function of GAM1338 is therefore inhibition of Absent in melanoma 1 (AIM1, Accession XP_166300.1), a gene which is altered in association with tumor suppression in a model of human melanoma and therefore may be associated with Malignant melanoma. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Malignant melanoma, and of other diseases and clinical conditions associated with AIM1.

[37597] The function of AIM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM136.1.A kinase (prka) anchor protein 8 (AKAP8, Accession NP_005849.1) is another GAM1338 target gene, herein designated TARGET GENE. AKAP8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AKAP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKAP8 BINDING SITE, designated SEQ ID:2643, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37598] Another function of GAM1338 is therefore inhibition of A kinase (prka) anchor protein 8 (AKAP8, Accession NP_005849.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP8.

[37599] Aldehyde dehydrogenase 1 family, member b1 (ALDH1B1, Accession NP_000683.3) is another GAM1338 target gene, herein designated TARGET GENE. ALDH1B1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALDH1B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of ALDH1B1 BINDING SITE, designated SEQ ID:19434, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37600] Another function of GAM1338 is therefore inhibition of Aldehyde dehydrogenase 1 family, member b1 (ALDH1B1, Accession NP_000683.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH1B1.

[37601] Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1) is another GAM1338 target gene, herein designated TARGET GENE. ALOX15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALOX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALOX15 BINDING SITE, designated SEQ ID:18901, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37602] Another function of GAM1338 is therefore inhibition of Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1), a gene which converts arachidonic acid to

15s- hydroperoxyeicosatetraenoic acid. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALOX15.

[37603] The function of ALOX15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.AMID (Accession NP_116186.1) is another GAM1338 target gene, herein designated TARGET GENE. AMID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AMID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMID BINDING SITE, designated SEQ ID:2328, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37604] Another function of GAM1338 is therefore inhibition of AMID (Accession NP_116186.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMID.

[37605] Ankyrin repeat domain 6 (ANKRD6, Accession NP_055757.1) is another GAM1338 target gene, herein

designated TARGET GENE. ANKRD6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ANKRD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANKRD6 BINDING SITE, designated SEQ ID:11653, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37606] Another function of GAM1338 is therefore inhibition of Ankyrin repeat domain 6 (ANKRD6, Accession NP_055757.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKRD6.

[37607] AP1S3 (Accession XP_291023.1) is another GAM1338 target gene, herein designated TARGET GENE. AP1S3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1S3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1S3 BINDING SITE, designated SEQ ID:15779, to the nucleotide sequence of GAM1338

RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37608] Another function of GAM1338 is therefore inhibition of AP1S3 (Accession XP_291023.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1S3.

[37609] Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) is another GAM1338 target gene, herein designated TARGET GENE. AP3S2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AP3S2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP3S2 BINDING SITE, designated SEQ ID:6113, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37610] Another function of GAM1338 is therefore inhibition of Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3S2.

[37611] Apoptotic protease activating factor (APAF1, Accession

NP_001151.1) is another GAM1338 target gene, herein designated TARGET GENE. APAF1 BINDING SITE1 and APAF1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APAF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE1 and APAF1 BINDING SITE2, designated SEQ ID:803 and SEQ ID:803 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37612] Another function of GAM1338 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_001151.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[37613] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apoptotic protease activating factor (APAF1,

Accession NP_001151.1) is another GAM1338 target gene, herein designated TARGET GENE. APAF1 BINDING SITE1 and APAF1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APAF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE1 and APAF1 BINDING SITE2, designated SEQ ID:1306 and SEQ ID:1306 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37614] Another function of GAM1338 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_001151.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[37615] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM30.1.APM1 (Accession NP_004788.1) is another GAM1338 target gene, herein designated TARGET GENE. APM1 BINDING SITE1 through APM1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by APM1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APM1 BINDING SITE1 through APM1 BINDING SITE3, designated SEQ ID:13551, SEQ ID:1962 and SEQ ID:2268 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37616] Another function of GAM1338 is therefore inhibition of APM1 (Accession NP_004788.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1.

[37617] Apolipoprotein l, 2 (APOL2, Accession NP_112092.1) is another GAM1338 target gene, herein designated TARGET GENE. APOL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of APOL2 BINDING SITE, designated SEQ ID:16087, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37618] Another function of GAM1338 is therefore inhibition of Apolipoprotein l, 2 (APOL2, Accession NP_112092.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL2.

[37619] Apolipoprotein l, 2 (APOL2, Accession NP_663612.1) is another GAM1338 target gene, herein designated TARGET GENE. APOL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL2 BINDING SITE, designated SEQ ID:16087, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37620] Another function of GAM1338 is therefore inhibition of Apolipoprotein l, 2 (APOL2, Accession NP_663612.1) . Accordingly, utilities of GAM1338 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with APOL2.

[37621] Amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2, Accession NP_006371.2) is another GAM1338 target gene, herein designated TARGET GENE. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APPBP2 BINDING SITE, designated SEQ ID:20094, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37622] Another function of GAM1338 is therefore inhibition of Amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2, Accession NP_006371.2), a gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore may be associated with Alzheimer's disease. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Alzheimer's disease, and of other diseases and clinical conditions associated with APPBP2.

[37623] The function of APPBP2 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.APPL (Accession NP_036228.1) is another GAM1338 target gene, herein designated TARGET GENE. APPL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APPL BINDING SITE, designated SEQ ID:12386, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37624] Another function of GAM1338 is therefore inhibition of APPL (Accession NP_036228.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APPL.

[37625] Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1) is another GAM1338 target gene, herein designated TARGET GENE. AQP6 BINDING SITE1 and AQP6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by AQP6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE1 and AQP6 BINDING SITE2, designated SEQ ID:16104 and SEQ ID:2103 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37626] Another function of GAM1338 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[37627] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1) is another GAM1338 target gene, herein designated TARGET GENE. AQP6 BINDING SITE1 and AQP6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by AQP6, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE1 and AQP6 BINDING SITE2, designated SEQ ID:2103 and SEQ ID:13404 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37628] Another function of GAM1338 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[37629] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Ras homolog gene family, member f (in filopodia) (ARHF, Accession NP_061907.1) is another GAM1338 target gene, herein designated TARGET GENE. ARHF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHF, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHF BINDING SITE, designated SEQ ID:3172, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37630] Another function of GAM1338 is therefore inhibition of Ras homolog gene family, member f (in filopodia) (ARHF, Accession NP_061907.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHF.

[37631] Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) is another GAM1338 target gene, herein designated TARGET GENE. ARHGAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP1 BINDING SITE, designated SEQ ID:8690, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37632] Another function of GAM1338 is therefore inhibition of

Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP1.

[37633] ARHGAP11A (Accession NP_055598.1) is another GAM1338 target gene, herein designated TARGET GENE. ARHGAP11A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGAP11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP11A BINDING SITE, designated SEQ ID:7085, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37634] Another function of GAM1338 is therefore inhibition of ARHGAP11A (Accession NP_055598.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP11A.

[37635] ARPP-19 (Accession NP_006619.1) is another GAM1338 target gene, herein designated TARGET GENE. ARPP-19 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by ARPP-19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARPP-19 BINDING SITE, designated SEQ ID:18664, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37636] Another function of GAM1338 is therefore inhibition of ARPP-19 (Accession NP_006619.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARPP-19.

[37637] Ankyrin repeat and socs box-containing 16 (ASB16, Accession NP_543139.4) is another GAM1338 target gene, herein designated TARGET GENE. ASB16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASB16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB16 BINDING SITE, designated SEQ ID:11661, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37638] Another function of GAM1338 is therefore inhibition of Ankyrin repeat and socs box-containing 16 (ASB16, Accession NP_543139.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB16.

[37639] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) is another GAM1338 target gene, herein designated TARGET GENE. ASB6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ASB6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE, designated SEQ ID:1654, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37640] Another function of GAM1338 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[37641] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) is another GAM1338 target gene,

herein designated TARGET GENE. ASB6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ASB6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE, designated SEQ ID:1654, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37642] Another function of GAM1338 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[37643] ASE-1 (Accession NP_036231.1) is another GAM1338 target gene, herein designated TARGET GENE. ASE-1 BINDING SITE1 and ASE-1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ASE-1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASE-1 BINDING SITE1 and ASE-1 BINDING SITE2, designated SEQ ID:9988 and SEQ ID:9101

respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37644] Another function of GAM1338 is therefore inhibition of ASE-1 (Accession NP_036231.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASE-1.

[37645] ATF7IP2 (Accession NP_079273.1) is another GAM1338 target gene, herein designated TARGET GENE. ATF7IP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATF7IP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATF7IP2 BINDING SITE, designated SEQ ID:12397, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37646] Another function of GAM1338 is therefore inhibition of ATF7IP2 (Accession NP_079273.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATF7IP2.

[37647] Ataxia telangiectasia mutated (includes complementation

groups a, c and d) (ATM, Accession NP_612150.1) is another GAM1338 target gene, herein designated TARGET GENE. ATM BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ATM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATM BINDING SITE, designated SEQ ID:5585, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37648] Another function of GAM1338 is therefore inhibition of Ataxia telangiectasia mutated (includes complementation groups a, c and d) (ATM, Accession NP_612150.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATM.

[37649] Atpase, na+/k+ transporting, beta 2 polypeptide (ATP1B2, Accession NP_001669.1) is another GAM1338 target gene, herein designated TARGET GENE. ATP1B2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP1B2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP1B2 BINDING SITE, designated SEQ ID:19749, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37650] Another function of GAM1338 is therefore inhibition of Atpase, na+/k+ transporting, beta 2 polypeptide (ATP1B2, Accession NP_001669.1), a gene which catalyzes the hydrolysis of ATP coupled with the exchange of Na +/K+ ions across the plasma membrane. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B2.

[37651] The function of ATP1B2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Atpase, (na+)/k+ transporting, beta 4 polypeptide (ATP1B4, Accession NP_036201.1) is another GAM1338 target gene, herein designated TARGET GENE. ATP1B4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP1B4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of ATP1B4 BINDING SITE, designated SEQ ID:15678, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37652] Another function of GAM1338 is therefore inhibition of Atpase, (na+)/k+ transporting, beta 4 polypeptide (ATP1B4, Accession NP_036201.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B4.

[37653] ATP6V1A (Accession NP_001681.2) is another GAM1338 target gene, herein designated TARGET GENE. ATP6V1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP6V1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP6V1A BINDING SITE, designated SEQ ID:19693, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37654] Another function of GAM1338 is therefore inhibition of ATP6V1A (Accession NP_001681.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with ATP6V1A.

[37655] Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) is another GAM1338 target gene, herein designated TARGET GENE. ATP7A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:19505, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37656] Another function of GAM1338 is therefore inhibition of Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A.

[37657] Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) is another GAM1338 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:5485, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37658] Another function of GAM1338 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[37659] Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) is another GAM1338 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:5485, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37660] Another function of GAM1338 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[37661] BA108L7.2 (Accession NP_112233.2) is another GAM1338 target gene, herein designated TARGET GENE. BA108L7.2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BA108L7.2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BA108L7.2 BINDING SITE, designated SEQ ID:4652, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37662] Another function of GAM1338 is therefore inhibition of BA108L7.2 (Accession NP_112233.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BA108L7.2.

[37663] Bcl2-associated athanogene 5 (BAG5, Accession NP_004864.1) is another GAM1338 target gene, herein designated TARGET GENE. BAG5 BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by BAG5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAG5 BINDING SITE, designated SEQ ID:19878, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37664] Another function of GAM1338 is therefore inhibition of Bcl2-associated athanogene 5 (BAG5, Accession NP_004864.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAG5.

[37665] Bromodomain adjacent to zinc finger domain, 2a (BAZ2A, Accession NP_038477.1) is another GAM1338 target gene, herein designated TARGET GENE. BAZ2A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BAZ2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAZ2A BINDING SITE, designated SEQ ID:16740, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[37666] Another function of GAM1338 is therefore inhibition of Bromodomain adjacent to zinc finger domain, 2a (BAZ2A, Accession NP_038477.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAZ2A.

[37667] B-cell cll/lymphoma 10 (BCL10, Accession NP_003912.1) is another GAM1338 target gene, herein designated TARGET GENE. BCL10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCL10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCL10 BINDING SITE, designated SEQ ID:17565, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37668] Another function of GAM1338 is therefore inhibition of B-cell cll/lymphoma 10 (BCL10, Accession NP_003912.1), a gene which is a positive regulator of lymphocyte proliferation, NF- kappaB activator. and therefore may be associated with Malt lymphoma, follicular lymphoma. Accordingly, utilities of GAM1338 include diagnosis, prevention

and treatment of Malt lymphoma, follicular lymphoma, and of other diseases and clinical conditions associated with BCL10.

[37669] The function of BCL10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Bradykinin receptor b1 (BDKRB1, Accession NP_000701.2) is another GAM1338 target gene, herein designated TARGET GENE. BDKRB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BDKRB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BDKRB1 BINDING SITE, designated SEQ ID:13940, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37670] Another function of GAM1338 is therefore inhibition of Bradykinin receptor b1 (BDKRB1, Accession NP_000701.2), a gene which mediates intracellular calcium flux. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDKRB1.

[37671] The function of BDKRB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.B double prime 1, subunit of rna polymerase iii transcription initiation factor iiib (BDP1, Accession NP_060899.1) is another GAM1338 target gene, herein designated TARGET GENE. BDP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BDP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BDP1 BINDING SITE, designated SEQ ID:4304, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37672] Another function of GAM1338 is therefore inhibition of B double prime 1, subunit of rna polymerase iii transcription initiation factor iiib (BDP1, Accession NP_060899.1), a gene which activates RNA polymerase III transcription. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDP1.

[37673] The function of BDP1 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM146.1.BENE (Accession NP_005425.1) is another GAM1338 target gene, herein designated TARGET GENE. BENE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BENE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BENE BINDING SITE, designated SEQ ID:3688, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37674] Another function of GAM1338 is therefore inhibition of BENE (Accession NP_005425.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BENE.

[37675] BHD (Accession NP_659434.2) is another GAM1338 target gene, herein designated TARGET GENE. BHD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BHD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of BHD BINDING SITE, designated SEQ ID:13142, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37676] Another function of GAM1338 is therefore inhibition of BHD (Accession NP_659434.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BHD.

[37677] BNIP-S (Accession NP_612122.1) is another GAM1338 target gene, herein designated TARGET GENE. BNIP-S BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BNIP-S, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BNIP-S BINDING SITE, designated SEQ ID:17763, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37678] Another function of GAM1338 is therefore inhibition of BNIP-S (Accession NP_612122.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BNIP-S.

[37679] BRIP1 (Accession NP_114432.1) is another GAM1338 tar-

get gene, herein designated TARGET GENE. BRIP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BRIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BRIP1 BINDING SITE, designated SEQ ID:721, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37680] Another function of GAM1338 is therefore inhibition of BRIP1 (Accession NP_114432.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRIP1.

[37681] Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession NP_008979.2) is another GAM1338 target gene, herein designated TARGET GENE. BTN3A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTN3A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTN3A1 BINDING SITE, designated SEQ ID:17858, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA,

also designated SEQ ID:360.

[37682] Another function of GAM1338 is therefore inhibition of Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession NP_008979.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN3A1.

[37683] BXDC1 (Accession XP_166303.1) is another GAM1338 target gene, herein designated TARGET GENE. BXDC1 BINDING SITE1 and BXDC1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by BXDC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BXDC1 BINDING SITE1 and BXDC1 BINDING SITE2, designated SEQ ID:711 and SEQ ID:7070 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37684] Another function of GAM1338 is therefore inhibition of BXDC1 (Accession XP_166303.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BXDC1.

[37685] BY55 (Accession NP_008984.1) is another GAM1338 tar-

get gene, herein designated TARGET GENE. BY55 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BY55, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BY55 BINDING SITE, designated SEQ ID:17712, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37686] Another function of GAM1338 is therefore inhibition of BY55 (Accession NP_008984.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BY55.

[37687] Chromosome 11 open reading frame 17 (C11orf17, Accession NP_065693.2) is another GAM1338 target gene, herein designated TARGET GENE. C11orf17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C11orf17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C11orf17 BINDING SITE, designated SEQ ID:13793, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA,

also designated SEQ ID:360.

[37688] Another function of GAM1338 is therefore inhibition of Chromosome 11 open reading frame 17 (C11orf17, Accession NP_065693.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf17.

[37689] Chromosome 13 open reading frame 1 (C13orf1, Accession NP_065189.1) is another GAM1338 target gene, herein designated TARGET GENE. C13orf1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C13orf1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C13orf1 BINDING SITE, designated SEQ ID:2596, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37690] Another function of GAM1338 is therefore inhibition of Chromosome 13 open reading frame 1 (C13orf1, Accession NP_065189.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C13orf1.

[37691] C14orf113 (Accession NP_060100.1) is another GAM1338

target gene, herein designated TARGET GENE. C14orf113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf113 BINDING SITE, designated SEQ ID:19688, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37692] Another function of GAM1338 is therefore inhibition of C14orf113 (Accession NP_060100.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf113.

[37693] C14orf143 (Accession NP_660274.1) is another GAM1338 target gene, herein designated TARGET GENE. C14orf143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf143 BINDING SITE, designated SEQ ID:11599, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[37694] Another function of GAM1338 is therefore inhibition of C14orf143 (Accession NP_660274.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf143.

[37695] C14orf92 (Accession NP_055643.1) is another GAM1338 target gene, herein designated TARGET GENE. C14orf92 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf92, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf92 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37696] Another function of GAM1338 is therefore inhibition of C14orf92 (Accession NP_055643.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf92.

[37697] Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) is another GAM1338 target gene,

herein designated TARGET GENE. C1orf24 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C1orf24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:601, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37698] Another function of GAM1338 is therefore inhibition of Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24.

[37699] C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) is another GAM1338 target gene, herein designated TARGET GENE. C1QTNF6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1QTNF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1QTNF6 BINDING SITE, designated SEQ ID:18746, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37700] Another function of GAM1338 is therefore inhibition of C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QTNF6.

[37701] Chromosome 20 open reading frame 129 (C20orf129, Accession NP_112181.1) is another GAM1338 target gene, herein designated TARGET GENE. C20orf129 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf129, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf129 BINDING SITE, designated SEQ ID:13924, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37702] Another function of GAM1338 is therefore inhibition of Chromosome 20 open reading frame 129 (C20orf129, Accession NP_112181.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with C20orf129.

[37703] Chromosome 22 open reading frame 19 (C22orf19, Accession NP_003669.2) is another GAM1338 target gene, herein designated TARGET GENE. C22orf19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C22orf19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C22orf19 BINDING SITE, designated SEQ ID:14748, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37704] Another function of GAM1338 is therefore inhibition of Chromosome 22 open reading frame 19 (C22orf19, Accession NP_003669.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C22orf19.

[37705] C4orf9 (Accession XP_035572.1) is another GAM1338 target gene, herein designated TARGET GENE. C4orf9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C4orf9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of C4orf9 BINDING SITE, designated SEQ ID:13142, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37706] Another function of GAM1338 is therefore inhibition of C4orf9 (Accession XP_035572.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C4orf9.

[37707] Chromosome 6 open reading frame 33 (C6orf33, Accession NP_588608.1) is another GAM1338 target gene, herein designated TARGET GENE. C6orf33 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf33, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf33 BINDING SITE, designated SEQ ID:7278, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37708] Another function of GAM1338 is therefore inhibition of Chromosome 6 open reading frame 33 (C6orf33, Accession NP_588608.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with C6orf33.

[37709] C6orf5 (Accession NP_056339.2) is another GAM1338 target gene, herein designated TARGET GENE. C6orf5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf5 BINDING SITE, designated SEQ ID:10778, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37710] Another function of GAM1338 is therefore inhibition of C6orf5 (Accession NP_056339.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf5.

[37711] C6orf57 (Accession NP_660310.1) is another GAM1338 target gene, herein designated TARGET GENE. C6orf57 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf57, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf57 BINDING SITE, designated SEQ ID:6442, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37712] Another function of GAM1338 is therefore inhibition of C6orf57 (Accession NP_660310.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf57.

[37713] Complement component 7 (C7, Accession NP_000578.1) is another GAM1338 target gene, herein designated TARGET GENE. C7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C7 BINDING SITE, designated SEQ ID:11697, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37714] Another function of GAM1338 is therefore inhibition of Complement component 7 (C7, Accession NP_000578.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C7.

[37715] Chromosome 9 open reading frame 5 (C9orf5, Accession

NP_114401.1) is another GAM1338 target gene, herein designated TARGET GENE. C9orf5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C9orf5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C9orf5 BINDING SITE, designated SEQ ID:15709, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37716] Another function of GAM1338 is therefore inhibition of Chromosome 9 open reading frame 5 (C9orf5, Accession NP_114401.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf5.

[37717] Chromosome 9 open reading frame 9 (C9orf9, Accession NP_061829.2) is another GAM1338 target gene, herein designated TARGET GENE. C9orf9 BINDING SITE1 and C9orf9 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C9orf9, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

C9orf9 BINDING SITE1 and C9orf9 BINDING SITE2, designated SEQ ID:19273 and SEQ ID:13797 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37718] Another function of GAM1338 is therefore inhibition of Chromosome 9 open reading frame 9 (C9orf9, Accession NP_061829.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf9.

[37719] Calcium modulating ligand (CAMLG, Accession NP_001736.1) is another GAM1338 target gene, herein designated TARGET GENE. CAMLG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAMLG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMLG BINDING SITE, designated SEQ ID:9364, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37720] Another function of GAM1338 is therefore inhibition of Calcium modulating ligand (CAMLG, Accession NP_001736.1), a gene which is likely involved in the mo-

bilization of calcium as a result of the tcr/cd3 complex interaction. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMLG.

[37721] The function of CAMLG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.CAPRI (Accession NP_008920.3) is another GAM1338 target gene, herein designated TARGET GENE. CAPRI BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAPRI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAPRI BINDING SITE, designated SEQ ID:12829, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37722] Another function of GAM1338 is therefore inhibition of CAPRI (Accession NP_008920.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPRI.

[37723] Caspase recruitment domain family, member 6 (CARD6, Accession NP_115976.2) is another GAM1338 target gene,

herein designated TARGET GENE. CARD6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CARD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CARD6 BINDING SITE, designated SEQ ID:13142, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37724] Another function of GAM1338 is therefore inhibition of Caspase recruitment domain family, member 6 (CARD6, Accession NP_115976.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD6.

[37725] Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116766.1) is another GAM1338 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE, designated SEQ ID:18463, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37726] Another function of GAM1338 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116766.1), a gene which involves in the activation cascade of caspases responsible

for apoptosis execution. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[37727] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116764.1) is another GAM1338 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE, designated SEQ ID:18463, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37728] Another function of GAM1338 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116764.1), a gene which

involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[37729] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_116765.1) is another GAM1338 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE, designated SEQ ID:18463, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37730] Another function of GAM1338 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-reg-

ulated 2) (CASP2, Accession NP_116765.1), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[37731] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_001215.1) is another GAM1338 target gene, herein designated TARGET GENE. CASP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE, designated SEQ ID:18463, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37732] Another function of GAM1338 is therefore inhibition of Caspase 2, apoptosis-related cysteine protease (neural

precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NP_001215.1), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2.

[37733] The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_001219.2) is another GAM1338 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37734] Another function of GAM1338 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8,

Accession NP_001219.2), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[37735] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203520.1) is another GAM1338 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ

ID:360.

[37736] Another function of GAM1338 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203520.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[37737] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203521.1) is another GAM1338 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37738] Another function of GAM1338 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203521.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[37739] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203519.1) is another GAM1338 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA

encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37740] Another function of GAM1338 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203519.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[37741] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession

NP_787060.1) is another GAM1338 target gene, herein designated TARGET GENE. CBFA2T2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CBFA2T2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CBFA2T2 BINDING SITE, designated SEQ ID:3868, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37742] Another function of GAM1338 is therefore inhibition of Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_787060.1), a gene which is a putative transcription factor. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T2.

[37743] The function of CBFA2T2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_005084.1) is another GAM1338 target gene, herein

designated TARGET GENE. CBFA2T2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CBFA2T2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CBFA2T2 BINDING SITE, designated SEQ ID:3868, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37744] Another function of GAM1338 is therefore inhibition of Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_005084.1), a gene which is a putative transcription factor. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T2.

[37745] The function of CBFA2T2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Chemokine (c-c motif) ligand 16 (CCL16, Accession NP_004581.1) is another GAM1338 target gene, herein designated TARGET GENE. CCL16 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by CCL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL16 BINDING SITE, designated SEQ ID:10633, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37746] Another function of GAM1338 is therefore inhibition of Chemokine (c-c motif) ligand 16 (CCL16, Accession NP_004581.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL16.

[37747] Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) is another GAM1338 target gene, herein designated TARGET GENE. CCL22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCL22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL22 BINDING SITE, designated SEQ ID:11649, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37748] Another function of GAM1338 is therefore inhibition of Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL22.

[37749] Cyclin f (CCNF, Accession NP_001752.1) is another GAM1338 target gene, herein designated TARGET GENE. CCNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCNF BINDING SITE, designated SEQ ID:14395, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37750] Another function of GAM1338 is therefore inhibition of Cyclin f (CCNF, Accession NP_001752.1), a gene which likely to be involved in the control of the cell cycle during s phase and g2. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNF.

[37751] The function of CCNF and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM130.1.Ccr4 carbon catabolite repression 4-like (s. cerevisiae) (CCRN4L, Accession NP_036250.2) is another GAM1338 target gene, herein designated TARGET GENE. CCRN4L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCRN4L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCRN4L BINDING SITE, designated SEQ ID:15829, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37752] Another function of GAM1338 is therefore inhibition of Ccr4 carbon catabolite repression 4-like (s. cerevisiae) (CCRN4L, Accession NP_036250.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCRN4L.

[37753] Cd209 antigen (CD209, Accession NP_066978.1) is another GAM1338 target gene, herein designated TARGET GENE. CD209 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD209, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD209 BINDING SITE, designated SEQ ID:8229, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37754] Another function of GAM1338 is therefore inhibition of Cd209 antigen (CD209, Accession NP_066978.1), a gene which may play an important role in the CD4- independent association of HIV with cells. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD209.

[37755] The function of CD209 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Cd24 antigen (small cell lung carcinoma cluster 4 antigen) (CD24, Accession NP_037362.1) is another GAM1338 target gene, herein designated TARGET GENE. CD24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

CD24 BINDING SITE, designated SEQ ID:18593, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37756] Another function of GAM1338 is therefore inhibition of Cd24 antigen (small cell lung carcinoma cluster 4 antigen) (CD24, Accession NP_037362.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD24.

[37757] Cdc14 cell division cycle 14 homolog b (s. cerevisiae) (CDC14B, Accession NP_201589.1) is another GAM1338 target gene, herein designated TARGET GENE. CDC14B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDC14B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC14B BINDING SITE, designated SEQ ID:7919, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37758] Another function of GAM1338 is therefore inhibition of Cdc14 cell division cycle 14 homolog b (s. cerevisiae) (CDC14B, Accession NP_201589.1) . Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC14B.

[37759] Cdc6 cell division cycle 6 homolog (s. cerevisiae) (CDC6, Accession NP_001245.1) is another GAM1338 target gene, herein designated TARGET GENE. CDC6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDC6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC6 BINDING SITE, designated SEQ ID:7495, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37760] Another function of GAM1338 is therefore inhibition of Cdc6 cell division cycle 6 homolog (s. cerevisiae) (CDC6, Accession NP_001245.1), a gene which is a component of the origin recognition complex (orc) that binds origins of replication. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC6.

[37761] The function of CDC6 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM189.1.CDCP1 (Accession NP_073753.3) is another GAM1338 target gene, herein designated TARGET GENE. CDCP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDCP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDCP1 BINDING SITE, designated SEQ ID:20095, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37762] Another function of GAM1338 is therefore inhibition of CDCP1 (Accession NP_073753.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDCP1.

[37763] Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) is another GAM1338 target gene, herein designated TARGET GENE. CDH1 BINDING SITE1 and CDH1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CDH1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of CDH1 BINDING SITE1 and CDH1 BINDING SITE2, designated SEQ ID:3667 and SEQ ID:5919 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37764] Another function of GAM1338 is therefore inhibition of Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH1.

[37765] Cadherin 17, li cadherin (liver-intestine) (CDH17, Accession NP_004054.2) is another GAM1338 target gene, herein designated TARGET GENE. CDH17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDH17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH17 BINDING SITE, designated SEQ ID:5407, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37766] Another function of GAM1338 is therefore inhibition of Cadherin 17, li cadherin (liver-intestine) (CDH17, Acces-

sion NP_004054.2), a gene which may have a role in the morphological organization of liver and intestine and involved in intestinal peptide transport. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH17.

[37767] The function of CDH17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.CDK11 (Accession XP_166324.1) is another GAM1338 target gene, herein designated TARGET GENE. CDK11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDK11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDK11 BINDING SITE, designated SEQ ID:5408, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37768] Another function of GAM1338 is therefore inhibition of CDK11 (Accession XP_166324.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDK11.

[37769] CDKAL1 (Accession NP_060244.1) is another GAM1338 target gene, herein designated TARGET GENE. CDKAL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDKAL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDKAL1 BINDING SITE, designated SEQ ID:12153, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37770] Another function of GAM1338 is therefore inhibition of CDKAL1 (Accession NP_060244.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKAL1.

[37771] Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) is another GAM1338 target gene, herein designated TARGET GENE. CEACAM8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CEACAM8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of CEACAM8 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37772] Another function of GAM1338 is therefore inhibition of Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEACAM8.

[37773] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) is another GAM1338 target gene, herein designated TARGET GENE. CECR1 BINDING SITE1 and CECR1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CECR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE1 and CECR1 BINDING SITE2, designated SEQ ID:15125 and SEQ ID:11209 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37774] Another function of GAM1338 is therefore inhibition of

Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[37775] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) is another GAM1338 target gene, herein designated TARGET GENE. CECR1 BINDING SITE1 and CECR1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CECR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE1 and CECR1 BINDING SITE2, designated SEQ ID:11209 and SEQ ID:15125 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37776] Another function of GAM1338 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[37777] Centromere protein h (CENPH, Accession NP_075060.1) is

another GAM1338 target gene, herein designated TARGET GENE. CENPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CENPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENPH BINDING SITE, designated SEQ ID:7835, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37778] Another function of GAM1338 is therefore inhibition of Centromere protein h (CENPH, Accession NP_075060.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENPH.

[37779] Centromere protein j (CENPJ, Accession NP_060921.2) is another GAM1338 target gene, herein designated TARGET GENE. CENPJ BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CENPJ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENPJ BINDING SITE, designated SEQ ID:8802,

to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37780] Another function of GAM1338 is therefore inhibition of Centromere protein j (CENPJ, Accession NP_060921.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENPJ.

[37781] CGI-150 (Accession NP_057164.1) is another GAM1338 target gene, herein designated TARGET GENE. CGI-150 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CGI-150, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-150 BINDING SITE, designated SEQ ID:19951, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37782] Another function of GAM1338 is therefore inhibition of CGI-150 (Accession NP_057164.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-150.

[37783] Chromatin accessibility complex 1 (CHRAC1, Accession

NP_059140.1) is another GAM1338 target gene, herein designated TARGET GENE. CHRAC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHRAC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHRAC1 BINDING SITE, designated SEQ ID:18375, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37784] Another function of GAM1338 is therefore inhibition of Chromatin accessibility complex 1 (CHRAC1, Accession NP_059140.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRAC1.

[37785] Carbohydrate (chondroitin) synthase 1 (CHSY1, Accession NP_055733.2) is another GAM1338 target gene, herein designated TARGET GENE. CHSY1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHSY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHSY1 BINDING SITE, designated

SEQ ID:18370, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37786] Another function of GAM1338 is therefore inhibition of Carbohydrate (chondroitin) synthase 1 (CHSY1, Accession NP_055733.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHSY1.

[37787] Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2) is another GAM1338 target gene, herein designated TARGET GENE. CIAS1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CIAS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIAS1 BINDING SITE, designated SEQ ID:7985, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37788] Another function of GAM1338 is therefore inhibition of Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2), a gene which may mediate protein- protein interactions; contains a leucine rich repeat and there-

fore may be associated with Familial cold autoinflammatory syndrome, muckle- wells syndrome. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Familial cold autoinflammatory syndrome, muckle- wells syndrome, and of other diseases and clinical conditions associated with CIAS1.

[37789] The function of CIAS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM90.1.CIP29 (Accession NP_115740.3) is another GAM1338 target gene, herein designated TARGET GENE. CIP29 BINDING SITE1 and CIP29 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CIP29, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIP29 BINDING SITE1 and CIP29 BINDING SITE2, designated SEQ ID:11639 and SEQ ID:20120 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37790] Another function of GAM1338 is therefore inhibition of CIP29 (Accession NP_115740.3) . Accordingly, utilities of

GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIP29.

[37791] C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2) is another GAM1338 target gene, herein designated TARGET GENE. CLECSF12 BINDING SITE1 and CLECSF12 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CLECSF12, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLECSF12 BINDING SITE1 and CLECSF12 BINDING SITE2, designated SEQ ID:1868 and SEQ ID:10233 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37792] Another function of GAM1338 is therefore inhibition of C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2), a gene which is a pattern- recognition receptor . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLECSF12.

[37793] The function of CLECSF12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Cell matrix adhesion regulator (CMAR, Accession NP_005191.2) is another GAM1338 target gene, herein designated TARGET GENE. CMAR BINDING SITE1 and CMAR BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CMAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CMAR BINDING SITE1 and CMAR BINDING SITE2, designated SEQ ID:6738 and SEQ ID:19999 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37794] Another function of GAM1338 is therefore inhibition of Cell matrix adhesion regulator (CMAR, Accession NP_005191.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CMAR.

[37795] Calponin 2 (CNN2, Accession NP_004359.1) is another GAM1338 target gene, herein designated TARGET GENE. CNN2 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by CNN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNN2 BINDING SITE, designated SEQ ID:6909, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37796] Another function of GAM1338 is therefore inhibition of Calponin 2 (CNN2, Accession NP_004359.1), a gene which may be involved in the structural organization and/or anchorage of actin filaments. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNN2.

[37797] The function of CNN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.2',3'-cyclic nucleotide 3' phosphodiesterase (CNP, Accession NP_149124.1) is another GAM1338 target gene, herein designated TARGET GENE. CNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of CNP BINDING SITE, designated SEQ ID:5014, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37798] Another function of GAM1338 is therefore inhibition of 2',3'-cyclic nucleotide 3' phosphodiesterase (CNP, Accession NP_149124.1), a gene which can link tubulin to membranes and may regulate cytoplasmic microtubule distribution. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNP.

[37799] The function of CNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) is another GAM1338 target gene, herein designated TARGET GENE. COLEC12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COLEC12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COLEC12 BINDING SITE, designated

SEQ ID:13793, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37800] Another function of GAM1338 is therefore inhibition of Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC12.

[37801] Coronin, actin binding protein, 1c (CORO1C, Accession NP_055140.1) is another GAM1338 target gene, herein designated TARGET GENE. CORO1C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CORO1C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CORO1C BINDING SITE, designated SEQ ID:1439, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37802] Another function of GAM1338 is therefore inhibition of Coronin, actin binding protein, 1c (CORO1C, Accession NP_055140.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with CORO1C.

[37803] Cox15 homolog, cytochrome c oxidase assembly protein (yeast) (COX15, Accession NP_510870.1) is another GAM1338 target gene, herein designated TARGET GENE. COX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COX15 BINDING SITE, designated SEQ ID:18262, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37804] Another function of GAM1338 is therefore inhibition of Cox15 homolog, cytochrome c oxidase assembly protein (yeast) (COX15, Accession NP_510870.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COX15.

[37805] Carboxypeptidase a4 (CPA4, Accession NP_057436.1) is another GAM1338 target gene, herein designated TARGET GENE. CPA4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPA4,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPA4 BINDING SITE, designated SEQ ID:10987, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37806] Another function of GAM1338 is therefore inhibition of Carboxypeptidase a4 (CPA4, Accession NP_057436.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPA4.

[37807] CPR8 (Accession NP_065790.1) is another GAM1338 target gene, herein designated TARGET GENE. CPR8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CPR8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPR8 BINDING SITE, designated SEQ ID:9163, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37808] Another function of GAM1338 is therefore inhibition of CPR8 (Accession NP_065790.1) . Accordingly, utilities of

GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPR8.

[37809] Carbamoyl-phosphate synthetase 1, mitochondrial (CPS1, Accession NP_001866.2) is another GAM1338 target gene, herein designated TARGET GENE. CPS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPS1 BINDING SITE, designated SEQ ID:4147, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37810] Another function of GAM1338 is therefore inhibition of Carbamoyl-phosphate synthetase 1, mitochondrial (CPS1, Accession NP_001866.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPS1.

[37811] Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) is another GAM1338 target gene, herein designated TARGET GENE. CPSF2 BINDING SITE1 and CPSF2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by

CPSF2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPSF2 BINDING SITE1 and CPSF2 BINDING SITE2, designated SEQ ID:6739 and SEQ ID:6347 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37812] Another function of GAM1338 is therefore inhibition of Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPSF2.

[37813] Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000564.1) is another GAM1338 target gene, herein designated TARGET GENE. CR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CR1 BINDING SITE, designated SEQ ID:13868, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37814] Another function of GAM1338 is therefore inhibition of Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000564.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CR1.

[37815] Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000642.2) is another GAM1338 target gene, herein designated TARGET GENE. CR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CR1 BINDING SITE, designated SEQ ID:13868, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37816] Another function of GAM1338 is therefore inhibition of Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000642.2)

. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CR1.

[37817] Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) is another GAM1338 target gene, herein designated TARGET GENE. CRLF3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRLF3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRLF3 BINDING SITE, designated SEQ ID:9675, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37818] Another function of GAM1338 is therefore inhibition of Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRLF3.

[37819] Cofactor required for sp1 transcriptional activation, subunit 6, 77kda (CRSP6, Accession NP_004259.3) is another GAM1338 target gene, herein designated TARGET GENE. CRSP6 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by CRSP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRSP6 BINDING SITE, designated SEQ ID:12005, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37820] Another function of GAM1338 is therefore inhibition of Cofactor required for sp1 transcriptional activation, subunit 6, 77kda (CRSP6, Accession NP_004259.3), a gene which is required for Sp1 mediated transcriptional activation with TAF(II)s. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRSP6.

[37821] The function of CRSP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Cartilage associated protein (CRTAP, Accession NP_006362.1) is another GAM1338 target gene, herein designated TARGET GENE. CRTAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRTAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRTAP BINDING SITE, designated SEQ ID:776, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37822] Another function of GAM1338 is therefore inhibition of Cartilage associated protein (CRTAP, Accession NP_006362.1), a gene which is a novel developmentally regulated chick embryo protein. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRTAP.

[37823] The function of CRTAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Crystallin, zeta (quinone reductase)-like 1 (CRYZL1, Accession NP_665857.1) is another GAM1338 target gene, herein designated TARGET GENE. CRYZL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRYZL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRYZL1 BINDING SITE, designated

SEQ ID:2539, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37824] Another function of GAM1338 is therefore inhibition of Crystallin, zeta (quinone reductase)-like 1 (CRYZL1, Accession NP_665857.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRYZL1.

[37825] Crystallin, zeta (quinone reductase)-like 1 (CRYZL1, Accession NP_660354.1) is another GAM1338 target gene, herein designated TARGET GENE. CRYZL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRYZL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRYZL1 BINDING SITE, designated SEQ ID:2539, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37826] Another function of GAM1338 is therefore inhibition of Crystallin, zeta (quinone reductase)-like 1 (CRYZL1, Accession NP_660354.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with CRYZL1.

[37827] CSE-C (Accession NP_061851.1) is another GAM1338 target gene, herein designated TARGET GENE. CSE-C BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CSE-C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSE-C BINDING SITE, designated SEQ ID:2336, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37828] Another function of GAM1338 is therefore inhibition of CSE-C (Accession NP_061851.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE-C.

[37829] Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_803185.1) is another GAM1338 target gene, herein designated TARGET GENE. CSE1L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CSE1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of CSE1L BINDING SITE, designated SEQ ID:3997, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37830] Another function of GAM1338 is therefore inhibition of Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_803185.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE1L.

[37831] Casein kinase 2, alpha prime polypeptide (CSNK2A2, Accession NP_001887.1) is another GAM1338 target gene, herein designated TARGET GENE. CSNK2A2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CSNK2A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSNK2A2 BINDING SITE, designated SEQ ID:15382, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37832] Another function of GAM1338 is therefore inhibition of Casein kinase 2, alpha prime polypeptide (CSNK2A2, Accession NP_001887.1), a gene which catalyzes the phos-

phorylation of serine or threonine residues in proteins. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK2A2.

[37833] The function of CSNK2A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Cardiotrophin 1 (CTF1, Accession NP_001321.1) is another GAM1338 target gene, herein designated TARGET GENE. CTF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTF1 BINDING SITE, designated SEQ ID:6515, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37834] Another function of GAM1338 is therefore inhibition of Cardiotrophin 1 (CTF1, Accession NP_001321.1), a gene which may play a role in cardiac hypertrophy. and therefore may be associated with Cardiac hypertrophy. Accordingly, utilities of GAM1338 include diagnosis, prevention

and treatment of Cardiac hypertrophy, and of other diseases and clinical conditions associated with CTF1.

[37835] The function of CTF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Cathepsin s (CTSS, Accession NP_004070.3) is another GAM1338 target gene, herein designated TARGET GENE. CTSS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSS BINDING SITE, designated SEQ ID:7946, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37836] Another function of GAM1338 is therefore inhibition of Cathepsin s (CTSS, Accession NP_004070.3), a gene which is a lysosomal cysteine (thiol) protease that cleaves elastin. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSS.

[37837] The function of CTSS and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM72.1.Chemokine (c-x-c motif) ligand 16 (CXCL16, Accession NP_071342.1) is another GAM1338 target gene, herein designated TARGET GENE. CXCL16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CXCL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CXCL16 BINDING SITE, designated SEQ ID:11701, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37838] Another function of GAM1338 is therefore inhibition of Chemokine (c-x-c motif) ligand 16 (CXCL16, Accession NP_071342.1), a gene which induces calcium mobilization. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCL16.

[37839] The function of CXCL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Chemokine (c-x-c motif) ligand 6 (granulocyte chemotactic protein 2) (CXCL6, Accession

NP_002984.1) is another GAM1338 target gene, herein designated TARGET GENE. CXCL6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CXCL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CXCL6 BINDING SITE, designated SEQ ID:7236, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37840] Another function of GAM1338 is therefore inhibition of Chemokine (c-x-c motif) ligand 6 (granulocyte chemotactic protein 2) (CXCL6, Accession NP_002984.1), a gene which is chemotactic for neutrophil granulocytes. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCL6.

[37841] The function of CXCL6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.1.CYCS (Accession NP_061820.1) is another GAM1338 target gene, herein designated TARGET GENE. CYCS BINDING SITE1 through CYCS BINDING SITE3 are tar-

get binding sites found in untranslated regions of mRNA encoded by CYCS, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYCS BINDING SITE1 through CYCS BINDING SITE3, designated SEQ ID:15642, SEQ ID:14950 and SEQ ID:19693 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37842] Another function of GAM1338 is therefore inhibition of CYCS (Accession NP_061820.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYCS.

[37843] Cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2, Accession NP_001331.1) is another GAM1338 target gene, herein designated TARGET GENE. CYLC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYLC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYLC2 BINDING SITE, designated SEQ ID:12632, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[37844] Another function of GAM1338 is therefore inhibition of Cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2, Accession NP_001331.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYLC2.

[37845] Cytochrome p450, subfamily i (aromatic compound-inducible), polypeptide 2 (CYP1A2, Accession NP_000752.1) is another GAM1338 target gene, herein designated TARGET GENE. CYP1A2 BINDING SITE1 through CYP1A2 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by CYP1A2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP1A2 BINDING SITE1 through CYP1A2 BINDING SITE3, designated SEQ ID:6816, SEQ ID:8688 and SEQ ID:13973 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37846] Another function of GAM1338 is therefore inhibition of Cytochrome p450, subfamily i (aromatic compound-inducible), polypeptide 2 (CYP1A2, Accession NP_000752.1), a gene which intervenes in an NADPH- de-

pendent electron transport pathway. and therefore may be associated with Porphyria cutanea tarda. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Porphyria cutanea tarda, and of other diseases and clinical conditions associated with CYP1A2.

[37847] The function of CYP1A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1) is another GAM1338 target gene, herein designated TARGET GENE. CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CYP2B6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2, designated SEQ ID:3011 and SEQ ID:4525 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37848] Another function of GAM1338 is therefore inhibition of Cytochrome p450, subfamily iib

(phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1), a gene which oxidizes a variety of structurally unrelated compounds, including steroids, fatty acids, and xenobiotics. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP2B6.

[37849] The function of CYP2B6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily ivf, polypeptide 3 (leukotriene b4 omega hydroxylase) (CYP4F3, Accession NP_000887.1) is another GAM1338 target gene, herein designated TARGET GENE. CYP4F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP4F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP4F3 BINDING SITE, designated SEQ ID:1417, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37850] Another function of GAM1338 is therefore inhibition of Cytochrome p450, subfamily ivf, polypeptide 3

(leukotriene b4 omega hydroxylase) (CYP4F3, Accession NP_000887.1), a gene which converts leukotriene B4 into the less active 20- hydroxy- leukotriene B4. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP4F3.

[37851] The function of CYP4F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.1.CYP51A1 (Accession NP_000777.1) is another GAM1338 target gene, herein designated TARGET GENE. CYP51A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP51A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP51A1 BINDING SITE, designated SEQ ID:10631, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37852] Another function of GAM1338 is therefore inhibition of CYP51A1 (Accession NP_000777.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with CYP51A1.

[37853] Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1) is another GAM1338 target gene, herein designated TARGET GENE. CYP8B1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP8B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP8B1 BINDING SITE, designated SEQ ID:5584, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37854] Another function of GAM1338 is therefore inhibition of Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1), a gene which functions in bile acid biosynthesis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP8B1.

[37855] The function of CYP8B1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM47.1.Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) is another GAM1338 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:6035, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37856] Another function of GAM1338 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[37857] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) is another GAM1338 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:6035, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37858] Another function of GAM1338 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[37859] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835364.1) is another GAM1338 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:6035, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37860] Another function of GAM1338 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin)

(DCX, Accession NP_835364.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[37861] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) is another GAM1338 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:6035, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37862] Another function of GAM1338 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[37863] Dead/h (asp-glu-ala-asp/his) box polypeptide 31 (DDX31, Accession NP_619526.1) is another GAM1338 target gene, herein designated TARGET GENE. DDX31 BINDING SITE is a target binding site found in the 3` un-

translated region of multiple transcripts of mRNA encoded by DDX31, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX31 BINDING SITE, designated SEQ ID:17894, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37864] Another function of GAM1338 is therefore inhibition of Dead/h (asp-glu-ala-asp/his) box polypeptide 31 (DDX31, Accession NP_619526.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX31.

[37865] Desmin (DES, Accession NP_001918.2) is another GAM1338 target gene, herein designated TARGET GENE. DES BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DES BINDING SITE, designated SEQ ID:5111, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37866] Another function of GAM1338 is therefore inhibition of Desmin (DES, Accession NP_001918.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DES.

[37867] Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1) is another GAM1338 target gene, herein designated TARGET GENE. DFFB BINDING SITE1 and DFFB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DFFB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DFFB BINDING SITE1 and DFFB BINDING SITE2, designated SEQ ID:7574 and SEQ ID:7848 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37868] Another function of GAM1338 is therefore inhibition of Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1), a gene which induces DNA fragmentation and chromatin condensation during apoptosis. Accord-

ingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DFFB.

[37869] The function of DFFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1) is another GAM1338 target gene, herein designated TARGET GENE. DIAPH2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DIAPH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DIAPH2 BINDING SITE, designated SEQ ID:12586, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37870] Another function of GAM1338 is therefore inhibition of Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1), a gene which may affect in oogenesis and therefore may be associated with Premature ovarian failure . Accordingly, utilities of GAM1338 include diagnosis,

prevention and treatment of Premature ovarian failure ., and of other diseases and clinical conditions associated with DIAPH2.

[37871] The function of DIAPH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1) is another GAM1338 target gene, herein designated TARGET GENE. DISC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DISC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DISC1 BINDING SITE, designated SEQ ID:13620, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37872] Another function of GAM1338 is therefore inhibition of Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1), a gene which has globular N- terminal domain(s) and a helical C- terminal domain. and therefore may be associated with Schizophrenia . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of Schizophrenia ., and of other diseases and clinical conditions associated with DISC1.

[37873] The function of DISC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.DKFZP434B044 (Accession NP_113664.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP434B044 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434B044, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434B044 BINDING SITE, designated SEQ ID:11474, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37874] Another function of GAM1338 is therefore inhibition of DKFZP434B044 (Accession NP_113664.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434B044.

[37875] DKFZP434B1727 (Accession NP_115519.1) is another GAM1338 target gene, herein designated TARGET GENE.

DKFZP434B1727 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434B1727, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434B1727 BINDING SITE, designated SEQ ID:1107, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37876] Another function of GAM1338 is therefore inhibition of DKFZP434B1727 (Accession NP_115519.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434B1727.

[37877] DKFZp434C0923 (Accession NP_060068.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp434C0923 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434C0923, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434C0923 BINDING SITE, designated SEQ ID:7947, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37878] Another function of GAM1338 is therefore inhibition of DKFZp434C0923 (Accession NP_060068.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434C0923.

[37879] DKFZP434C212 (Accession XP_044196.3) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP434C212 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434C212, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434C212 BINDING SITE, designated SEQ ID:5299, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37880] Another function of GAM1338 is therefore inhibition of DKFZP434C212 (Accession XP_044196.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C212.

[37881] DKFZP434D146 (Accession NP_056410.2) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP434D146 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434D146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434D146 BINDING SITE, designated SEQ ID:4843, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37882] Another function of GAM1338 is therefore inhibition of DKFZP434D146 (Accession NP_056410.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434D146.

[37883] DKFZp434E2220 (Accession NP_060082.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp434E2220 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp434E2220, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of DKFZp434E2220 BINDING SITE, designated SEQ ID:18031, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37884] Another function of GAM1338 is therefore inhibition of DKFZp434E2220 (Accession NP_060082.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E2220.

[37885] DKFZP434F0318 (Accession NP_110444.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP434F0318 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F0318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434F0318 BINDING SITE, designated SEQ ID:14671, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37886] Another function of GAM1338 is therefore inhibition of DKFZP434F0318 (Accession NP_110444.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZP434F0318.

[37887] DKFZp434F1719 (Accession NP_115624.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp434F1719 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434F1719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434F1719 BINDING SITE, designated SEQ ID:4173, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37888] Another function of GAM1338 is therefore inhibition of DKFZp434F1719 (Accession NP_115624.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434F1719.

[37889] DKFZp547H025 (Accession NP_064546.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp547H025 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547H025, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547H025 BINDING SITE, designated SEQ ID:1994, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37890] Another function of GAM1338 is therefore inhibition of DKFZp547H025 (Accession NP_064546.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547H025.

[37891] DKFZp547P234 (Accession NP_694590.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp547P234 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547P234, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547P234 BINDING SITE, designated SEQ ID:3007, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37892] Another function of GAM1338 is therefore inhibition of

DKFZp547P234 (Accession NP_694590.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547P234.

[37893] DKFZP564D166 (Accession NP_108648.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP564D166 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DKFZP564D166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564D166 BINDING SITE, designated SEQ ID:13202, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37894] Another function of GAM1338 is therefore inhibition of DKFZP564D166 (Accession NP_108648.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D166.

[37895] DKFZP564G092 (Accession NP_056416.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP564G092 BINDING SITE is a target binding site

found in the 5` untranslated region of mRNA encoded by DKFZP564G092, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564G092 BINDING SITE, designated SEQ ID:519, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37896] Another function of GAM1338 is therefore inhibition of DKFZP564G092 (Accession NP_056416.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564G092.

[37897] DKFZP564I122 (Accession XP_032397.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP564I122 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564I122, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564I122 BINDING SITE, designated SEQ ID:19815, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[37898] Another function of GAM1338 is therefore inhibition of DKFZP564I122 (Accession XP_032397.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564I122.

[37899] DKFZP564J0863 (Accession NP_056274.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP564J0863 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564J0863, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564J0863 BINDING SITE, designated SEQ ID:18946, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37900] Another function of GAM1338 is therefore inhibition of DKFZP564J0863 (Accession NP_056274.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564J0863.

[37901] DKFZP564K0322 (Accession NP_114429.1) is another

GAM1338 target gene, herein designated TARGET GENE. DKFZP564K0322 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564K0322, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564K0322 BINDING SITE, designated SEQ ID:1414, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37902] Another function of GAM1338 is therefore inhibition of DKFZP564K0322 (Accession NP_114429.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564K0322.

[37903] DKFZp564K142 (Accession NP_115497.2) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp564K142 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp564K142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp564K142 BINDING SITE,

designated SEQ ID:811, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37904] Another function of GAM1338 is therefore inhibition of DKFZp564K142 (Accession NP_115497.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp564K142.

[37905] DKFZP564O0523 (Accession NP_115496.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP564O0523 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O0523, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564O0523 BINDING SITE, designated SEQ ID:1963, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37906] Another function of GAM1338 is therefore inhibition of DKFZP564O0523 (Accession NP_115496.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZP564O0523.

[37907] DKFZP566D1346 (Accession NP_110443.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP566D1346 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP566D1346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566D1346 BINDING SITE, designated SEQ ID:12834, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37908] Another function of GAM1338 is therefore inhibition of DKFZP566D1346 (Accession NP_110443.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566D1346.

[37909] DKFZP566I1024 (Accession NP_056226.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP566I1024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP566I1024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566I1024 BINDING SITE, designated SEQ ID:2402, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37910] Another function of GAM1338 is therefore inhibition of DKFZP566I1024 (Accession NP_056226.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566I1024.

[37911] DKFZP586D0919 (Accession NP_056248.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZP586D0919 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586D0919, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586D0919 BINDING SITE, designated SEQ ID:5664, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37912] Another function of GAM1338 is therefore inhibition of DKFZP586D0919 (Accession NP_056248.1) . Accordingly,

utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586D0919.

[37913] DKFZp667B1218 (Accession NP_808881.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp667B1218 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp667B1218, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667B1218 BINDING SITE, designated SEQ ID:13142, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37914] Another function of GAM1338 is therefore inhibition of DKFZp667B1218 (Accession NP_808881.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp667B1218.

[37915] DKFZp667E0512 (Accession XP_117353.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp667E0512 BINDING SITE1 and DKFZp667E0512 BINDING SITE2 are target binding sites found in untrans-

lated regions of mRNA encoded by DKFZp667E0512, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667E0512 BINDING SITE1 and DKFZp667E0512 BINDING SITE2, designated SEQ ID:17043 and SEQ ID:9198 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37916] Another function of GAM1338 is therefore inhibition of DKFZp667E0512 (Accession XP_117353.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp667E0512.

[37917] DKFZp761B107 (Accession NP_775734.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp761B107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761B107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B107 BINDING SITE, designated SEQ ID:5298, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37918] Another function of GAM1338 is therefore inhibition of DKFZp761B107 (Accession NP_775734.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B107.

[37919] DKFZp761B128 (Accession NP_689650.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp761B128 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761B128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B128 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37920] Another function of GAM1338 is therefore inhibition of DKFZp761B128 (Accession NP_689650.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B128.

[37921] DKFZp761H039 (Accession NP_061181.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp761H039 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761H039, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761H039 BINDING SITE, designated SEQ ID:12709, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37922] Another function of GAM1338 is therefore inhibition of DKFZp761H039 (Accession NP_061181.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761H039.

[37923] DKFZp761J139 (Accession NP_115656.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp761J139 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761J139, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of DKFZp761J139 BINDING SITE, designated SEQ ID:969, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37924] Another function of GAM1338 is therefore inhibition of DKFZp761J139 (Accession NP_115656.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761J139.

[37925] DKFZp761N1114 (Accession XP_086327.6) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp761N1114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761N1114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761N1114 BINDING SITE, designated SEQ ID:10882, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37926] Another function of GAM1338 is therefore inhibition of DKFZp761N1114 (Accession XP_086327.6) . Accordingly, utilities of GAM1338 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZp761N1114.

[37927] DKFZp761O0113 (Accession NP_060879.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp761O0113 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761O0113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761O0113 BINDING SITE, designated SEQ ID:11194, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37928] Another function of GAM1338 is therefore inhibition of DKFZp761O0113 (Accession NP_060879.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761O0113.

[37929] DKFZp761P1121 (Accession NP_690870.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp761P1121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761P1121, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761P1121 BINDING SITE, designated SEQ ID:1413, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37930] Another function of GAM1338 is therefore inhibition of DKFZp761P1121 (Accession NP_690870.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761P1121.

[37931] DKFZp762C2414 (Accession NP_848637.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp762C2414 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762C2414, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762C2414 BINDING SITE, designated SEQ ID:11830, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37932] Another function of GAM1338 is therefore inhibition of

DKFZp762C2414 (Accession NP_848637.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762C2414.

[37933] DKFZp762H185 (Accession XP_172976.2) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp762H185 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762H185, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762H185 BINDING SITE, designated SEQ ID:2137, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37934] Another function of GAM1338 is therefore inhibition of DKFZp762H185 (Accession XP_172976.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762H185.

[37935] DKFZp762I137 (Accession NP_689624.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp762I137 BINDING SITE is a target binding site found

in the 3` untranslated region of mRNA encoded by DKFZp762I137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762I137 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37936] Another function of GAM1338 is therefore inhibition of DKFZp762I137 (Accession NP_689624.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762I137.

[37937] DKFZp762I194 (Accession NP_689597.1) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp762I194 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762I194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762I194 BINDING SITE, designated SEQ ID:19272, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[37938] Another function of GAM1338 is therefore inhibition of DKFZp762I194 (Accession NP_689597.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762I194.

[37939] DKFZp762L0311 (Accession NP_061189.2) is another GAM1338 target gene, herein designated TARGET GENE. DKFZp762L0311 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762L0311, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762L0311 BINDING SITE, designated SEQ ID:13546, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37940] Another function of GAM1338 is therefore inhibition of DKFZp762L0311 (Accession NP_061189.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762L0311.

[37941] Dynein, axonemal, heavy polypeptide 11 (DNAH11, Ac-

cession NP_003768.1) is another GAM1338 target gene, herein designated TARGET GENE. DNAH11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DNAH11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DNAH11 BINDING SITE, designated SEQ ID:18338, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37942] Another function of GAM1338 is therefore inhibition of Dynein, axonemal, heavy polypeptide 11 (DNAH11, Accession NP_003768.1), a gene which may function as a motor protein. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAH11.

[37943] The function of DNAH11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.DRIM (Accession NP_055318.1) is another GAM1338 target gene, herein designated TARGET GENE. DRIM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DRIM, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DRIM BINDING SITE, designated SEQ ID:2324, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37944] Another function of GAM1338 is therefore inhibition of DRIM (Accession NP_055318.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRIM.

[37945] Dentatorubral-pallidoluysian atrophy (atrophin-1) (DRPLA, Accession NP_001931.1) is another GAM1338 target gene, herein designated TARGET GENE. DRPLA BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DRPLA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DRPLA BINDING SITE, designated SEQ ID:8154, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37946] Another function of GAM1338 is therefore inhibition of Dentatorubral-pallidoluysian atrophy (atrophin-1) (DRPLA,

Accession NP_001931.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRPLA.

[37947] Desmocollin 3 (DSC3, Accession NP_001932.1) is another GAM1338 target gene, herein designated TARGET GENE. DSC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE, designated SEQ ID:2085, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37948] Another function of GAM1338 is therefore inhibition of Desmocollin 3 (DSC3, Accession NP_001932.1), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC3.

[37949] The function of DSC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM30.1.Desmocollin 3 (DSC3, Accession NP_077741.1) is another GAM1338 target gene, herein designated TARGET GENE. DSC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE, designated SEQ ID:2085, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37950] Another function of GAM1338 is therefore inhibition of Desmocollin 3 (DSC3, Accession NP_077741.1), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC3.

[37951] The function of DSC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Down syndrome critical region gene 6 (DSCR6, Accession NP_061835.1) is another GAM1338 target gene, herein designated TARGET GENE. DSCR6

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSCR6 BINDING SITE, designated SEQ ID:17339, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37952] Another function of GAM1338 is therefore inhibition of Down syndrome critical region gene 6 (DSCR6, Accession NP_061835.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSCR6.

[37953] DUPLIN (Accession XP_208760.3) is another GAM1338 target gene, herein designated TARGET GENE. DUPLIN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DUPLIN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUPLIN BINDING SITE, designated SEQ ID:2517, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37954] Another function of GAM1338 is therefore inhibition of DUPLIN (Accession XP_208760.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUPLIN.

[37955] DUSP18 (Accession NP_689724.2) is another GAM1338 target gene, herein designated TARGET GENE. DUSP18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DUSP18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP18 BINDING SITE, designated SEQ ID:19123, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37956] Another function of GAM1338 is therefore inhibition of DUSP18 (Accession NP_689724.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP18.

[37957] Dual specificity phosphatase 19 (DUSP19, Accession NP_543152.1) is another GAM1338 target gene, herein designated TARGET GENE. DUSP19 BINDING SITE1 and DUSP19 BINDING SITE2 are target binding sites found in

untranslated regions of mRNA encoded by DUSP19, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP19 BINDING SITE1 and DUSP19 BINDING SITE2, designated SEQ ID:710 and SEQ ID:969 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37958] Another function of GAM1338 is therefore inhibition of Dual specificity phosphatase 19 (DUSP19, Accession NP_543152.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP19.

[37959] Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NP_567824.1) is another GAM1338 target gene, herein designated TARGET GENE. DYRK1A BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by DYRK1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DYRK1A BINDING SITE, designated SEQ ID:14469, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37960] Another function of GAM1338 is therefore inhibition of Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NP_567824.1), a gene which regulates cell proliferation and may be involved in brain development . and therefore may be associated with Down syndrome. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Down syndrome, and of other diseases and clinical conditions associated with DYRK1A.

[37961] The function of DYRK1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Endometrial bleeding associated factor (left-right determination, factor a; transforming growth factor beta superfamily) (EBAF, Accession NP_003231.2) is another GAM1338 target gene, herein designated TARGET GENE. EBAF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EBAF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of EBAF BINDING SITE, designated SEQ ID:7720, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37962] Another function of GAM1338 is therefore inhibition of Endometrial bleeding associated factor (left-right determination, factor a; transforming growth factor beta superfamily) (EBAF, Accession NP_003231.2), a gene which LEFT- RIGHT AXIS MALFORMATIONS and therefore is associated with Left- right axis malformations. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Left- right axis malformations, and of other diseases and clinical conditions associated with EBAF.

[37963] The function of EBAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.EEF2K (Accession NP_037434.1) is another GAM1338 target gene, herein designated TARGET GENE. EEF2K BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EEF2K, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EEF2K BINDING SITE, designated SEQ ID:11618, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37964] Another function of GAM1338 is therefore inhibition of EEF2K (Accession NP_037434.1), a gene which phosphorylates serine or threonine on the eukaryotic elongation factor- 2 and therefore may be associated with Systemic lupus erythematosus and cancer. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Systemic lupus erythematosus and cancer, and of other diseases and clinical conditions associated with EEF2K.

[37965] The function of EEF2K and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Eh-domain containing 1 (EHD1, Accession NP_006786.2) is another GAM1338 target gene, herein designated TARGET GENE. EHD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EHD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EHD1 BINDING SITE, designated SEQ ID:14949, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ

ID:360.

[37966] Another function of GAM1338 is therefore inhibition of Eh-domain containing 1 (EHD1, Accession NP_006786.2), a gene which may be involved in ligand- initiated endocytosis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHD1.

[37967] The function of EHD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.Eh-domain containing 2 (EHD2, Accession NP_055416.2) is another GAM1338 target gene, herein designated TARGET GENE. EHD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EHD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EHD2 BINDING SITE, designated SEQ ID:6934, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37968] Another function of GAM1338 is therefore inhibition of Eh-domain containing 2 (EHD2, Accession NP_055416.2) .

Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHD2.

[37969] Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kda (EIF2S3, Accession NP_001406.1) is another GAM1338 target gene, herein designated TARGET GENE. EIF2S3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF2S3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF2S3 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37970] Another function of GAM1338 is therefore inhibition of Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kda (EIF2S3, Accession NP_001406.1), a gene which functions in the early steps of protein synthesis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2S3.

[37971] The function of EIF2S3 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM189.1.Eukaryotic translation initiation factor 5a2 (EIF5A2, Accession NP_065123.1) is another GAM1338 target gene, herein designated TARGET GENE. EIF5A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF5A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF5A2 BINDING SITE, designated SEQ ID:1333, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37972] Another function of GAM1338 is therefore inhibition of Eukaryotic translation initiation factor 5a2 (EIF5A2, Accession NP_065123.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF5A2.

[37973] ELP3 (Accession NP_060561.3) is another GAM1338 target gene, herein designated TARGET GENE. ELP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ELP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of ELP3 BINDING SITE, designated SEQ ID:6182, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37974] Another function of GAM1338 is therefore inhibition of ELP3 (Accession NP_060561.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELP3.

[37975] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690882.1) is another GAM1338 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37976] Another function of GAM1338 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690882.1) . Ac-

cordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[37977] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_038475.2) is another GAM1338 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37978] Another function of GAM1338 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_038475.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[37979] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690883.1) is

another GAM1338 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37980] Another function of GAM1338 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690883.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[37981] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690885.1) is another GAM1338 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37982] Another function of GAM1338 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690885.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[37983] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690880.1) is another GAM1338 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37984] Another function of GAM1338 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690880.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[37985] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690881.1) is another GAM1338 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37986] Another function of GAM1338 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690881.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with EMR2.

[37987] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690884.1) is another GAM1338 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37988] Another function of GAM1338 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690884.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[37989] Endonuclease g-like 1 (ENDOGL1, Accession NP_005098.1) is another GAM1338 target gene, herein designated TARGET GENE. ENDOGL1 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by ENDOGL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ENDOGL1 BINDING SITE, designated SEQ ID:4223, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37990] Another function of GAM1338 is therefore inhibition of Endonuclease g-like 1 (ENDOGL1, Accession NP_005098.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENDOGL1.

[37991] Epiregulin (EREG, Accession NP_001423.1) is another GAM1338 target gene, herein designated TARGET GENE. EREG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EREG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EREG BINDING SITE, designated SEQ ID:430, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37992] Another function of GAM1338 is therefore inhibition of

Epiregulin (EREG, Accession NP_001423.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EREG.

[37993] ET(B)R-LP-2 (Accession NP_004758.2) is another GAM1338 target gene, herein designated TARGET GENE. ET(B)R-LP-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ET(B)R-LP-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ET(B)R-LP-2 BINDING SITE, designated SEQ ID:6465, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37994] Another function of GAM1338 is therefore inhibition of ET(B)R-LP-2 (Accession NP_004758.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ET(B)R-LP-2.

[37995] Ellis van creveld syndrome (EVC, Accession NP_714928.1) is another GAM1338 target gene, herein designated TARGET GENE. EVC BINDING SITE is a target binding site found

in the 3` untranslated region of multiple transcripts of mRNA encoded by EVC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:4148, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[37996] Another function of GAM1338 is therefore inhibition of Ellis van creveld syndrome (EVC, Accession NP_714928.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC.

[37997] Ellis van creveld syndrome (EVC, Accession NP_055371.1) is another GAM1338 target gene, herein designated TARGET GENE. EVC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EVC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:4148, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ

ID:360.

[37998] Another function of GAM1338 is therefore inhibition of Ellis van creveld syndrome (EVC, Accession NP_055371.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC.

[37999] Ecotropic viral integration site 5 (EVI5, Accession NP_005656.2) is another GAM1338 target gene, herein designated TARGET GENE. EVI5 BINDING SITE1 and EVI5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by EVI5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVI5 BINDING SITE1 and EVI5 BINDING SITE2, designated SEQ ID:16074 and SEQ ID:18007 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38000] Another function of GAM1338 is therefore inhibition of Ecotropic viral integration site 5 (EVI5, Accession NP_005656.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVI5.

[38001] F11R (Accession NP_653085.1) is another GAM1338 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:16292, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38002] Another function of GAM1338 is therefore inhibition of F11R (Accession NP_653085.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[38003] F11R (Accession NP_653087.1) is another GAM1338 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:16292, to the nucleotide sequence of GAM1338 RNA, herein des-

ignated GAM RNA, also designated SEQ ID:360.

[38004] Another function of GAM1338 is therefore inhibition of F11R (Accession NP_653087.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[38005] F11R (Accession NP_058642.1) is another GAM1338 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:16292, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38006] Another function of GAM1338 is therefore inhibition of F11R (Accession NP_058642.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[38007] F11R (Accession NP_653086.1) is another GAM1338 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:16292, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38008] Another function of GAM1338 is therefore inhibition of F11R (Accession NP_653086.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[38009] Coagulation factor ii (thrombin) receptor-like 3 (F2RL3, Accession NP_003941.1) is another GAM1338 target gene, herein designated TARGET GENE. F2RL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F2RL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F2RL3 BINDING SITE, designated SEQ ID:13324, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38010] Another function of GAM1338 is therefore inhibition of Coagulation factor ii (thrombin) receptor-like 3 (F2RL3,

Accession NP_003941.1), a gene which Protease- activated receptor 4; G protein- coupled receptor that increases phosphoinositide hydrolysis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2RL3.

[38011] The function of F2RL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1) is another GAM1338 target gene, herein designated TARGET GENE. F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F3 BINDING SITE, designated SEQ ID:15547, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38012] Another function of GAM1338 is therefore inhibition of Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1), a gene which functions in normal hemostasis. Accordingly, utilities of GAM1338 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with F3.

[38013] The function of F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Coagulation factor v (proaccelerin, labile factor) (F5, Accession NP_000121.1) is another GAM1338 target gene, herein designated TARGET GENE. F5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by F5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F5 BINDING SITE, designated SEQ ID:4594, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38014] Another function of GAM1338 is therefore inhibition of Coagulation factor v (proaccelerin, labile factor) (F5, Accession NP_000121.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F5.

[38015] Coagulation factor viii-associated (intronic transcript) (F8A, Accession NP_036283.2) is another GAM1338 target

gene, herein designated TARGET GENE. F8A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F8A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F8A BINDING SITE, designated SEQ ID:16334, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38016] Another function of GAM1338 is therefore inhibition of Coagulation factor viii-associated (intronic transcript) (F8A, Accession NP_036283.2), a gene which has a possible housekeeping role. and therefore may be associated with Huntington disease. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Huntington disease., and of other diseases and clinical conditions associated with F8A.

[38017] The function of F8A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM689.1.Family with sequence similarity 13, member a1 (FAM13A1, Accession NP_055698.1) is another GAM1338 target gene, herein designated TARGET GENE.

FAM13A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FAM13A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FAM13A1 BINDING SITE, designated SEQ ID:17686, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38018] Another function of GAM1338 is therefore inhibition of Family with sequence similarity 13, member a1 (FAM13A1, Accession NP_055698.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAM13A1.

[38019] Fanconi anemia, complementation group e (FANCE, Accession NP_068741.1) is another GAM1338 target gene, herein designated TARGET GENE. FANCE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCE BINDING SITE, designated SEQ ID:16751, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38020] Another function of GAM1338 is therefore inhibition of Fanconi anemia, complementation group e (FANCE, Accession NP_068741.1), a gene which is a possible regulator of lymphocyte and platelet function. and therefore is associated with Fanconi anemia, complementation group e. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Fanconi anemia, complementation group e., and of other diseases and clinical conditions associated with FANCE.

[38021] The function of FANCE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Fanconi anemia, complementation group f (FANCF, Accession NP_073562.1) is another GAM1338 target gene, herein designated TARGET GENE. FANCF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCF BINDING SITE, designated SEQ ID:14445, to the nu-

cleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38022] Another function of GAM1338 is therefore inhibition of Fanconi anemia, complementation group f (FANCF, Accession NP_073562.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCF.

[38023] F-box and leucine-rich repeat protein 7 (FBXL7, Accession NP_036436.1) is another GAM1338 target gene, herein designated TARGET GENE. FBXL7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FBXL7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXL7 BINDING SITE, designated SEQ ID:10986, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38024] Another function of GAM1338 is therefore inhibition of F-box and leucine-rich repeat protein 7 (FBXL7, Accession NP_036436.1), a gene which may be involved in in phosphorylation- dependent ubiquitination. Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with FBXL7.

[38025] The function of FBXL7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Fc fragment of iga, receptor for (FCAR, Accession NP_001991.1) is another GAM1338 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:10505, SEQ ID:18209 and SEQ ID:18209 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38026] Another function of GAM1338 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_001991.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associ-

ated with Iga nephropathy. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[38027] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Accession NP_579812.1) is another GAM1338 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:18209, SEQ ID:441 and SEQ ID:18209 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38028] Another function of GAM1338 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579812.1), a gene which binds to the fc region of im-

munoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[38029] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Accession NP_579813.1) is another GAM1338 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:441, SEQ ID:18209 and SEQ ID:18209 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38030] Another function of GAM1338 is therefore inhibition of Fc

fragment of iga, receptor for (FCAR, Accession NP_579813.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[38031] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Accession NP_579811.1) is another GAM1338 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:18209, SEQ ID:10188 and SEQ ID:1759 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA,

also designated SEQ ID:360.

[38032] Another function of GAM1338 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579811.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[38033] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) is another GAM1338 target gene, herein designated TARGET GENE. FER1L4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FER1L4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FER1L4 BINDING SITE, designated SEQ ID:1759, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ

ID:360.

[38034] Another function of GAM1338 is therefore inhibition of Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER1L4.

[38035] Fgd1 family, member 2 (FGD2, Accession NP_775829.1) is another GAM1338 target gene, herein designated TARGET GENE. FGD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FGD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGD2 BINDING SITE, designated SEQ ID:14487, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38036] Another function of GAM1338 is therefore inhibition of Fgd1 family, member 2 (FGD2, Accession NP_775829.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGD2.

[38037] Fibroblast growth factor 5 (FGF5, Accession NP_149134.1) is another GAM1338 target gene, herein designated TAR-

GET GENE. FGF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE, designated SEQ ID:3375, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38038] Another function of GAM1338 is therefore inhibition of Fibroblast growth factor 5 (FGF5, Accession NP_149134.1), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5.

[38039] The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.1.Fibroblast growth factor 5 (FGF5, Accession NP_004455.1) is another GAM1338 target gene, herein designated TARGET GENE. FGF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGF5, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE, designated SEQ ID:3375, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38040] Another function of GAM1338 is therefore inhibition of Fibroblast growth factor 5 (FGF5, Accession NP_004455.1), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5.

[38041] The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.1.Four and a half lim domains 2 (FHL2, Accession NP_001441.2) is another GAM1338 target gene, herein designated TARGET GENE. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FHL2 BINDING SITE,

designated SEQ ID:19820, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38042] Another function of GAM1338 is therefore inhibition of Four and a half lim domains 2 (FHL2, Accession NP_001441.2), a gene which Contains four LIM domains and an additional zinc finger. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHL2.

[38043] The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.FISH (Accession NP_055446.1) is another GAM1338 target gene, herein designated TARGET GENE. FISH BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FISH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FISH BINDING SITE, designated SEQ ID:16564, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38044] Another function of GAM1338 is therefore inhibition of

FISH (Accession NP_055446.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FISH.

[38045] Fk506 binding protein 9, 63 kda (FKBP9, Accession NP_009201.1) is another GAM1338 target gene, herein designated TARGET GENE. FKBP9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FKBP9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FKBP9 BINDING SITE, designated SEQ ID:2718, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38046] Another function of GAM1338 is therefore inhibition of Fk506 binding protein 9, 63 kda (FKBP9, Accession NP_009201.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKBP9.

[38047] FLJ00060 (Accession XP_028154.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ00060 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ00060, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ00060 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38048] Another function of GAM1338 is therefore inhibition of FLJ00060 (Accession XP_028154.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00060.

[38049] FLJ10101 (Accession NP_078994.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10101 BINDING SITE1 and FLJ10101 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ10101, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10101 BINDING SITE1 and FLJ10101 BINDING SITE2, designated SEQ ID:10153 and SEQ ID:9878 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38050] Another function of GAM1338 is therefore inhibition of FLJ10101 (Accession NP_078994.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10101.

[38051] FLJ10298 (Accession NP_060520.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10298 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10298, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10298 BINDING SITE, designated SEQ ID:468, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38052] Another function of GAM1338 is therefore inhibition of FLJ10298 (Accession NP_060520.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10298.

[38053] FLJ10346 (Accession NP_060535.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10346 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by FLJ10346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10346 BINDING SITE, designated SEQ ID:7836, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38054] Another function of GAM1338 is therefore inhibition of FLJ10346 (Accession NP_060535.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10346.

[38055] FLJ10520 (Accession NP_060594.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10520 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10520, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10520 BINDING SITE, designated SEQ ID:8795, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38056] Another function of GAM1338 is therefore inhibition of

FLJ10520 (Accession NP_060594.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10520.

[38057] FLJ10535 (Accession NP_060599.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10535 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10535, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10535 BINDING SITE, designated SEQ ID:10633, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38058] Another function of GAM1338 is therefore inhibition of FLJ10535 (Accession NP_060599.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10535.

[38059] FLJ10560 (Accession NP_060608.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10560 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10560, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10560 BINDING SITE, designated SEQ ID:16115, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38060] Another function of GAM1338 is therefore inhibition of FLJ10560 (Accession NP_060608.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10560.

[38061] FLJ10569 (Accession NP_060612.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10569 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10569, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10569 BINDING SITE, designated SEQ ID:7662, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38062] Another function of GAM1338 is therefore inhibition of FLJ10569 (Accession NP_060612.1) . Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10569.

[38063] FLJ10640 (Accession NP_061896.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10640 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10640, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10640 BINDING SITE, designated SEQ ID:16789, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38064] Another function of GAM1338 is therefore inhibition of FLJ10640 (Accession NP_061896.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10640.

[38065] FLJ10713 (Accession NP_060659.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10713 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10713, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10713 BINDING SITE, designated SEQ ID:12092, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38066] Another function of GAM1338 is therefore inhibition of FLJ10713 (Accession NP_060659.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10713.

[38067] FLJ10743 (Accession NP_060671.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10743 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10743, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10743 BINDING SITE, designated SEQ ID:2269, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38068] Another function of GAM1338 is therefore inhibition of FLJ10743 (Accession NP_060671.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ10743.

[38069] FLJ10846 (Accession NP_060711.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10846 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10846, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10846 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38070] Another function of GAM1338 is therefore inhibition of FLJ10846 (Accession NP_060711.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10846.

[38071] FLJ10847 (Accession NP_060712.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10847 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10847, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ10847 BINDING SITE, designated SEQ ID:18108, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38072] Another function of GAM1338 is therefore inhibition of FLJ10847 (Accession NP_060712.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10847.

[38073] FLJ10901 (Accession NP_060735.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10901 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10901, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10901 BINDING SITE, designated SEQ ID:13292, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38074] Another function of GAM1338 is therefore inhibition of FLJ10901 (Accession NP_060735.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ10901.

[38075] FLJ10922 (Accession NP_060743.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ10922 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10922 BINDING SITE, designated SEQ ID:6574, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38076] Another function of GAM1338 is therefore inhibition of FLJ10922 (Accession NP_060743.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10922.

[38077] FLJ11274 (Accession NP_060845.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ11274 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ11274, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ11274 BINDING SITE, designated SEQ ID:7307, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38078] Another function of GAM1338 is therefore inhibition of FLJ11274 (Accession NP_060845.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11274.

[38079] FLJ11323 (Accession NP_060860.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ11323 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ11323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11323 BINDING SITE, designated SEQ ID:13280, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38080] Another function of GAM1338 is therefore inhibition of FLJ11323 (Accession NP_060860.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ11323.

[38081] FLJ11467 (Accession NP_079239.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ11467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11467 BINDING SITE, designated SEQ ID:9552, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38082] Another function of GAM1338 is therefore inhibition of FLJ11467 (Accession NP_079239.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11467.

[38083] FLJ11710 (Accession NP_079122.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ11710 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11710, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ11710 BINDING SITE, designated SEQ ID:6034, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38084] Another function of GAM1338 is therefore inhibition of FLJ11710 (Accession NP_079122.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11710.

[38085] FLJ11715 (Accession NP_078840.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ11715 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11715, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11715 BINDING SITE, designated SEQ ID:4281, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38086] Another function of GAM1338 is therefore inhibition of FLJ11715 (Accession NP_078840.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11715.

[38087] FLJ11783 (Accession NP_079167.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ11783 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11783, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11783 BINDING SITE, designated SEQ ID:11128, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38088] Another function of GAM1338 is therefore inhibition of FLJ11783 (Accession NP_079167.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11783.

[38089] FLJ11800 (Accession NP_079250.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ11800 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11800, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11800 BINDING SITE, designated SEQ ID:17222, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38090] Another function of GAM1338 is therefore inhibition of FLJ11800 (Accession NP_079250.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11800.

[38091] FLJ12363 (Accession NP_115543.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12363 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12363, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12363 BINDING SITE, designated SEQ ID:14486, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38092] Another function of GAM1338 is therefore inhibition of FLJ12363 (Accession NP_115543.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12363.

[38093] FLJ12409 (Accession NP_079381.1) is another GAM1338

target gene, herein designated TARGET GENE. FLJ12409 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12409, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12409 BINDING SITE, designated SEQ ID:19506, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38094] Another function of GAM1338 is therefore inhibition of FLJ12409 (Accession NP_079381.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12409.

[38095] FLJ12572 (Accession NP_075056.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12572 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ12572, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12572 BINDING SITE, designated SEQ ID:14282, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38096] Another function of GAM1338 is therefore inhibition of FLJ12572 (Accession NP_075056.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12572.

[38097] FLJ12586 (Accession NP_078896.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12586 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ12586, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12586 BINDING SITE, designated SEQ ID:13509, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38098] Another function of GAM1338 is therefore inhibition of FLJ12586 (Accession NP_078896.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12586.

[38099] FLJ12649 (Accession XP_291344.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12649

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12649, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12649 BINDING SITE, designated SEQ ID:1963, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38100] Another function of GAM1338 is therefore inhibition of FLJ12649 (Accession XP_291344.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12649.

[38101] FLJ12687 (Accession NP_079193.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12687 BINDING SITE, designated SEQ ID:4553, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38102] Another function of GAM1338 is therefore inhibition of FLJ12687 (Accession NP_079193.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12687.

[38103] FLJ12787 (Accession NP_115551.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12787 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12787, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12787 BINDING SITE, designated SEQ ID:8076, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38104] Another function of GAM1338 is therefore inhibition of FLJ12787 (Accession NP_115551.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12787.

[38105] FLJ12800 (Accession NP_075054.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12800 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ12800, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12800 BINDING SITE, designated SEQ ID:3651, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38106] Another function of GAM1338 is therefore inhibition of FLJ12800 (Accession NP_075054.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12800.

[38107] FLJ12888 (Accession NP_079221.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12888 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12888, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12888 BINDING SITE, designated SEQ ID:1302, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38108] Another function of GAM1338 is therefore inhibition of

FLJ12888 (Accession NP_079221.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12888.

[38109] FLJ12903 (Accession NP_073590.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12903 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12903, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12903 BINDING SITE, designated SEQ ID:15276, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38110] Another function of GAM1338 is therefore inhibition of FLJ12903 (Accession NP_073590.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12903.

[38111] FLJ12960 (Accession NP_078914.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12960 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12960, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12960 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38112] Another function of GAM1338 is therefore inhibition of FLJ12960 (Accession NP_078914.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12960.

[38113] FLJ12973 (Accession NP_079184.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12973 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12973, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12973 BINDING SITE, designated SEQ ID:14027, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38114] Another function of GAM1338 is therefore inhibition of FLJ12973 (Accession NP_079184.1) . Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12973.

[38115] FLJ12975 (Accession NP_079085.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12975 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12975 BINDING SITE, designated SEQ ID:836, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38116] Another function of GAM1338 is therefore inhibition of FLJ12975 (Accession NP_079085.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12975.

[38117] FLJ12986 (Accession XP_290685.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ12986 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12986, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12986 BINDING SITE, designated SEQ ID:6642, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38118] Another function of GAM1338 is therefore inhibition of FLJ12986 (Accession XP_290685.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12986.

[38119] FLJ13072 (Accession XP_117117.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ13072 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13072, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13072 BINDING SITE, designated SEQ ID:6870, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38120] Another function of GAM1338 is therefore inhibition of FLJ13072 (Accession XP_117117.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13072.

[38121] FLJ13114 (Accession NP_078817.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ13114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13114 BINDING SITE, designated SEQ ID:7621, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38122] Another function of GAM1338 is therefore inhibition of FLJ13114 (Accession NP_078817.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13114.

[38123] FLJ13188 (Accession NP_071346.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ13188 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13188, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ13188 BINDING SITE, designated SEQ ID:12816, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38124] Another function of GAM1338 is therefore inhibition of FLJ13188 (Accession NP_071346.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13188.

[38125] FLJ13189 (Accession NP_079158.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ13189 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13189, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13189 BINDING SITE, designated SEQ ID:11334, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38126] Another function of GAM1338 is therefore inhibition of FLJ13189 (Accession NP_079158.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ13189.

[38127] FLJ13197 (Accession NP_078890.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ13197 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13197, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13197 BINDING SITE, designated SEQ ID:7946, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38128] Another function of GAM1338 is therefore inhibition of FLJ13197 (Accession NP_078890.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13197.

[38129] FLJ13263 (Accession NP_079401.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ13263 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13263, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ13263 BINDING SITE, designated SEQ ID:1789, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38130] Another function of GAM1338 is therefore inhibition of FLJ13263 (Accession NP_079401.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13263.

[38131] FLJ13456 (Accession XP_038291.5) is another GAM1338 target gene, herein designated TARGET GENE. FLJ13456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13456 BINDING SITE, designated SEQ ID:5409, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38132] Another function of GAM1338 is therefore inhibition of FLJ13456 (Accession XP_038291.5) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13456.

[38133] FLJ13590 (Accession NP_079116.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ13590 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13590, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13590 BINDING SITE, designated SEQ ID:6935, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38134] Another function of GAM1338 is therefore inhibition of FLJ13590 (Accession NP_079116.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13590.

[38135] FLJ13769 (Accession NP_079288.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ13769 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13769, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13769 BINDING SITE, designated SEQ ID:4401, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38136] Another function of GAM1338 is therefore inhibition of FLJ13769 (Accession NP_079288.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13769.

[38137] FLJ13910 (Accession NP_073617.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ13910 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13910, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13910 BINDING SITE, designated SEQ ID:8349, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38138] Another function of GAM1338 is therefore inhibition of FLJ13910 (Accession NP_073617.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13910.

[38139] FLJ13984 (Accession NP_079046.1) is another GAM1338

target gene, herein designated TARGET GENE. FLJ13984 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13984, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13984 BINDING SITE, designated SEQ ID:16972, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38140] Another function of GAM1338 is therefore inhibition of FLJ13984 (Accession NP_079046.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13984.

[38141] FLJ14327 (Accession NP_079188.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ14327 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14327, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14327 BINDING SITE, designated SEQ ID:14346, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38142] Another function of GAM1338 is therefore inhibition of FLJ14327 (Accession NP_079188.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14327.

[38143] FLJ14351 (Accession NP_079008.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ14351 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14351, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14351 BINDING SITE, designated SEQ ID:8244, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38144] Another function of GAM1338 is therefore inhibition of FLJ14351 (Accession NP_079008.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14351.

[38145] FLJ14442 (Accession NP_116174.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ14442

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14442 BINDING SITE, designated SEQ ID:16517, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38146] Another function of GAM1338 is therefore inhibition of FLJ14442 (Accession NP_116174.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14442.

[38147] FLJ14803 (Accession NP_116231.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ14803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14803 BINDING SITE, designated SEQ ID:3409, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38148] Another function of GAM1338 is therefore inhibition of FLJ14803 (Accession NP_116231.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14803.

[38149] FLJ14957 (Accession NP_116255.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ14957 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14957, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14957 BINDING SITE, designated SEQ ID:13179, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38150] Another function of GAM1338 is therefore inhibition of FLJ14957 (Accession NP_116255.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14957.

[38151] FLJ20045 (Accession NP_060108.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20045 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ20045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20045 BINDING SITE, designated SEQ ID:19070, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38152] Another function of GAM1338 is therefore inhibition of FLJ20045 (Accession NP_060108.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20045.

[38153] FLJ20079 (Accession NP_060126.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20079 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20079, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20079 BINDING SITE, designated SEQ ID:6780, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38154] Another function of GAM1338 is therefore inhibition of

FLJ20079 (Accession NP_060126.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20079.

[38155] FLJ20095 (Accession NP_060136.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20095 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20095, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20095 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38156] Another function of GAM1338 is therefore inhibition of FLJ20095 (Accession NP_060136.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20095.

[38157] FLJ20136 (Accession NP_060154.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20136 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20136, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20136 BINDING SITE, designated SEQ ID:15523, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38158] Another function of GAM1338 is therefore inhibition of FLJ20136 (Accession NP_060154.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20136.

[38159] FLJ20147 (Accession NP_060157.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20147 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20147, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20147 BINDING SITE, designated SEQ ID:11745, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38160] Another function of GAM1338 is therefore inhibition of FLJ20147 (Accession NP_060157.1) . Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20147.

[38161] FLJ20245 (Accession NP_060193.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20245 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20245, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20245 BINDING SITE, designated SEQ ID:19728, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38162] Another function of GAM1338 is therefore inhibition of FLJ20245 (Accession NP_060193.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20245.

[38163] FLJ20308 (Accession NP_060228.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20308 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20308, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20308 BINDING SITE, designated SEQ ID:5707, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38164] Another function of GAM1338 is therefore inhibition of FLJ20308 (Accession NP_060228.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20308.

[38165] FLJ20309 (Accession NP_060229.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20309 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20309, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20309 BINDING SITE, designated SEQ ID:2478, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38166] Another function of GAM1338 is therefore inhibition of FLJ20309 (Accession NP_060229.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20309.

[38167] FLJ20320 (Accession NP_060235.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20320 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20320, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20320 BINDING SITE, designated SEQ ID:9740, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38168] Another function of GAM1338 is therefore inhibition of FLJ20320 (Accession NP_060235.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20320.

[38169] FLJ20502 (Accession NP_060315.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20502 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20502, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ20502 BINDING SITE, designated SEQ ID:2719, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38170] Another function of GAM1338 is therefore inhibition of FLJ20502 (Accession NP_060315.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20502.

[38171] FLJ20511 (Accession NP_060323.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20511 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20511, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20511 BINDING SITE, designated SEQ ID:969, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38172] Another function of GAM1338 is therefore inhibition of FLJ20511 (Accession NP_060323.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20511.

[38173] FLJ20671 (Accession NP_060394.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20671 BINDING SITE1 and FLJ20671 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ20671, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20671 BINDING SITE1 and FLJ20671 BINDING SITE2, designated SEQ ID:13745 and SEQ ID:10861 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38174] Another function of GAM1338 is therefore inhibition of FLJ20671 (Accession NP_060394.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20671.

[38175] FLJ20700 (Accession NP_060402.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20700 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20700, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20700 BINDING SITE, designated SEQ ID:20156, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38176] Another function of GAM1338 is therefore inhibition of FLJ20700 (Accession NP_060402.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20700.

[38177] FLJ20813 (Accession NP_060431.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20813 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20813 BINDING SITE, designated SEQ ID:18464, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38178] Another function of GAM1338 is therefore inhibition of FLJ20813 (Accession NP_060431.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20813.

[38179] FLJ20886 (Accession NP_079475.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ20886 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20886, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20886 BINDING SITE, designated SEQ ID:6236, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38180] Another function of GAM1338 is therefore inhibition of FLJ20886 (Accession NP_079475.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20886.

[38181] FLJ21302 (Accession NP_075052.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ21302 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21302, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ21302 BINDING SITE, designated SEQ ID:11446, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38182] Another function of GAM1338 is therefore inhibition of FLJ21302 (Accession NP_075052.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21302.

[38183] FLJ21603 (Accession NP_079038.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ21603 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21603 BINDING SITE, designated SEQ ID:11662, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38184] Another function of GAM1338 is therefore inhibition of FLJ21603 (Accession NP_079038.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ21603.

[38185] FLJ21673 (Accession NP_112160.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ21673 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ21673, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21673 BINDING SITE, designated SEQ ID:1926, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38186] Another function of GAM1338 is therefore inhibition of FLJ21673 (Accession NP_112160.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21673.

[38187] FLJ21841 (Accession NP_078885.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ21841 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21841, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ21841 BINDING SITE, designated SEQ ID:5009, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38188] Another function of GAM1338 is therefore inhibition of FLJ21841 (Accession NP_078885.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21841.

[38189] FLJ22029 (Accession NP_079225.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ22029 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22029, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22029 BINDING SITE, designated SEQ ID:10676, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38190] Another function of GAM1338 is therefore inhibition of FLJ22029 (Accession NP_079225.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22029.

[38191] FLJ22167 (Accession NP_078809.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ22167 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22167 BINDING SITE, designated SEQ ID:2733, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38192] Another function of GAM1338 is therefore inhibition of FLJ22167 (Accession NP_078809.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22167.

[38193] FLJ22329 (Accession NP_078932.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ22329 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22329 BINDING SITE, designated SEQ ID:10803, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38194] Another function of GAM1338 is therefore inhibition of FLJ22329 (Accession NP_078932.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22329.

[38195] FLJ22531 (Accession NP_078926.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ22531 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22531, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22531 BINDING SITE, designated SEQ ID:3548, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38196] Another function of GAM1338 is therefore inhibition of FLJ22531 (Accession NP_078926.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22531.

[38197] FLJ22965 (Accession NP_071384.1) is another GAM1338

target gene, herein designated TARGET GENE. FLJ22965 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22965, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22965 BINDING SITE, designated SEQ ID:9754, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38198] Another function of GAM1338 is therefore inhibition of FLJ22965 (Accession NP_071384.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22965.

[38199] FLJ23053 (Accession NP_075058.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ23053 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23053, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23053 BINDING SITE, designated SEQ ID:16973, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38200] Another function of GAM1338 is therefore inhibition of FLJ23053 (Accession NP_075058.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23053.

[38201] FLJ23186 (Accession NP_078892.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ23186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23186 BINDING SITE, designated SEQ ID:10010, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38202] Another function of GAM1338 is therefore inhibition of FLJ23186 (Accession NP_078892.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23186.

[38203] FLJ23263 (Accession NP_079391.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ23263

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ23263, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23263 BINDING SITE, designated SEQ ID:13801, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38204] Another function of GAM1338 is therefore inhibition of FLJ23263 (Accession NP_079391.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23263.

[38205] FLJ23356 (Accession NP_115613.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ23356 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23356 BINDING SITE, designated SEQ ID:14440, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38206] Another function of GAM1338 is therefore inhibition of FLJ23356 (Accession NP_115613.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23356.

[38207] FLJ23392 (Accession NP_079060.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ23392 BINDING SITE1 through FLJ23392 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ23392, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23392 BINDING SITE1 through FLJ23392 BINDING SITE3, designated SEQ ID:431, SEQ ID:4022 and SEQ ID:11425 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38208] Another function of GAM1338 is therefore inhibition of FLJ23392 (Accession NP_079060.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23392.

[38209] FLJ23416 (Accession NP_115614.1) is another GAM1338

target gene, herein designated TARGET GENE. FLJ23416 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23416, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23416 BINDING SITE, designated SEQ ID:4771, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38210] Another function of GAM1338 is therefore inhibition of FLJ23416 (Accession NP_115614.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23416.

[38211] FLJ23556 (Accession NP_079156.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ23556 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23556, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23556 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38212] Another function of GAM1338 is therefore inhibition of FLJ23556 (Accession NP_079156.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23556.

[38213] FLJ23563 (Accession XP_041701.4) is another GAM1338 target gene, herein designated TARGET GENE. FLJ23563 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23563 BINDING SITE, designated SEQ ID:12755, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38214] Another function of GAM1338 is therefore inhibition of FLJ23563 (Accession XP_041701.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23563.

[38215] FLJ25795 (Accession NP_689633.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ25795

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25795, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25795 BINDING SITE, designated SEQ ID:18075, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38216] Another function of GAM1338 is therefore inhibition of FLJ25795 (Accession NP_689633.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25795.

[38217] FLJ30507 (Accession NP_694555.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ30507 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ30507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30507 BINDING SITE, designated SEQ ID:15050, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38218] Another function of GAM1338 is therefore inhibition of FLJ30507 (Accession NP_694555.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30507.

[38219] FLJ30532 (Accession NP_653325.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ30532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30532 BINDING SITE, designated SEQ ID:15898, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38220] Another function of GAM1338 is therefore inhibition of FLJ30532 (Accession NP_653325.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30532.

[38221] FLJ31139 (Accession NP_775928.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ31139 BINDING SITE1 through FLJ31139 BINDING SITE3 are target

binding sites found in untranslated regions of mRNA encoded by FLJ31139, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31139 BINDING SITE1 through FLJ31139 BINDING SITE3, designated SEQ ID:7279, SEQ ID:1817 and SEQ ID:19693 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38222] Another function of GAM1338 is therefore inhibition of FLJ31139 (Accession NP_775928.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31139.

[38223] FLJ31153 (Accession NP_653201.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ31153 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31153, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31153 BINDING SITE, designated SEQ ID:13799, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38224] Another function of GAM1338 is therefore inhibition of FLJ31153 (Accession NP_653201.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31153.

[38225] FLJ31338 (Accession NP_689682.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ31338 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31338, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31338 BINDING SITE, designated SEQ ID:7114, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38226] Another function of GAM1338 is therefore inhibition of FLJ31338 (Accession NP_689682.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31338.

[38227] FLJ31393 (Accession NP_694569.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ31393

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ31393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31393 BINDING SITE, designated SEQ ID:7878, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38228] Another function of GAM1338 is therefore inhibition of FLJ31393 (Accession NP_694569.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31393.

[38229] FLJ31401 (Accession NP_689877.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ31401 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31401, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31401 BINDING SITE, designated SEQ ID:11498, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38230] Another function of GAM1338 is therefore inhibition of FLJ31401 (Accession NP_689877.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31401.

[38231] FLJ31821 (Accession NP_694574.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ31821 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ31821, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31821 BINDING SITE, designated SEQ ID:17212, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38232] Another function of GAM1338 is therefore inhibition of FLJ31821 (Accession NP_694574.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31821.

[38233] FLJ32096 (Accession NP_776156.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ32096 BINDING SITE1 and FLJ32096 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by FLJ32096, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32096 BINDING SITE1 and FLJ32096 BINDING SITE2, designated SEQ ID:11067 and SEQ ID:20189 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38234] Another function of GAM1338 is therefore inhibition of FLJ32096 (Accession NP_776156.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32096.

[38235] FLJ32130 (Accession NP_689671.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ32130 BINDING SITE1 through FLJ32130 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ32130, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32130 BINDING SITE1 through FLJ32130 BINDING SITE3, designated SEQ ID:17307, SEQ

ID:9100 and SEQ ID:5404 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38236] Another function of GAM1338 is therefore inhibition of FLJ32130 (Accession NP_689671.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32130.

[38237] FLJ32206 (Accession NP_689710.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ32206 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32206, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32206 BINDING SITE, designated SEQ ID:14825, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38238] Another function of GAM1338 is therefore inhibition of FLJ32206 (Accession NP_689710.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32206.

[38239] FLJ32499 (Accession NP_653208.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ32499 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32499, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32499 BINDING SITE, designated SEQ ID:2883, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38240] Another function of GAM1338 is therefore inhibition of FLJ32499 (Accession NP_653208.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32499.

[38241] FLJ32731 (Accession NP_689632.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ32731 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32731, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32731 BINDING SITE, designated SEQ ID:7308, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38242] Another function of GAM1338 is therefore inhibition of FLJ32731 (Accession NP_689632.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32731.

[38243] FLJ32803 (Accession NP_694584.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ32803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32803 BINDING SITE, designated SEQ ID:7824, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38244] Another function of GAM1338 is therefore inhibition of FLJ32803 (Accession NP_694584.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32803.

[38245] FLJ32894 (Accession NP_653268.1) is another GAM1338

target gene, herein designated TARGET GENE. FLJ32894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32894 BINDING SITE, designated SEQ ID:3716, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38246] Another function of GAM1338 is therefore inhibition of FLJ32894 (Accession NP_653268.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32894.

[38247] FLJ32932 (Accession NP_690873.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ32932 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32932, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32932 BINDING SITE, designated SEQ ID:4748, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38248] Another function of GAM1338 is therefore inhibition of FLJ32932 (Accession NP_690873.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32932.

[38249] FLJ33318 (Accession NP_694961.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ33318 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33318 BINDING SITE, designated SEQ ID:17978, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38250] Another function of GAM1338 is therefore inhibition of FLJ33318 (Accession NP_694961.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33318.

[38251] FLJ33505 (Accession NP_689530.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ33505

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33505, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33505 BINDING SITE, designated SEQ ID:2450, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38252] Another function of GAM1338 is therefore inhibition of FLJ33505 (Accession NP_689530.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33505.

[38253] FLJ33655 (Accession NP_775912.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ33655 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33655, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33655 BINDING SITE, designated SEQ ID:6177, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38254] Another function of GAM1338 is therefore inhibition of FLJ33655 (Accession NP_775912.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33655.

[38255] FLJ34817 (Accession NP_689516.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ34817 BINDING SITE1 and FLJ34817 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ34817, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34817 BINDING SITE1 and FLJ34817 BINDING SITE2, designated SEQ ID:434 and SEQ ID:10174 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38256] Another function of GAM1338 is therefore inhibition of FLJ34817 (Accession NP_689516.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34817.

[38257] FLJ34922 (Accession NP_689483.1) is another GAM1338

target gene, herein designated TARGET GENE. FLJ34922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ34922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34922 BINDING SITE, designated SEQ ID:14214, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38258] Another function of GAM1338 is therefore inhibition of FLJ34922 (Accession NP_689483.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34922.

[38259] FLJ34969 (Accession XP_114353.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ34969 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ34969, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34969 BINDING SITE, designated SEQ ID:6348, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38260] Another function of GAM1338 is therefore inhibition of FLJ34969 (Accession XP_114353.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34969.

[38261] FLJ35105 (Accession NP_689890.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ35105 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ35105, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35105 BINDING SITE, designated SEQ ID:6840, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38262] Another function of GAM1338 is therefore inhibition of FLJ35105 (Accession NP_689890.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35105.

[38263] FLJ35681 (Accession NP_787096.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ35681

BINDING SITE1 and FLJ35681 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ35681, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35681 BINDING SITE1 and FLJ35681 BINDING SITE2, designated SEQ ID:3105 and SEQ ID:10703 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38264] Another function of GAM1338 is therefore inhibition of FLJ35681 (Accession NP_787096.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35681.

[38265] FLJ35848 (Accession XP_290755.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ35848 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35848, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35848 BINDING SITE, designated SEQ ID:12720, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38266] Another function of GAM1338 is therefore inhibition of FLJ35848 (Accession XP_290755.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35848.

[38267] FLJ36445 (Accession NP_694965.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ36445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36445 BINDING SITE, designated SEQ ID:10632, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38268] Another function of GAM1338 is therefore inhibition of FLJ36445 (Accession NP_694965.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36445.

[38269] FLJ37045 (Accession NP_787085.1) is another GAM1338

target gene, herein designated TARGET GENE. FLJ37045 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37045 BINDING SITE, designated SEQ ID:6414, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38270] Another function of GAM1338 is therefore inhibition of FLJ37045 (Accession NP_787085.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37045.

[38271] FLJ37078 (Accession NP_694588.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ37078 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ37078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37078 BINDING SITE, designated SEQ ID:3106, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38272] Another function of GAM1338 is therefore inhibition of FLJ37078 (Accession NP_694588.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37078.

[38273] FLJ37266 (Accession NP_787088.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ37266 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37266, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37266 BINDING SITE, designated SEQ ID:9900, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38274] Another function of GAM1338 is therefore inhibition of FLJ37266 (Accession NP_787088.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37266.

[38275] FLJ37300 (Accession NP_694941.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ37300

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37300, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37300 BINDING SITE, designated SEQ ID:11542, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38276] Another function of GAM1338 is therefore inhibition of FLJ37300 (Accession NP_694941.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37300.

[38277] FLJ37433 (Accession NP_848612.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ37433 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37433, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37433 BINDING SITE, designated SEQ ID:18178, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38278] Another function of GAM1338 is therefore inhibition of FLJ37433 (Accession NP_848612.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37433.

[38279] FLJ37543 (Accession NP_775938.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ37543 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37543, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37543 BINDING SITE, designated SEQ ID:435, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38280] Another function of GAM1338 is therefore inhibition of FLJ37543 (Accession NP_775938.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37543.

[38281] FLJ37970 (Accession XP_290514.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ37970 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ37970, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37970 BINDING SITE, designated SEQ ID:13645, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38282] Another function of GAM1338 is therefore inhibition of FLJ37970 (Accession XP_290514.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37970.

[38283] FLJ38101 (Accession NP_694993.2) is another GAM1338 target gene, herein designated TARGET GENE. FLJ38101 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38101 BINDING SITE, designated SEQ ID:6516, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38284] Another function of GAM1338 is therefore inhibition of

FLJ38101 (Accession NP_694993.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38101.

[38285] FLJ38149 (Accession XP_091919.5) is another GAM1338 target gene, herein designated TARGET GENE. FLJ38149 BINDING SITE1 through FLJ38149 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ38149, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38149 BINDING SITE1 through FLJ38149 BINDING SITE3, designated SEQ ID:2644, SEQ ID:11661 and SEQ ID:12581 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38286] Another function of GAM1338 is therefore inhibition of FLJ38149 (Accession XP_091919.5) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38149.

[38287] FLJ38281 (Accession NP_689814.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ38281

BINDING SITE1 and FLJ38281 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38281, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38281 BINDING SITE1 and FLJ38281 BINDING SITE2, designated SEQ ID:17962 and SEQ ID:19457 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38288] Another function of GAM1338 is therefore inhibition of FLJ38281 (Accession NP_689814.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38281.

[38289] FLJ38607 (Accession NP_689867.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ38607 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38607, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38607 BINDING SITE, designated SEQ ID:3109, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38290] Another function of GAM1338 is therefore inhibition of FLJ38607 (Accession NP_689867.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38607.

[38291] FLJ38792 (Accession NP_848615.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ38792 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38792, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38792 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38292] Another function of GAM1338 is therefore inhibition of FLJ38792 (Accession NP_848615.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38792.

[38293] FLJ38819 (Accession NP_665872.1) is another GAM1338

target gene, herein designated TARGET GENE. FLJ38819 BINDING SITE1 and FLJ38819 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38819, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38819 BINDING SITE1 and FLJ38819 BINDING SITE2, designated SEQ ID:3726 and SEQ ID:3017 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38294] Another function of GAM1338 is therefore inhibition of FLJ38819 (Accession NP_665872.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38819.

[38295] FLJ38991 (Accession NP_776188.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ38991 BINDING SITE1 and FLJ38991 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38991, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of FLJ38991 BINDING SITE1 and FLJ38991 BINDING SITE2, designated SEQ ID:5383 and SEQ ID:7191 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38296] Another function of GAM1338 is therefore inhibition of FLJ38991 (Accession NP_776188.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38991.

[38297] FLJ39415 (Accession NP_775952.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ39415 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39415, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39415 BINDING SITE, designated SEQ ID:17781, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38298] Another function of GAM1338 is therefore inhibition of FLJ39415 (Accession NP_775952.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ39415.

[38299] FLJ39599 (Accession NP_776164.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ39599 BINDING SITE1 through FLJ39599 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ39599, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39599 BINDING SITE1 through FLJ39599 BINDING SITE3, designated SEQ ID:16019, SEQ ID:16634 and SEQ ID:7948 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38300] Another function of GAM1338 is therefore inhibition of FLJ39599 (Accession NP_776164.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39599.

[38301] FLJ39639 (Accession XP_290687.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ39639 BINDING SITE1 and FLJ39639 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by FLJ39639, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39639 BINDING SITE1 and FLJ39639 BINDING SITE2, designated SEQ ID:7663 and SEQ ID:13371 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38302] Another function of GAM1338 is therefore inhibition of FLJ39639 (Accession XP_290687.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39639.

[38303] FLJ39821 (Accession NP_775971.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ39821 BINDING SITE1 and FLJ39821 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ39821, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39821 BINDING SITE1 and FLJ39821 BINDING SITE2, designated SEQ ID:8171 and SEQ ID:14284 respectively, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38304] Another function of GAM1338 is therefore inhibition of FLJ39821 (Accession NP_775971.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39821.

[38305] FLJ90231 (Accession NP_775852.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ90231 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90231, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90231 BINDING SITE, designated SEQ ID:18854, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38306] Another function of GAM1338 is therefore inhibition of FLJ90231 (Accession NP_775852.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90231.

[38307] FLJ90586 (Accession NP_699176.1) is another GAM1338

target gene, herein designated TARGET GENE. FLJ90586 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90586, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90586 BINDING SITE, designated SEQ ID:3767, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38308] Another function of GAM1338 is therefore inhibition of FLJ90586 (Accession NP_699176.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90586.

[38309] FLJ90723 (Accession NP_787115.1) is another GAM1338 target gene, herein designated TARGET GENE. FLJ90723 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90723, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90723 BINDING SITE, designated SEQ ID:16986, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38310] Another function of GAM1338 is therefore inhibition of FLJ90723 (Accession NP_787115.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90723.

[38311] Formin binding protein 1 (FNBP1, Accession XP_052666.3) is another GAM1338 target gene, herein designated TARGET GENE. FNBP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FNBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FNBP1 BINDING SITE, designated SEQ ID:8560, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38312] Another function of GAM1338 is therefore inhibition of Formin binding protein 1 (FNBP1, Accession XP_052666.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FNBP1.

[38313] Fsh primary response (lrpr1 homolog, rat) 1 (FSHPRH1,

Accession NP_006724.1) is another GAM1338 target gene, herein designated TARGET GENE. FSHPRH1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FSHPRH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FSHPRH1 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38314] Another function of GAM1338 is therefore inhibition of Fsh primary response (lrpr1 homolog, rat) 1 (FSHPRH1, Accession NP_006724.1), a gene which is involved in the response of gonadal tissues to follicle- stimulating hormone. and therefore may be associated with Hypergonadotropic ovarian dysgenesis (odg), x- linked disorders of gonadal development. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Hypergonadotropic ovarian dysgenesis (odg), x- linked disorders of gonadal development, and of other diseases and clinical conditions associated with FSHPRH1.

[38315] The function of FSHPRH1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM189.1.Follistatin-like 1 (FSTL1, Accession NP_009016.1) is another GAM1338 target gene, herein designated TARGET GENE. FSTL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FSTL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FSTL1 BINDING SITE, designated SEQ ID:3666, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38316] Another function of GAM1338 is therefore inhibition of Follistatin-like 1 (FSTL1, Accession NP_009016.1), a gene which may modulate the action of some growth factors on cell proliferation and differentiation. and therefore may be associated with Rheumatoid arthritis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Rheumatoid arthritis., and of other diseases and clinical conditions associated with FSTL1.

[38317] The function of FSTL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM279.1.Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) is another GAM1338 target gene, herein designated TARGET GENE. FUT1 BINDING SITE1 and FUT1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FUT1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FUT1 BINDING SITE1 and FUT1 BINDING SITE2, designated SEQ ID:3102 and SEQ ID:7472 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38318] Another function of GAM1338 is therefore inhibition of Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUT1.

[38319] Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075011.1) is another GAM1338 target gene,

herein designated TARGET GENE. G1P3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by G1P3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G1P3 BINDING SITE, designated SEQ ID:14496, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38320] Another function of GAM1338 is therefore inhibition of Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075011.1), a gene which is an interferon-stimulated gene (ISG). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G1P3.

[38321] The function of G1P3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_002029.3) is another GAM1338 target gene, herein designated TARGET GENE. G1P3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA en-

coded by G1P3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G1P3 BINDING SITE, designated SEQ ID:14496, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38322] Another function of GAM1338 is therefore inhibition of Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_002029.3), a gene which is an interferon-stimulated gene (ISG). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G1P3.

[38323] The function of G1P3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075010.1) is another GAM1338 target gene, herein designated TARGET GENE. G1P3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by G1P3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G1P3 BINDING SITE, designated SEQ ID:14496, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38324] Another function of GAM1338 is therefore inhibition of Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075010.1), a gene which is an interferon-stimulated gene (ISG). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G1P3.

[38325] The function of G1P3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.G2A (Accession NP_037477.1) is another GAM1338 target gene, herein designated TARGET GENE. G2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G2A BINDING SITE, designated SEQ ID:8834, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38326] Another function of GAM1338 is therefore inhibition of G2A (Accession NP_037477.1), a gene which may mediate some of the effects of extracellular atp on insulin secretion. and therefore may be associated with Autoimmune disease. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Autoimmune disease., and of other diseases and clinical conditions associated with G2A.

[38327] The function of G2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Glucose-6-phosphatase, catalytic (glycogen storage disease type i, von gierke disease) (G6PC, Accession NP_000142.1) is another GAM1338 target gene, herein designated TARGET GENE. G6PC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G6PC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G6PC BINDING SITE, designated SEQ ID:8902, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[38328] Another function of GAM1338 is therefore inhibition of Glucose-6-phosphatase, catalytic (glycogen storage disease type i, von gierke disease) (G6PC, Accession NP_000142.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G6PC.

[38329] GAL3ST-4 (Accession NP_078913.3) is another GAM1338 target gene, herein designated TARGET GENE. GAL3ST-4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAL3ST-4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAL3ST-4 BINDING SITE, designated SEQ ID:13405, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38330] Another function of GAM1338 is therefore inhibition of GAL3ST-4 (Accession NP_078913.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAL3ST-4.

[38331] GBP4 (Accession NP_443173.2) is another GAM1338 tar-

get gene, herein designated TARGET GENE. GBP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GBP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GBP4 BINDING SITE, designated SEQ ID:12569, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38332] Another function of GAM1338 is therefore inhibition of GBP4 (Accession NP_443173.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GBP4.

[38333] Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) is another GAM1338 target gene, herein designated TARGET GENE. GGA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE, designated SEQ ID:520, to the nucleotide sequence of GAM1338 RNA,

herein designated GAM RNA, also designated SEQ ID:360.

[38334] Another function of GAM1338 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[38335] Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) is another GAM1338 target gene, herein designated TARGET GENE. GGA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE, designated SEQ ID:520, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38336] Another function of GAM1338 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with GGA2.

[38337] Glucagon-like peptide 1 receptor (GLP1R, Accession NP_002053.2) is another GAM1338 target gene, herein designated TARGET GENE. GLP1R BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLP1R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GLP1R BINDING SITE, designated SEQ ID:13842, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38338] Another function of GAM1338 is therefore inhibition of Glucagon-like peptide 1 receptor (GLP1R, Accession NP_002053.2), a gene which is mediated by g proteins which activate adenylyl cyclase. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLP1R.

[38339] The function of GLP1R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM385.2.Gm2 ganglioside activator protein (GM2A, Accession NP_000396.1) is another GAM1338 target gene,

herein designated TARGET GENE. GM2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GM2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GM2A BINDING SITE, designated SEQ ID:2518, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38340] Another function of GAM1338 is therefore inhibition of Gm2 ganglioside activator protein (GM2A, Accession NP_000396.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GM2A.

[38341] GNE (Accession NP_005467.1) is another GAM1338 target gene, herein designated TARGET GENE. GNE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNE BINDING SITE, designated SEQ ID:7151, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also des-

ignated SEQ ID:360.

[38342] Another function of GAM1338 is therefore inhibition of GNE (Accession NP_005467.1), a gene which has roles in sialic acid biosynthesis and regulates cell surface sialylation. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNE.

[38343] The function of GNE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.GNPNAT1 (Accession XP_085119.1) is another GAM1338 target gene, herein designated TARGET GENE. GNPNAT1 BINDING SITE1 and GNPNAT1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GNPNAT1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNPNAT1 BINDING SITE1 and GNPNAT1 BINDING SITE2, designated SEQ ID:19027 and SEQ ID:10643 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38344] Another function of GAM1338 is therefore inhibition of

GNPNAT1 (Accession XP_085119.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNPNAT1.

[38345] GNRPX (Accession NP_060519.1) is another GAM1338 target gene, herein designated TARGET GENE. GNRPX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNRPX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNRPX BINDING SITE, designated SEQ ID:17848, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38346] Another function of GAM1338 is therefore inhibition of GNRPX (Accession NP_060519.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNRPX.

[38347] Golgi autoantigen, golgin subfamily a, 3 (GOLGA3, Accession NP_005886.2) is another GAM1338 target gene, herein designated TARGET GENE. GOLGA3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GOLGA3, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GOLGA3 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38348] Another function of GAM1338 is therefore inhibition of Golgi autoantigen, golgin subfamily a, 3 (GOLGA3, Accession NP_005886.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLGA3.

[38349] Glycoprotein v (platelet) (GP5, Accession NP_004479.1) is another GAM1338 target gene, herein designated TARGET GENE. GP5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GP5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GP5 BINDING SITE, designated SEQ ID:18832, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38350] Another function of GAM1338 is therefore inhibition of Glycoprotein v (platelet) (GP5, Accession NP_004479.1) .

Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GP5.

[38351] GPP34R (Accession NP_060648.2) is another GAM1338 target gene, herein designated TARGET GENE. GPP34R BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPP34R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPP34R BINDING SITE, designated SEQ ID:16162, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38352] Another function of GAM1338 is therefore inhibition of GPP34R (Accession NP_060648.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPP34R.

[38353] G protein-coupled receptor 114 (GPR114, Accession NP_722579.1) is another GAM1338 target gene, herein designated TARGET GENE. GPR114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR114 BINDING SITE, designated SEQ ID:13684, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38354] Another function of GAM1338 is therefore inhibition of G protein-coupled receptor 114 (GPR114, Accession NP_722579.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR114.

[38355] G protein-coupled receptor 26 (GPR26, Accession NP_703143.1) is another GAM1338 target gene, herein designated TARGET GENE. GPR26 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR26, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR26 BINDING SITE, designated SEQ ID:9581, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38356] Another function of GAM1338 is therefore inhibition of G protein-coupled receptor 26 (GPR26, Accession

NP_703143.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR26.

[38357] G protein-coupled receptor 4 (GPR4, Accession NP_005273.1) is another GAM1338 target gene, herein designated TARGET GENE. GPR4 BINDING SITE1 and GPR4 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GPR4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR4 BINDING SITE1 and GPR4 BINDING SITE2, designated SEQ ID:16936 and SEQ ID:15917 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38358] Another function of GAM1338 is therefore inhibition of G protein-coupled receptor 4 (GPR4, Accession NP_005273.1), a gene which stimulates to produce increased calcium by both SPC and LPC . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR4.

[38359] The function of GPR4 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.G protein-coupled receptor 56 (GPR56, Accession NP_005673.2) is another GAM1338 target gene, herein designated TARGET GENE. GPR56 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GPR56, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR56 BINDING SITE, designated SEQ ID:6235, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38360] Another function of GAM1338 is therefore inhibition of G protein-coupled receptor 56 (GPR56, Accession NP_005673.2), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR56.

[38361] The function of GPR56 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM63.1.G protein-coupled receptor 66 (GPR66, Accession NP_006047.2) is another GAM1338 target gene, herein designated TARGET GENE. GPR66 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR66, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR66 BINDING SITE, designated SEQ ID:4149, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38362] Another function of GAM1338 is therefore inhibition of G protein-coupled receptor 66 (GPR66, Accession NP_006047.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR66.

[38363] G protein-coupled receptor 81 (GPR81, Accession NP_115943.1) is another GAM1338 target gene, herein designated TARGET GENE. GPR81 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR81, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of GPR81 BINDING SITE, designated SEQ ID:9012, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38364] Another function of GAM1338 is therefore inhibition of G protein-coupled receptor 81 (GPR81, Accession NP_115943.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR81.

[38365] GR6 (Accession NP_031380.1) is another GAM1338 target gene, herein designated TARGET GENE. GR6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GR6 BINDING SITE, designated SEQ ID:11621, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38366] Another function of GAM1338 is therefore inhibition of GR6 (Accession NP_031380.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GR6.

[38367] GRAF (Accession NP_055886.1) is another GAM1338 target gene, herein designated TARGET GENE. GRAF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRAF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRAF BINDING SITE, designated SEQ ID:18118, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38368] Another function of GAM1338 is therefore inhibition of GRAF (Accession NP_055886.1), a gene which ia a GTPase activating protein for p21- rac and therefore may be associated with Juvenile myelomonocytic leukemia. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Juvenile myelomonocytic leukemia, and of other diseases and clinical conditions associated with GRAF.

[38369] The function of GRAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.GREB1 (Accession NP_055483.2) is another GAM1338 target gene, herein designated TARGET GENE.

GREB1 BINDING SITE1 and GREB1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by GREB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GREB1 BINDING SITE1 and GREB1 BINDING SITE2, designated SEQ ID:18182 and SEQ ID:2321 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38370] Another function of GAM1338 is therefore inhibition of GREB1 (Accession NP_055483.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GREB1.

[38371] Glutamate receptor, ionotropic, delta 1 (GRID1, Accession XP_043613.8) is another GAM1338 target gene, herein designated TARGET GENE. GRID1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRID1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRID1 BINDING SITE, designated SEQ ID:12320, to the nucleotide sequence of GAM1338

RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38372] Another function of GAM1338 is therefore inhibition of Glutamate receptor, ionotropic, delta 1 (GRID1, Accession XP_043613.8) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRID1.

[38373] Glutamate receptor, ionotropic, n-methyl d-aspartate-like 1a (GRINL1A, Accession NP_056347.1) is another GAM1338 target gene, herein designated TARGET GENE. GRINL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRINL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRINL1A BINDING SITE, designated SEQ ID:17379, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38374] Another function of GAM1338 is therefore inhibition of Glutamate receptor, ionotropic, n-methyl d-aspartate-like 1a (GRINL1A, Accession NP_056347.1), a gene which plays a role in the development and function of the mammalian brain. Accordingly, utilities of GAM1338 include diagno-

sis, prevention and treatment of diseases and clinical conditions associated with GRINL1A.

[38375] The function of GRINL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Glutamate receptor, metabotropic 6 (GRM6, Accession NP_000834.1) is another GAM1338 target gene, herein designated TARGET GENE. GRM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRM6 BINDING SITE, designated SEQ ID:5942, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38376] Another function of GAM1338 is therefore inhibition of Glutamate receptor, metabotropic 6 (GRM6, Accession NP_000834.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRM6.

[38377] GRWD (Accession NP_113673.2) is another GAM1338 target gene, herein designated TARGET GENE. GRWD BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRWD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRWD BINDING SITE, designated SEQ ID:6811, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38378] Another function of GAM1338 is therefore inhibition of GRWD (Accession NP_113673.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRWD.

[38379] GSDM (Accession XP_209009.1) is another GAM1338 target gene, herein designated TARGET GENE. GSDM BINDING SITE1 and GSDM BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by GSDM, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSDM BINDING SITE1 and GSDM BINDING SITE2, designated SEQ ID:13197 and SEQ ID:3037 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[38380] Another function of GAM1338 is therefore inhibition of GSDM (Accession XP_209009.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSDM.

[38381] GTF2IRD2 (Accession NP_775808.1) is another GAM1338 target gene, herein designated TARGET GENE. GTF2IRD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GTF2IRD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2IRD2 BINDING SITE, designated SEQ ID:3107, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38382] Another function of GAM1338 is therefore inhibition of GTF2IRD2 (Accession NP_775808.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2IRD2.

[38383] GTF2IRD2 (Accession NP_115579.3) is another GAM1338 target gene, herein designated TARGET GENE. GTF2IRD2

BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GTF2IRD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2IRD2 BINDING SITE, designated SEQ ID:3107, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38384] Another function of GAM1338 is therefore inhibition of GTF2IRD2 (Accession NP_115579.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2IRD2.

[38385] GTPBG3 (Accession NP_116009.1) is another GAM1338 target gene, herein designated TARGET GENE. GTPBG3 BINDING SITE1 and GTPBG3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GTPBG3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTPBG3 BINDING SITE1 and GTPBG3 BINDING SITE2, designated SEQ ID:15596 and SEQ

ID:7742 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38386] Another function of GAM1338 is therefore inhibition of GTPBG3 (Accession NP_116009.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTPBG3.

[38387] Glycogenin (GYG, Accession NP_004121.2) is another GAM1338 target gene, herein designated TARGET GENE. GYG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GYG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GYG BINDING SITE, designated SEQ ID:10290, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38388] Another function of GAM1338 is therefore inhibition of Glycogenin (GYG, Accession NP_004121.2), a gene which primes de novo glycogen synthesis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GYG.

[38389] The function of GYG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.H-plk (Accession NP_056936.1) is another GAM1338 target gene, herein designated TARGET GENE. H-plk BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by H-plk, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H-plk BINDING SITE, designated SEQ ID:8288, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38390] Another function of GAM1338 is therefore inhibition of H-plk (Accession NP_056936.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H-plk.

[38391] H63 (Accession NP_816929.1) is another GAM1338 target gene, herein designated TARGET GENE. H63 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H63, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of H63 BINDING SITE, designated SEQ ID:2008, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38392] Another function of GAM1338 is therefore inhibition of H63 (Accession NP_816929.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H63.

[38393] H63 (Accession NP_612432.2) is another GAM1338 target gene, herein designated TARGET GENE. H63 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H63, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H63 BINDING SITE, designated SEQ ID:2008, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38394] Another function of GAM1338 is therefore inhibition of H63 (Accession NP_612432.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H63.

[38395] Hepatitis a virus cellular receptor 2 (HAVCR2, Accession

NP_116171.2) is another GAM1338 target gene, herein designated TARGET GENE. HAVCR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HAVCR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HAVCR2 BINDING SITE, designated SEQ ID:16518, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38396] Another function of GAM1338 is therefore inhibition of Hepatitis a virus cellular receptor 2 (HAVCR2, Accession NP_116171.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAVCR2.

[38397] HE9 (Accession NP_741997.1) is another GAM1338 target gene, herein designated TARGET GENE. HE9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HE9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HE9 BINDING SITE, designated SEQ ID:13755, to the nucleotide se-

quence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38398] Another function of GAM1338 is therefore inhibition of HE9 (Accession NP_741997.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HE9.

[38399] HECA (Accession NP_057301.1) is another GAM1338 target gene, herein designated TARGET GENE. HECA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HECA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HECA BINDING SITE, designated SEQ ID:6145, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38400] Another function of GAM1338 is therefore inhibition of HECA (Accession NP_057301.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HECA.

[38401] HEMK (Accession NP_057257.1) is another GAM1338 target gene, herein designated TARGET GENE. HEMK BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by HEMK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HEMK BINDING SITE, designated SEQ ID:12517, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38402] Another function of GAM1338 is therefore inhibition of HEMK (Accession NP_057257.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEMK.

[38403] Hephaestin (HEPH, Accession NP_055614.1) is another GAM1338 target gene, herein designated TARGET GENE. HEPH BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by HEPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HEPH BINDING SITE, designated SEQ ID:4303, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38404] Another function of GAM1338 is therefore inhibition of

Hephaestin (HEPH, Accession NP_055614.1), a gene which is thought to be a membrane- bound protein responsible for transport of dietary iron from epithelial cells of the intestinal lumen into the circulatory system. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEPH.

[38405] The function of HEPH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Holocarboxylase synthetase (biotin-[proprionyl-coenzyme a-carboxylase (atp-hydrolysing)] ligase) (HLCS, Accession NP_000402.2) is another GAM1338 target gene, herein designated TARGET GENE. HLCS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HLCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:10628, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38406] Another function of GAM1338 is therefore inhibition of

Holocarboxylase synthetase (biotin-[proprionyl-coenzyme a-carboxylase (atp-hydrolysing)] ligase) (HLCS, Accession NP_000402.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLCS.

[38407] High-mobility group 20a (HMG20A, Accession NP_060670.1) is another GAM1338 target gene, herein designated TARGET GENE. HMG20A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HMG20A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HMG20A BINDING SITE, designated SEQ ID:19141, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38408] Another function of GAM1338 is therefore inhibition of High-mobility group 20a (HMG20A, Accession NP_060670.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMG20A.

[38409] HPRN (Accession NP_071938.1) is another GAM1338 target gene, herein designated TARGET GENE. HPRN BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HPRN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HPRN BINDING SITE, designated SEQ ID:11574, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38410] Another function of GAM1338 is therefore inhibition of HPRN (Accession NP_071938.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HPRN.

[38411] Histamine receptor h4 (HRH4, Accession NP_067637.2) is another GAM1338 target gene, herein designated TARGET GENE. HRH4 BINDING SITE1 through HRH4 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by HRH4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HRH4 BINDING SITE1 through HRH4 BINDING SITE3, designated SEQ ID:12079, SEQ ID:14595 and SEQ ID:5920 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA,

also designated SEQ ID:360.

[38412] Another function of GAM1338 is therefore inhibition of Histamine receptor h4 (HRH4, Accession NP_067637.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRH4.

[38413] HSD3B7 (Accession NP_079469.2) is another GAM1338 target gene, herein designated TARGET GENE. HSD3B7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSD3B7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSD3B7 BINDING SITE, designated SEQ ID:16293, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38414] Another function of GAM1338 is therefore inhibition of HSD3B7 (Accession NP_079469.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSD3B7.

[38415] HSMPP8 (Accession XP_167894.1) is another GAM1338 target gene, herein designated TARGET GENE. HSMPP8

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSMPP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSMPP8 BINDING SITE, designated SEQ ID:19749, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38416] Another function of GAM1338 is therefore inhibition of HSMPP8 (Accession XP_167894.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSMPP8.

[38417] HSPC065 (Accession NP_054876.2) is another GAM1338 target gene, herein designated TARGET GENE. HSPC065 BINDING SITE1 and HSPC065 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HSPC065, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPC065 BINDING SITE1 and HSPC065 BINDING SITE2, designated SEQ ID:7511 and SEQ ID:10877 respectively, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38418] Another function of GAM1338 is therefore inhibition of HSPC065 (Accession NP_054876.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC065.

[38419] 5-hydroxytryptamine (serotonin) receptor 1d (HTR1D, Accession NP_000855.1) is another GAM1338 target gene, herein designated TARGET GENE. HTR1D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTR1D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR1D BINDING SITE, designated SEQ ID:14604, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38420] Another function of GAM1338 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 1d (HTR1D, Accession NP_000855.1), a gene which belongs to g- protein coupled receptor. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with HTR1D.

[38421] The function of HTR1D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.5-hydroxytryptamine (serotonin) receptor 1e (HTR1E, Accession NP_000856.1) is another GAM1338 target gene, herein designated TARGET GENE. HTR1E BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR1E, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR1E BINDING SITE, designated SEQ ID:9063, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38422] Another function of GAM1338 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 1e (HTR1E, Accession NP_000856.1), a gene which belongs to g- protein coupled receptors. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR1E.

[38423] The function of HTR1E and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM161.1.Hormonally upregulated neu-associated kinase (HUNK, Accession NP_055401.1) is another GAM1338 target gene, herein designated TARGET GENE. HUNK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HUNK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUNK BINDING SITE, designated SEQ ID:1413, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38424] Another function of GAM1338 is therefore inhibition of Hormonally upregulated neu-associated kinase (HUNK, Accession NP_055401.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUNK.

[38425] Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1) is another GAM1338 target gene, herein designated TARGET GENE. HUS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HUS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUS1 BINDING SITE, designated SEQ ID:11161, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38426] Another function of GAM1338 is therefore inhibition of Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1), a gene which May form DNA damage- responsive protein complex . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUS1.

[38427] The function of HUS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Hyaluronoglucosaminidase 4 (HYAL4, Accession NP_036401.1) is another GAM1338 target gene, herein designated TARGET GENE. HYAL4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HYAL4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HYAL4 BINDING SITE, designated SEQ ID:19431, to the nucleotide se-

quence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38428] Another function of GAM1338 is therefore inhibition of Hyaluronoglucosaminidase 4 (HYAL4, Accession NP_036401.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HYAL4.

[38429] Intercellular adhesion molecule 1 (cd54), human rhinovirus receptor (ICAM1, Accession NP_000192.1) is another GAM1338 target gene, herein designated TARGET GENE. ICAM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ICAM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICAM1 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38430] Another function of GAM1338 is therefore inhibition of Intercellular adhesion molecule 1 (cd54), human rhinovirus receptor (ICAM1, Accession NP_000192.1), a gene which binds the integrin LFA- 1 (ITGB2) and promotes adhesion; member of the immunoglobulin superfamily and

therefore may be associated with Malaria, cerebral, susceptibility to. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Malaria, cerebral, susceptibility to, and of other diseases and clinical conditions associated with ICAM1.

[38431] The function of ICAM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.ICK (Accession NP_055735.1) is another GAM1338 target gene, herein designated TARGET GENE. ICK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ICK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:3106, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38432] Another function of GAM1338 is therefore inhibition of ICK (Accession NP_055735.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK.

[38433] ICK (Accession NP_057597.2) is another GAM1338 target

gene, herein designated TARGET GENE. ICK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ICK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:3106, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38434] Another function of GAM1338 is therefore inhibition of ICK (Accession NP_057597.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK.

[38435] Insulin-like growth factor 1 (somatomedin c) (IGF1, Accession NP_000609.1) is another GAM1338 target gene, herein designated TARGET GENE. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IGF1 BINDING SITE, designated SEQ ID:8230, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[38436] Another function of GAM1338 is therefore inhibition of Insulin-like growth factor 1 (somatomedin c) (IGF1, Accession NP_000609.1), a gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore may be associated with Growth retardation with sensorineural deafness and mental retardation. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Growth retardation with sensorineural deafness and mental retardation, and of other diseases and clinical conditions associated with IGF1.

[38437] The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Interleukin 11 (IL11, Accession NP_000632.1) is another GAM1338 target gene, herein designated TARGET GENE. IL11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL11 BINDING SITE, designated SEQ ID:17785,

to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38438] Another function of GAM1338 is therefore inhibition of Interleukin 11 (IL11, Accession NP_000632.1), a gene which stimulates the proliferation of hematopoietic stem cells and megakaryocyte progenitor cells and induces megakaryocyte maturation. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL11.

[38439] The function of IL11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM41.1.Interleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NP_757366.1) is another GAM1338 target gene, herein designated TARGET GENE. IL16 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by IL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL16 BINDING SITE, designated SEQ ID:11272, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38440] Another function of GAM1338 is therefore inhibition of Interleukin 16 (lymphocyte chemoattractant factor) (IL16, Accession NP_757366.1), a gene which modulates T- cell activation. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL16.

[38441] The function of IL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Interleukin 21 receptor (IL21R, Accession NP_851564.1) is another GAM1338 target gene, herein designated TARGET GENE. IL21R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL21R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL21R BINDING SITE, designated SEQ ID:2012, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38442] Another function of GAM1338 is therefore inhibition of Interleukin 21 receptor (IL21R, Accession NP_851564.1), a gene which is involved in receptor mediated endocytosis

and transduces the mitogenic signals of il- 2. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL21R.

[38443] The function of IL21R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Interleukin 21 receptor (IL21R, Accession NP_068570.1) is another GAM1338 target gene, herein designated TARGET GENE. IL21R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL21R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL21R BINDING SITE, designated SEQ ID:2012, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38444] Another function of GAM1338 is therefore inhibition of Interleukin 21 receptor (IL21R, Accession NP_068570.1), a gene which is involved in receptor mediated endocytosis and transduces the mitogenic signals of il- 2. Accordingly, utilities of GAM1338 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with IL21R.

[38445] The function of IL21R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Interleukin 21 receptor (IL21R, Accession NP_851565.1) is another GAM1338 target gene, herein designated TARGET GENE. IL21R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL21R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL21R BINDING SITE, designated SEQ ID:2012, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38446] Another function of GAM1338 is therefore inhibition of Interleukin 21 receptor (IL21R, Accession NP_851565.1), a gene which is involved in receptor mediated endocytosis and transduces the mitogenic signals of il- 2. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL21R.

[38447] The function of IL21R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Interleukin 28 receptor, alpha (IL28RA, Accession NP_775088.1) is another GAM1338 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:17486, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38448] Another function of GAM1338 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_775088.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[38449] Interleukin 28 receptor, alpha (IL28RA, Accession NP_734464.1) is another GAM1338 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:17486, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38450] Another function of GAM1338 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_734464.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[38451] Interleukin 28 receptor, alpha (IL28RA, Accession NP_775087.1) is another GAM1338 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:17486, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38452] Another function of GAM1338 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_775087.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[38453] IMPACT (Accession NP_060909.1) is another GAM1338 target gene, herein designated TARGET GENE. IMPACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IMPACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IMPACT BINDING SITE, designated SEQ ID:19846, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38454] Another function of GAM1338 is therefore inhibition of IMPACT (Accession NP_060909.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMPACT.

[38455] Imp (inosine monophosphate) dehydrogenase 1 (IMPDH1, Accession NP_000874.1) is another GAM1338 target gene, herein designated TARGET GENE. IMPDH1 BINDING SITE is a target binding site found in the 5` untranslated region

of mRNA encoded by IMPDH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IMPDH1 BINDING SITE, designated SEQ ID:15608, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38456] Another function of GAM1338 is therefore inhibition of Imp (inosine monophosphate) dehydrogenase 1 (IMPDH1, Accession NP_000874.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMPDH1.

[38457] INHBE (Accession NP_113667.1) is another GAM1338 target gene, herein designated TARGET GENE. INHBE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INHBE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INHBE BINDING SITE, designated SEQ ID:9633, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38458] Another function of GAM1338 is therefore inhibition of

INHBE (Accession NP_113667.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INHBE.

[38459] Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) is another GAM1338 target gene, herein designated TARGET GENE. INMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INMT BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38460] Another function of GAM1338 is therefore inhibition of Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INMT.

[38461] Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) is another GAM1338 target gene, herein designated TARGET GENE. IRF4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by IRF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRF4 BINDING SITE, designated SEQ ID:16311, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38462] Another function of GAM1338 is therefore inhibition of Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRF4.

[38463] IRTA1 (Accession NP_112572.1) is another GAM1338 target gene, herein designated TARGET GENE. IRTA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IRTA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRTA1 BINDING SITE, designated SEQ ID:18021, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38464] Another function of GAM1338 is therefore inhibition of

IRTA1 (Accession NP_112572.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRTA1.

[38465] Iroquois homeobox protein 5 (IRX5, Accession NP_005844.1) is another GAM1338 target gene, herein designated TARGET GENE. IRX5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IRX5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRX5 BINDING SITE, designated SEQ ID:5486, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38466] Another function of GAM1338 is therefore inhibition of Iroquois homeobox protein 5 (IRX5, Accession NP_005844.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRX5.

[38467] Inositol 1,4,5-triphosphate receptor, type 2 (ITPR2, Accession NP_002214.1) is another GAM1338 target gene, herein designated TARGET GENE. ITPR2 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by ITPR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITPR2 BINDING SITE, designated SEQ ID:2513, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38468] Another function of GAM1338 is therefore inhibition of Inositol 1,4,5-triphosphate receptor, type 2 (ITPR2, Accession NP_002214.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPR2.

[38469] Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3, Accession NP_000206.1) is another GAM1338 target gene, herein designated TARGET GENE. JAK3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JAK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JAK3 BINDING SITE, designated SEQ ID:6262, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38470] Another function of GAM1338 is therefore inhibition of Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3, Accession NP_000206.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAK3.

[38471] JM11 (Accession NP_296375.1) is another GAM1338 target gene, herein designated TARGET GENE. JM11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JM11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JM11 BINDING SITE, designated SEQ ID:15361, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38472] Another function of GAM1338 is therefore inhibition of JM11 (Accession NP_296375.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JM11.

[38473] Jerky homolog (mouse) (JRK, Accession NP_003715.1) is another GAM1338 target gene, herein designated TARGET GENE. JRK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JRK, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JRK BINDING SITE, designated SEQ ID:1529, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38474] Another function of GAM1338 is therefore inhibition of Jerky homolog (mouse) (JRK, Accession NP_003715.1), a gene which might function as a DNA- binding protein. and therefore may be associated with Absence epilepsy. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Absence epilepsy, and of other diseases and clinical conditions associated with JRK.

[38475] The function of JRK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.2.Potassium voltage-gated channel, isk-related family, member 3 (KCNE3, Accession NP_005463.1) is another GAM1338 target gene, herein designated TARGET GENE. KCNE3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KCNE3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNE3 BINDING SITE, designated SEQ ID:6918, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38476] Another function of GAM1338 is therefore inhibition of Potassium voltage-gated channel, isk-related family, member 3 (KCNE3, Accession NP_005463.1), a gene which ancillary protein that co- assemble with a potassium channel alpha- subunit to modulate the gating kinetics and enhance stability of the multimeric complex (by similarity). and therefore may be associated with Hypokalemic periodic paralysis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Hypokalemic periodic paralysis, and of other diseases and clinical conditions associated with KCNE3.

[38477] The function of KCNE3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Potassium inwardly-rectifying channel, subfamily j, member 11 (KCNJ11, Accession NP_000516.2) is another GAM1338 target gene, herein designated TARGET GENE. KCNJ11 BINDING SITE is a target binding site found

in the 5` untranslated region of mRNA encoded by KCNJ11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ11 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38478] Another function of GAM1338 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 11 (KCNJ11, Accession NP_000516.2), a gene which is controlled by g proteins. inward rectifier k+ channels are characterized by a greater tendancy to allow potassium to flow into the cell rather than out of it. and therefore is associated with Persistent hyperinsulinemic hypoglycemia of infancy. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Persistent hyperinsulinemic hypoglycemia of infancy, and of other diseases and clinical conditions associated with KCNJ11.

[38479] The function of KCNJ11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Potassium inwardly-rectifying channel, sub-

family j, member 16 (KCNJ16, Accession NP_061128.1) is another GAM1338 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNJ16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:10579, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38480] Another function of GAM1338 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_061128.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[38481] Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733938.1) is another GAM1338 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNJ16, corresponding to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:10579, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38482] Another function of GAM1338 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733938.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[38483] Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733937.1) is another GAM1338 target gene, herein designated TARGET GENE. KCNJ16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KCNJ16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ16 BINDING SITE, designated SEQ ID:10579, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[38484] Another function of GAM1338 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 16 (KCNJ16, Accession NP_733937.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ16.

[38485] KENAE (Accession NP_789786.1) is another GAM1338 target gene, herein designated TARGET GENE. KENAE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KENAE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KENAE BINDING SITE, designated SEQ ID:18180, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38486] Another function of GAM1338 is therefore inhibition of KENAE (Accession NP_789786.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KENAE.

[38487] KIAA0063 (Accession NP_055691.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0063

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0063, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0063 BINDING SITE, designated SEQ ID:13142, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38488] Another function of GAM1338 is therefore inhibition of KIAA0063 (Accession NP_055691.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0063.

[38489] KIAA0087 (Accession NP_055584.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0087 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0087, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0087 BINDING SITE, designated SEQ ID:14875, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38490] Another function of GAM1338 is therefore inhibition of KIAA0087 (Accession NP_055584.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0087.

[38491] KIAA0117 (Accession XP_290939.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0117 BINDING SITE, designated SEQ ID:1353, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38492] Another function of GAM1338 is therefore inhibition of KIAA0117 (Accession XP_290939.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0117.

[38493] KIAA0182 (Accession XP_050495.4) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0182 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA0182, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0182 BINDING SITE, designated SEQ ID:2720, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38494] Another function of GAM1338 is therefore inhibition of KIAA0182 (Accession XP_050495.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0182.

[38495] KIAA0186 (Accession NP_066545.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0186 BINDING SITE, designated SEQ ID:6841, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38496] Another function of GAM1338 is therefore inhibition of

KIAA0186 (Accession NP_066545.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0186.

[38497] KIAA0205 (Accession NP_055688.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0205 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0205, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0205 BINDING SITE, designated SEQ ID:17371, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38498] Another function of GAM1338 is therefore inhibition of KIAA0205 (Accession NP_055688.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0205.

[38499] KIAA0237 (Accession NP_055562.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0237 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0237, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0237 BINDING SITE, designated SEQ ID:4878, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38500] Another function of GAM1338 is therefore inhibition of KIAA0237 (Accession NP_055562.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0237.

[38501] KIAA0295 (Accession XP_042833.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0295 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0295, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0295 BINDING SITE, designated SEQ ID:19689, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38502] Another function of GAM1338 is therefore inhibition of KIAA0295 (Accession XP_042833.2) . Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0295.

[38503] KIAA0435 (Accession NP_055616.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0435 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0435, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0435 BINDING SITE, designated SEQ ID:14441, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38504] Another function of GAM1338 is therefore inhibition of KIAA0435 (Accession NP_055616.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0435.

[38505] KIAA0446 (Accession XP_044155.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0446 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0446, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0446 BINDING SITE, designated SEQ ID:20115, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38506] Another function of GAM1338 is therefore inhibition of KIAA0446 (Accession XP_044155.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0446.

[38507] KIAA0459 (Accession XP_027862.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:3442, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38508] Another function of GAM1338 is therefore inhibition of KIAA0459 (Accession XP_027862.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA0459.

[38509] KIAA0469 (Accession NP_055666.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0469 BINDING SITE1 and KIAA0469 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0469, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0469 BINDING SITE1 and KIAA0469 BINDING SITE2, designated SEQ ID:14283 and SEQ ID:1413 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38510] Another function of GAM1338 is therefore inhibition of KIAA0469 (Accession NP_055666.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469.

[38511] KIAA0475 (Accession NP_055679.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0475 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:7946, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38512] Another function of GAM1338 is therefore inhibition of KIAA0475 (Accession NP_055679.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475.

[38513] KIAA0493 (Accession XP_034717.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0493 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0493 BINDING SITE, designated SEQ ID:6597, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38514] Another function of GAM1338 is therefore inhibition of KIAA0493 (Accession XP_034717.1) . Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0493.

[38515] KIAA0513 (Accession NP_055547.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0513 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0513, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE, designated SEQ ID:11210, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38516] Another function of GAM1338 is therefore inhibition of KIAA0513 (Accession NP_055547.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513.

[38517] KIAA0527 (Accession XP_171054.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0527 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0527, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0527 BINDING SITE, designated SEQ ID:19044, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38518] Another function of GAM1338 is therefore inhibition of KIAA0527 (Accession XP_171054.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0527.

[38519] KIAA0555 (Accession NP_055605.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0555 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0555, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0555 BINDING SITE, designated SEQ ID:19623, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38520] Another function of GAM1338 is therefore inhibition of KIAA0555 (Accession NP_055605.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA0555.

[38521] KIAA0561 (Accession XP_038150.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0561 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0561, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0561 BINDING SITE, designated SEQ ID:12972, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38522] Another function of GAM1338 is therefore inhibition of KIAA0561 (Accession XP_038150.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0561.

[38523] KIAA0562 (Accession NP_055519.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA0562 BINDING SITE, designated SEQ ID:10458, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38524] Another function of GAM1338 is therefore inhibition of KIAA0562 (Accession NP_055519.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0562.

[38525] KIAA0563 (Accession NP_055649.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0563 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0563 BINDING SITE, designated SEQ ID:19679, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38526] Another function of GAM1338 is therefore inhibition of KIAA0563 (Accession NP_055649.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0563.

[38527] KIAA0682 (Accession NP_055667.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0682 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA0682, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0682 BINDING SITE, designated SEQ ID:2671, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38528] Another function of GAM1338 is therefore inhibition of KIAA0682 (Accession NP_055667.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0682.

[38529] KIAA0831 (Accession NP_055739.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0831 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0831, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA0831 BINDING SITE, designated SEQ ID:16264, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38530] Another function of GAM1338 is therefore inhibition of KIAA0831 (Accession NP_055739.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0831.

[38531] KIAA0841 (Accession XP_049237.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0841 BINDING SITE1 and KIAA0841 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0841, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0841 BINDING SITE1 and KIAA0841 BINDING SITE2, designated SEQ ID:1519 and SEQ ID:901 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38532] Another function of GAM1338 is therefore inhibition of KIAA0841 (Accession XP_049237.1) . Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0841.

[38533] KIAA0861 (Accession NP_055893.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0861 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0861, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0861 BINDING SITE, designated SEQ ID:10629, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38534] Another function of GAM1338 is therefore inhibition of KIAA0861 (Accession NP_055893.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0861.

[38535] KIAA0924 (Accession NP_055712.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0924 BINDING SITE1 and KIAA0924 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0924, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0924 BINDING SITE1 and KIAA0924 BINDING SITE2, designated SEQ ID:19935 and SEQ ID:864 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38536] Another function of GAM1338 is therefore inhibition of KIAA0924 (Accession NP_055712.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0924.

[38537] KIAA0935 (Accession XP_052620.6) is another GAM1338 target gene, herein designated TARGET GENE. KIAA0935 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0935, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0935 BINDING SITE, designated SEQ ID:10957, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38538] Another function of GAM1338 is therefore inhibition of

KIAA0935 (Accession XP_052620.6) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0935.

[38539] KIAA1002 (Accession XP_290584.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1002 BINDING SITE1 and KIAA1002 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1002, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1002 BINDING SITE1 and KIAA1002 BINDING SITE2, designated SEQ ID:12518 and SEQ ID:8660 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38540] Another function of GAM1338 is therefore inhibition of KIAA1002 (Accession XP_290584.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1002.

[38541] KIAA1040 (Accession XP_051091.3) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1040

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1040, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1040 BINDING SITE, designated SEQ ID:5138, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38542] Another function of GAM1338 is therefore inhibition of KIAA1040 (Accession XP_051091.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1040.

[38543] KIAA1041 (Accession NP_055762.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1041 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1041, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1041 BINDING SITE, designated SEQ ID:11112, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38544] Another function of GAM1338 is therefore inhibition of KIAA1041 (Accession NP_055762.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1041.

[38545] KIAA1052 (Accession NP_055771.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1052 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1052 BINDING SITE, designated SEQ ID:1530, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38546] Another function of GAM1338 is therefore inhibition of KIAA1052 (Accession NP_055771.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1052.

[38547] KIAA1054 (Accession XP_043493.5) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1054 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1054, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1054 BINDING SITE, designated SEQ ID:7973, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38548] Another function of GAM1338 is therefore inhibition of KIAA1054 (Accession XP_043493.5) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1054.

[38549] KIAA1128 (Accession NP_061872.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1128 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1128 BINDING SITE, designated SEQ ID:8868, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38550] Another function of GAM1338 is therefore inhibition of

KIAA1128 (Accession NP_061872.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1128.

[38551] KIAA1143 (Accession XP_044014.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1143 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38552] Another function of GAM1338 is therefore inhibition of KIAA1143 (Accession XP_044014.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1143.

[38553] KIAA1155 (Accession XP_030864.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1155 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1155, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1155 BINDING SITE, designated SEQ ID:5405, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38554] Another function of GAM1338 is therefore inhibition of KIAA1155 (Accession XP_030864.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1155.

[38555] KIAA1170 (Accession XP_045907.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1170 BINDING SITE, designated SEQ ID:7575, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38556] Another function of GAM1338 is therefore inhibition of KIAA1170 (Accession XP_045907.2) . Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1170.

[38557] KIAA1185 (Accession NP_065761.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1185 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1185, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1185 BINDING SITE, designated SEQ ID:9213, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38558] Another function of GAM1338 is therefore inhibition of KIAA1185 (Accession NP_065761.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1185.

[38559] KIAA1193 (Accession XP_041843.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1193, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1193 BINDING SITE, designated SEQ ID:1683, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38560] Another function of GAM1338 is therefore inhibition of KIAA1193 (Accession XP_041843.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1193.

[38561] KIAA1198 (Accession NP_065765.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE5 are target binding sites found in untranslated regions of mRNA encoded by KIAA1198, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE5, designated SEQ ID:17224, SEQ ID:17617, SEQ ID:17786, SEQ ID:8170 and SEQ ID:5522 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38562] Another function of GAM1338 is therefore inhibition of KIAA1198 (Accession NP_065765.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1198.

[38563] KIAA1209 (Accession XP_027307.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1209 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1209, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1209 BINDING SITE, designated SEQ ID:10878, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38564] Another function of GAM1338 is therefore inhibition of KIAA1209 (Accession XP_027307.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1209.

[38565] KIAA1210 (Accession XP_172801.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1210 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1210, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1210 BINDING SITE, designated SEQ ID:1409, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38566] Another function of GAM1338 is therefore inhibition of KIAA1210 (Accession XP_172801.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1210.

[38567] KIAA1257 (Accession XP_031577.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1257 BINDING SITE1 through KIAA1257 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by KIAA1257, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1257 BINDING SITE1 through KIAA1257 BINDING SITE3, designated SEQ ID:14928, SEQ ID:3109 and SEQ ID:13137 respectively, to the nucleotide sequence of GAM1338 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:360.

[38568] Another function of GAM1338 is therefore inhibition of KIAA1257 (Accession XP_031577.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1257.

[38569] KIAA1268 (Accession XP_291055.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1268 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1268 BINDING SITE, designated SEQ ID:6348, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38570] Another function of GAM1338 is therefore inhibition of KIAA1268 (Accession XP_291055.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1268.

[38571] KIAA1287 (Accession NP_065799.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1287

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1287, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1287 BINDING SITE, designated SEQ ID:13685, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38572] Another function of GAM1338 is therefore inhibition of KIAA1287 (Accession NP_065799.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1287.

[38573] KIAA1393 (Accession XP_050793.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1393 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1393 BINDING SITE, designated SEQ ID:6495, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38574] Another function of GAM1338 is therefore inhibition of KIAA1393 (Accession XP_050793.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1393.

[38575] KIAA1465 (Accession XP_027396.4) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1465 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1465, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1465 BINDING SITE, designated SEQ ID:13306, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38576] Another function of GAM1338 is therefore inhibition of KIAA1465 (Accession XP_027396.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1465.

[38577] KIAA1493 (Accession XP_034415.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1493 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1493 BINDING SITE, designated SEQ ID:11663, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38578] Another function of GAM1338 is therefore inhibition of KIAA1493 (Accession XP_034415.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1493.

[38579] KIAA1518 (Accession XP_170889.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1518 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA1518, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1518 BINDING SITE, designated SEQ ID:17375, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38580] Another function of GAM1338 is therefore inhibition of KIAA1518 (Accession XP_170889.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1518.

[38581] KIAA1530 (Accession XP_042661.5) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1530 BINDING SITE1 and KIAA1530 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1530, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1530 BINDING SITE1 and KIAA1530 BINDING SITE2, designated SEQ ID:12345 and SEQ ID:6360 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38582] Another function of GAM1338 is therefore inhibition of KIAA1530 (Accession XP_042661.5) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1530.

[38583] KIAA1559 (Accession XP_054472.2) is another GAM1338

target gene, herein designated TARGET GENE. KIAA1559 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1559, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1559 BINDING SITE, designated SEQ ID:14408, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38584] Another function of GAM1338 is therefore inhibition of KIAA1559 (Accession XP_054472.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1559.

[38585] KIAA1571 (Accession XP_027744.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1571 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1571, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1571 BINDING SITE, designated SEQ ID:13037, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38586] Another function of GAM1338 is therefore inhibition of KIAA1571 (Accession XP_027744.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1571.

[38587] KIAA1615 (Accession NP_066002.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1615, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2, designated SEQ ID:12534 and SEQ ID:8578 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38588] Another function of GAM1338 is therefore inhibition of KIAA1615 (Accession NP_066002.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1615.

[38589] KIAA1671 (Accession XP_037809.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1671 BINDING SITE1 and KIAA1671 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1671, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1671 BINDING SITE1 and KIAA1671 BINDING SITE2, designated SEQ ID:17814 and SEQ ID:6490 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38590] Another function of GAM1338 is therefore inhibition of KIAA1671 (Accession XP_037809.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1671.

[38591] KIAA1712 (Accession NP_085136.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by KIAA1712, corresponding to target binding sites such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2, designated SEQ ID:12038 and SEQ ID:12038 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38592] Another function of GAM1338 is therefore inhibition of KIAA1712 (Accession NP_085136.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1712.

[38593] KIAA1712 (Accession NP_085136.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by KIAA1712, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2, designated SEQ ID:8796 and SEQ ID:8796 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38594] Another function of GAM1338 is therefore inhibition of KIAA1712 (Accession NP_085136.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1712.

[38595] KIAA1724 (Accession XP_040280.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1724 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1724, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1724 BINDING SITE, designated SEQ ID:12049, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38596] Another function of GAM1338 is therefore inhibition of KIAA1724 (Accession XP_040280.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1724.

[38597] KIAA1737 (Accession NP_219494.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1737 BINDING SITE1 and KIAA1737 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by KIAA1737, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1737 BINDING SITE1 and KIAA1737 BINDING SITE2, designated SEQ ID:12203 and SEQ ID:19235 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38598] Another function of GAM1338 is therefore inhibition of KIAA1737 (Accession NP_219494.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1737.

[38599] KIAA1784 (Accession NP_115820.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1784 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1784, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1784 BINDING SITE, designated SEQ ID:18884, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38600] Another function of GAM1338 is therefore inhibition of KIAA1784 (Accession NP_115820.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1784.

[38601] KIAA1822 (Accession XP_041566.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1822 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1822 BINDING SITE, designated SEQ ID:9237, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38602] Another function of GAM1338 is therefore inhibition of KIAA1822 (Accession XP_041566.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1822.

[38603] KIAA1827 (Accession XP_290834.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1827

BINDING SITE1 and KIAA1827 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1827, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1827 BINDING SITE1 and KIAA1827 BINDING SITE2, designated SEQ ID:2385 and SEQ ID:19431 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38604] Another function of GAM1338 is therefore inhibition of KIAA1827 (Accession XP_290834.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1827.

[38605] KIAA1829 (Accession XP_030378.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1829 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1829, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1829 BINDING SITE, designated SEQ ID:12386, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38606] Another function of GAM1338 is therefore inhibition of KIAA1829 (Accession XP_030378.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1829.

[38607] KIAA1836 (Accession XP_114087.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1836 BINDING SITE, designated SEQ ID:17519, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38608] Another function of GAM1338 is therefore inhibition of KIAA1836 (Accession XP_114087.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1836.

[38609] KIAA1892 (Accession NP_056212.1) is another GAM1338

target gene, herein designated TARGET GENE. KIAA1892 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1892, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1892 BINDING SITE, designated SEQ ID:19465, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38610] Another function of GAM1338 is therefore inhibition of KIAA1892 (Accession NP_056212.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1892.

[38611] KIAA1922 (Accession XP_057040.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1922 BINDING SITE, designated SEQ ID:18258, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38612] Another function of GAM1338 is therefore inhibition of KIAA1922 (Accession XP_057040.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1922.

[38613] KIAA1924 (Accession NP_694971.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1924 BINDING SITE1 and KIAA1924 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1924, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1924 BINDING SITE1 and KIAA1924 BINDING SITE2, designated SEQ ID:12570 and SEQ ID:7825 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38614] Another function of GAM1338 is therefore inhibition of KIAA1924 (Accession NP_694971.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1924.

[38615] KIAA1971 (Accession XP_058720.4) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1971 BINDING SITE1 through KIAA1971 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by KIAA1971, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1971 BINDING SITE1 through KIAA1971 BINDING SITE3, designated SEQ ID:19552, SEQ ID:4023 and SEQ ID:13441 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38616] Another function of GAM1338 is therefore inhibition of KIAA1971 (Accession XP_058720.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1971.

[38617] KIAA1987 (Accession XP_113870.1) is another GAM1338 target gene, herein designated TARGET GENE. KIAA1987 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1987, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA1987 BINDING SITE, designated SEQ ID:18263, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38618] Another function of GAM1338 is therefore inhibition of KIAA1987 (Accession XP_113870.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1987.

[38619] KIAA2028 (Accession XP_059415.2) is another GAM1338 target gene, herein designated TARGET GENE. KIAA2028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA2028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA2028 BINDING SITE, designated SEQ ID:11722, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38620] Another function of GAM1338 is therefore inhibition of KIAA2028 (Accession XP_059415.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA2028.

[38621] Kruppel-like factor 12 (KLF12, Accession NP_009180.3) is another GAM1338 target gene, herein designated TARGET GENE. KLF12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLF12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLF12 BINDING SITE, designated SEQ ID:7570, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38622] Another function of GAM1338 is therefore inhibition of Kruppel-like factor 12 (KLF12, Accession NP_009180.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF12.

[38623] Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_002253.1) is another GAM1338 target gene, herein designated TARGET GENE. KLRD1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLRD1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLRD1 BINDING SITE, designated SEQ ID:8689, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38624] Another function of GAM1338 is therefore inhibition of Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_002253.1), a gene which is a receptor for the recognition of mhc class i hla- e molecules by nk cells and some cytotoxic t- cells. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLRD1.

[38625] The function of KLRD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_031360.1) is another GAM1338 target gene, herein designated TARGET GENE. KLRD1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLRD1, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLRD1 BINDING SITE, designated SEQ ID:8689, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38626] Another function of GAM1338 is therefore inhibition of Killer cell lectin-like receptor subfamily d, member 1 (KLRD1, Accession NP_031360.1), a gene which is a receptor for the recognition of mhc class i hla- e molecules by nk cells and some cytotoxic t- cells. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLRD1.

[38627] The function of KLRD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NP_003670.1) is another GAM1338 target gene, herein designated TARGET GENE. KMO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KMO, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KMO BINDING SITE, designated SEQ ID:5730, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38628] Another function of GAM1338 is therefore inhibition of Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NP_003670.1), a gene which may play a role in encephalic photoreception. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KMO.

[38629] The function of KMO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Kinase suppressor of ras (KSR, Accession XP_290793.1) is another GAM1338 target gene, herein designated TARGET GENE. KSR BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KSR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KSR BINDING SITE, designated

SEQ ID:15951, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38630] Another function of GAM1338 is therefore inhibition of Kinase suppressor of ras (KSR, Accession XP_290793.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KSR.

[38631] Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) is another GAM1338 target gene, herein designated TARGET GENE. LAMP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAMP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMP3 BINDING SITE, designated SEQ ID:970, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38632] Another function of GAM1338 is therefore inhibition of Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with LAMP3.

[38633] Lipocalin 7 (LCN7, Accession NP_071447.1) is another GAM1338 target gene, herein designated TARGET GENE. LCN7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCN7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCN7 BINDING SITE, designated SEQ ID:3972, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38634] Another function of GAM1338 is therefore inhibition of Lipocalin 7 (LCN7, Accession NP_071447.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCN7.

[38635] LCX (Accession XP_167612.2) is another GAM1338 target gene, herein designated TARGET GENE. LCX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCX BINDING

SITE, designated SEQ ID:7409, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38636] Another function of GAM1338 is therefore inhibition of LCX (Accession XP_167612.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCX.

[38637] LGP1 (Accession NP_115873.1) is another GAM1338 target gene, herein designated TARGET GENE. LGP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LGP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LGP1 BINDING SITE, designated SEQ ID:20143, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38638] Another function of GAM1338 is therefore inhibition of LGP1 (Accession NP_115873.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGP1.

[38639] LIN-28 (Accession NP_078950.1) is another GAM1338 target gene, herein designated TARGET GENE. LIN-28

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LIN-28, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LIN-28 BINDING SITE, designated SEQ ID:6030, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38640] Another function of GAM1338 is therefore inhibition of LIN-28 (Accession NP_078950.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIN-28.

[38641] LNK (Accession NP_005466.1) is another GAM1338 target gene, herein designated TARGET GENE. LNK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LNK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LNK BINDING SITE, designated SEQ ID:9510, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38642] Another function of GAM1338 is therefore inhibition of

LNK (Accession NP_005466.1), a gene which links T- cell receptor activation signal to phospholipase c- gamma- 1, grb- 2 and phosphatidylinositol 3- kinase (by similarity). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNK.

[38643] The function of LNK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.LOC112687 (Accession XP_053145.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC112687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112687 BINDING SITE, designated SEQ ID:4875, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38644] Another function of GAM1338 is therefore inhibition of LOC112687 (Accession XP_053145.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC112687.

[38645] LOC113444 (Accession NP_612437.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC113444 BINDING SITE1 through LOC113444 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC113444, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC113444 BINDING SITE1 through LOC113444 BINDING SITE3, designated SEQ ID:14262, SEQ ID:15369 and SEQ ID:15847 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38646] Another function of GAM1338 is therefore inhibition of LOC113444 (Accession NP_612437.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113444.

[38647] LOC115123 (Accession XP_055276.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC115123 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC115123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115123 BINDING SITE, designated SEQ ID:8312, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38648] Another function of GAM1338 is therefore inhibition of LOC115123 (Accession XP_055276.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115123.

[38649] LOC115129 (Accession XP_055292.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC115129 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC115129, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115129 BINDING SITE, designated SEQ ID:11459, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[38650] Another function of GAM1338 is therefore inhibition of LOC115129 (Accession XP_055292.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115129.

[38651] LOC115648 (Accession NP_663299.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC115648 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC115648, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115648 BINDING SITE, designated SEQ ID:6386, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38652] Another function of GAM1338 is therefore inhibition of LOC115648 (Accession NP_663299.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115648.

[38653] LOC116411 (Accession XP_058095.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC116411 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC116411, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC116411 BINDING SITE, designated SEQ ID:1487, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38654] Another function of GAM1338 is therefore inhibition of LOC116411 (Accession XP_058095.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116411.

[38655] LOC118490 (Accession XP_060981.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC118490 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC118490, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118490 BINDING SITE, desig-

nated SEQ ID:11022, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38656] Another function of GAM1338 is therefore inhibition of LOC118490 (Accession XP_060981.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118490.

[38657] LOC118812 (Accession NP_849154.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:7879, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38658] Another function of GAM1338 is therefore inhibition of LOC118812 (Accession NP_849154.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC118812.

[38659] LOC118812 (Accession XP_058346.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:7879, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38660] Another function of GAM1338 is therefore inhibition of LOC118812 (Accession XP_058346.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118812.

[38661] LOC120526 (Accession XP_058475.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC120526 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC120526, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC120526 BINDING SITE, designated SEQ ID:14215, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38662] Another function of GAM1338 is therefore inhibition of LOC120526 (Accession XP_058475.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120526.

[38663] LOC121952 (Accession XP_062872.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC121952 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC121952, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC121952 BINDING SITE, designated SEQ ID:17591, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38664] Another function of GAM1338 is therefore inhibition of LOC121952 (Accession XP_062872.2) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121952.

[38665] LOC124221 (Accession XP_058785.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC124221 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC124221, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC124221 BINDING SITE, designated SEQ ID:14470, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38666] Another function of GAM1338 is therefore inhibition of LOC124221 (Accession XP_058785.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124221.

[38667] LOC124871 (Accession XP_058857.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC124871 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC124871, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC124871 BINDING SITE, designated SEQ ID:1585, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38668] Another function of GAM1338 is therefore inhibition of LOC124871 (Accession XP_058857.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124871.

[38669] LOC125061 (Accession XP_058889.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC125061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC125061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC125061 BINDING SITE, designated SEQ ID:9098, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38670] Another function of GAM1338 is therefore inhibition of LOC125061 (Accession XP_058889.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125061.

[38671] LOC126669 (Accession XP_060121.4) is another GAM1338 target gene, herein designated TARGET GENE. LOC126669 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC126669, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126669 BINDING SITE, designated SEQ ID:8179, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38672] Another function of GAM1338 is therefore inhibition of LOC126669 (Accession XP_060121.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126669.

[38673] LOC127253 (Accession XP_059122.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC127253 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC127253, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC127253 BINDING SITE, designated SEQ ID:2617, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38674] Another function of GAM1338 is therefore inhibition of LOC127253 (Accession XP_059122.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127253.

[38675] LOC127841 (Accession XP_059184.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC127841 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC127841, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC127841 BINDING SITE, designated SEQ ID:5401, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38676] Another function of GAM1338 is therefore inhibition of LOC127841 (Accession XP_059184.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127841.

[38677] LOC128387 (Accession XP_059243.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC128387 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC128387, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC128387 BINDING SITE, designated SEQ ID:2302, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38678] Another function of GAM1338 is therefore inhibition of LOC128387 (Accession XP_059243.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128387.

[38679] LOC132241 (Accession XP_059583.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC132241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC132241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC132241 BINDING SITE, designated SEQ ID:13281, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38680] Another function of GAM1338 is therefore inhibition of LOC132241 (Accession XP_059583.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132241.

[38681] LOC135293 (Accession XP_072402.4) is another GAM1338 target gene, herein designated TARGET GENE. LOC135293 BINDING SITE1 and LOC135293 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC135293, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC135293 BINDING SITE1 and LOC135293 BINDING SITE2, designated SEQ ID:15178 and SEQ ID:11660 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38682] Another function of GAM1338 is therefore inhibition of LOC135293 (Accession XP_072402.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135293.

[38683] LOC135763 (Accession NP_612639.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC135763 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135763, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135763 BINDING SITE, designated SEQ ID:14442, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38684] Another function of GAM1338 is therefore inhibition of LOC135763 (Accession NP_612639.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135763.

[38685] LOC135818 (Accession XP_059804.4) is another GAM1338 target gene, herein designated TARGET GENE. LOC135818 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135818 BINDING SITE, designated SEQ ID:7348, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38686] Another function of GAM1338 is therefore inhibition of LOC135818 (Accession XP_059804.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135818.

[38687] LOC137886 (Accession XP_059929.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC137886 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC137886, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC137886 BINDING SITE, designated SEQ ID:18258, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38688] Another function of GAM1338 is therefore inhibition of LOC137886 (Accession XP_059929.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137886.

[38689] LOC139422 (Accession XP_066687.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC139422 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC139422, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC139422 BINDING SITE, designated SEQ ID:17958, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38690] Another function of GAM1338 is therefore inhibition of LOC139422 (Accession XP_066687.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139422.

[38691] LOC143241 (Accession NP_620167.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC143241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC143241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143241 BINDING SITE, designated SEQ ID:13142, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38692] Another function of GAM1338 is therefore inhibition of LOC143241 (Accession NP_620167.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143241.

[38693] LOC144404 (Accession XP_084852.6) is another GAM1338 target gene, herein designated TARGET GENE.

LOC144404 BINDING SITE1 and LOC144404 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC144404, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144404 BINDING SITE1 and LOC144404 BINDING SITE2, designated SEQ ID:8561 and SEQ ID:11669 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38694] Another function of GAM1338 is therefore inhibition of LOC144404 (Accession XP_084852.6) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144404.

[38695] LOC144481 (Accession XP_096611.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC144481 BINDING SITE1 and LOC144481 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC144481, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144481

BINDING SITE1 and LOC144481 BINDING SITE2, designated SEQ ID:17022 and SEQ ID:16400 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38696] Another function of GAM1338 is therefore inhibition of LOC144481 (Accession XP_096611.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144481.

[38697] LOC144742 (Accession XP_084949.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC144742 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144742, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144742 BINDING SITE, designated SEQ ID:15441, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38698] Another function of GAM1338 is therefore inhibition of LOC144742 (Accession XP_084949.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC144742.

[38699] LOC144766 (Accession XP_084963.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC144766 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144766, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144766 BINDING SITE, designated SEQ ID:19847, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38700] Another function of GAM1338 is therefore inhibition of LOC144766 (Accession XP_084963.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144766.

[38701] LOC144776 (Accession XP_084964.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC144776 BINDING SITE1 and LOC144776 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC144776, corresponding to

target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144776 BINDING SITE1 and LOC144776 BINDING SITE2, designated SEQ ID:14978 and SEQ ID:16958 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38702] Another function of GAM1338 is therefore inhibition of LOC144776 (Accession XP_084964.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144776.

[38703] LOC144817 (Accession XP_084972.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC144817 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144817 BINDING SITE, designated SEQ ID:12382, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38704] Another function of GAM1338 is therefore inhibition of LOC144817 (Accession XP_084972.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144817.

[38705] LOC144871 (Accession XP_096698.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC144871 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144871, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144871 BINDING SITE, designated SEQ ID:10644, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38706] Another function of GAM1338 is therefore inhibition of LOC144871 (Accession XP_096698.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144871.

[38707] LOC145268 (Accession XP_085072.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC145268 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145268 BINDING SITE, designated SEQ ID:15408, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38708] Another function of GAM1338 is therefore inhibition of LOC145268 (Accession XP_085072.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145268.

[38709] LOC145453 (Accession XP_085120.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC145453 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145453, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145453 BINDING SITE, designated SEQ ID:8486, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38710] Another function of GAM1338 is therefore inhibition of LOC145453 (Accession XP_085120.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145453.

[38711] LOC145725 (Accession XP_085211.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC145725 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145725 BINDING SITE, designated SEQ ID:418, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38712] Another function of GAM1338 is therefore inhibition of LOC145725 (Accession XP_085211.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145725.

[38713] LOC145757 (Accession XP_085227.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC145757 BINDING SITE1 and LOC145757 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC145757, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145757 BINDING SITE1 and LOC145757 BINDING SITE2, designated SEQ ID:13797 and SEQ ID:3109 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38714] Another function of GAM1338 is therefore inhibition of LOC145757 (Accession XP_085227.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145757.

[38715] LOC145842 (Accession XP_085254.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC145842 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145842 BINDING SITE, designated SEQ ID:16182, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38716] Another function of GAM1338 is therefore inhibition of LOC145842 (Accession XP_085254.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145842.

[38717] LOC146177 (Accession NP_778229.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC146177 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146177 BINDING SITE, designated SEQ ID:15157, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38718] Another function of GAM1338 is therefore inhibition of LOC146177 (Accession NP_778229.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146177.

[38719] LOC146229 (Accession XP_085387.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC146229 BINDING SITE1 through LOC146229 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC146229, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146229 BINDING SITE1 through LOC146229 BINDING SITE4, designated SEQ ID:3109, SEQ ID:8345, SEQ ID:13931 and SEQ ID:5010 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38720] Another function of GAM1338 is therefore inhibition of LOC146229 (Accession XP_085387.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146229.

[38721] LOC146346 (Accession XP_085430.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC146346 BINDING SITE1 and LOC146346 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC146346, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146346 BINDING SITE1 and LOC146346 BINDING SITE2, designated SEQ ID:6781 and SEQ ID:16312 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38722] Another function of GAM1338 is therefore inhibition of LOC146346 (Accession XP_085430.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146346.

[38723] LOC146429 (Accession XP_096998.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC146429 BINDING SITE1 and LOC146429 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC146429, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146429

BINDING SITE1 and LOC146429 BINDING SITE2, designated SEQ ID:13213 and SEQ ID:8579 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38724] Another function of GAM1338 is therefore inhibition of LOC146429 (Accession XP_096998.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146429.

[38725] LOC146603 (Accession XP_085514.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC146603 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146603 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38726] Another function of GAM1338 is therefore inhibition of LOC146603 (Accession XP_085514.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC146603.

[38727] LOC146784 (Accession XP_085588.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC146784 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146784, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146784 BINDING SITE, designated SEQ ID:13452, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38728] Another function of GAM1338 is therefore inhibition of LOC146784 (Accession XP_085588.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146784.

[38729] LOC146839 (Accession XP_097107.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC146839 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146839, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146839 BINDING SITE, designated SEQ ID:11661, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38730] Another function of GAM1338 is therefore inhibition of LOC146839 (Accession XP_097107.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146839.

[38731] LOC146894 (Accession NP_660316.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC146894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146894 BINDING SITE, designated SEQ ID:2386, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38732] Another function of GAM1338 is therefore inhibition of

LOC146894 (Accession NP_660316.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146894.

[38733] LOC146895 (Accession XP_097120.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC146895 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146895, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146895 BINDING SITE, designated SEQ ID:8862, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38734] Another function of GAM1338 is therefore inhibition of LOC146895 (Accession XP_097120.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146895.

[38735] LOC146901 (Accession XP_097121.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC146901 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC146901, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146901 BINDING SITE, designated SEQ ID:12152, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38736] Another function of GAM1338 is therefore inhibition of LOC146901 (Accession XP_097121.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146901.

[38737] LOC146909 (Accession XP_085634.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC146909 BINDING SITE1 and LOC146909 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC146909, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146909 BINDING SITE1 and LOC146909 BINDING SITE2, designated SEQ ID:14280 and SEQ ID:20010 respectively, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38738] Another function of GAM1338 is therefore inhibition of LOC146909 (Accession XP_085634.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146909.

[38739] LOC147071 (Accession XP_054031.5) is another GAM1338 target gene, herein designated TARGET GENE. LOC147071 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147071, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147071 BINDING SITE, designated SEQ ID:6735, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38740] Another function of GAM1338 is therefore inhibition of LOC147071 (Accession XP_054031.5) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147071.

[38741] LOC147080 (Accession XP_097182.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC147080 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147080, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147080 BINDING SITE, designated SEQ ID:18093, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38742] Another function of GAM1338 is therefore inhibition of LOC147080 (Accession XP_097182.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147080.

[38743] LOC147166 (Accession XP_085722.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC147166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147166 BINDING SITE, designated SEQ ID:546, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38744] Another function of GAM1338 is therefore inhibition of LOC147166 (Accession XP_085722.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147166.

[38745] LOC147343 (Accession XP_097225.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC147343 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147343, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC147343 BINDING SITE, designated SEQ ID:15088, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38746] Another function of GAM1338 is therefore inhibition of LOC147343 (Accession XP_097225.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147343.

[38747] LOC147407 (Accession XP_084000.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC147407 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147407, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147407 BINDING SITE, designated SEQ ID:12382, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38748] Another function of GAM1338 is therefore inhibition of LOC147407 (Accession XP_084000.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147407.

[38749] LOC147622 (Accession XP_097255.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC147622 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147622, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147622 BINDING SITE, designated SEQ ID:10349, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38750] Another function of GAM1338 is therefore inhibition of LOC147622 (Accession XP_097255.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147622.

[38751] LOC147841 (Accession XP_085924.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC147841 BINDING SITE1 and LOC147841 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC147841, corresponding to

target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147841 BINDING SITE1 and LOC147841 BINDING SITE2, designated SEQ ID:18175 and SEQ ID:15453 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38752] Another function of GAM1338 is therefore inhibition of LOC147841 (Accession XP_085924.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147841.

[38753] LOC147947 (Accession XP_085974.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC147947 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147947, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147947 BINDING SITE, designated SEQ ID:438, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38754] Another function of GAM1338 is therefore inhibition of LOC147947 (Accession XP_085974.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147947.

[38755] LOC148137 (Accession NP_653293.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC148137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148137 BINDING SITE, designated SEQ ID:13130, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38756] Another function of GAM1338 is therefore inhibition of LOC148137 (Accession NP_653293.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148137.

[38757] LOC148198 (Accession XP_047554.4) is another GAM1338 target gene, herein designated TARGET GENE.

LOC148198 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148198, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148198 BINDING SITE, designated SEQ ID:7524, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38758] Another function of GAM1338 is therefore inhibition of LOC148198 (Accession XP_047554.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148198.

[38759] LOC148708 (Accession XP_086286.4) is another GAM1338 target gene, herein designated TARGET GENE. LOC148708 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148708 BINDING SITE, designated SEQ ID:18164, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38760] Another function of GAM1338 is therefore inhibition of LOC148708 (Accession XP_086286.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148708.

[38761] LOC148709 (Accession XP_086281.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC148709 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148709, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148709 BINDING SITE, designated SEQ ID:8427, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38762] Another function of GAM1338 is therefore inhibition of LOC148709 (Accession XP_086281.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148709.

[38763] LOC149149 (Accession XP_097598.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC149149 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149149 BINDING SITE, designated SEQ ID:9725, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38764] Another function of GAM1338 is therefore inhibition of LOC149149 (Accession XP_097598.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149149.

[38765] LOC149371 (Accession NP_787072.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC149371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC149371 BINDING SITE, designated SEQ ID:14762, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38766] Another function of GAM1338 is therefore inhibition of LOC149371 (Accession NP_787072.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149371.

[38767] LOC149464 (Accession XP_097645.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC149464 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149464, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149464 BINDING SITE, designated SEQ ID:14821, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38768] Another function of GAM1338 is therefore inhibition of LOC149464 (Accession XP_097645.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC149464.

[38769] LOC149466 (Accession XP_086546.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC149466 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149466, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149466 BINDING SITE, designated SEQ ID:982, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38770] Another function of GAM1338 is therefore inhibition of LOC149466 (Accession XP_086546.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149466.

[38771] LOC149478 (Accession XP_086536.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC149478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149478, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149478 BINDING SITE, designated SEQ ID:2514, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38772] Another function of GAM1338 is therefore inhibition of LOC149478 (Accession XP_086536.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149478.

[38773] LOC149506 (Accession XP_097661.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC149506 BINDING SITE1 and LOC149506 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC149506, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE1 and LOC149506 BINDING SITE2, designated SEQ ID:17503 and SEQ ID:5777 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38774] Another function of GAM1338 is therefore inhibition of LOC149506 (Accession XP_097661.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149506.

[38775] LOC149692 (Accession XP_097706.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC149692 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149692, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149692 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38776] Another function of GAM1338 is therefore inhibition of LOC149692 (Accession XP_097706.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149692.

[38777] LOC149703 (Accession XP_097719.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC149703 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149703, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149703 BINDING SITE, designated SEQ ID:19805, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38778] Another function of GAM1338 is therefore inhibition of LOC149703 (Accession XP_097719.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149703.

[38779] LOC150054 (Accession XP_097797.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC150054 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150054, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150054 BINDING SITE, designated SEQ ID:18175, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38780] Another function of GAM1338 is therefore inhibition of LOC150054 (Accession XP_097797.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150054.

[38781] LOC150225 (Accession XP_097870.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC150225 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150225, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150225 BINDING SITE, designated SEQ ID:1664, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38782] Another function of GAM1338 is therefore inhibition of LOC150225 (Accession XP_097870.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150225.

[38783] LOC150356 (Accession XP_086884.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC150356 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150356 BINDING SITE, designated SEQ ID:19150, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38784] Another function of GAM1338 is therefore inhibition of LOC150356 (Accession XP_086884.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150356.

[38785] LOC150407 (Accession XP_086906.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC150407 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150407, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC150407 BINDING SITE, designated SEQ ID:2430, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38786] Another function of GAM1338 is therefore inhibition of LOC150407 (Accession XP_086906.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150407.

[38787] LOC150587 (Accession XP_097917.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC150587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150587 BINDING SITE, designated SEQ ID:8861, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38788] Another function of GAM1338 is therefore inhibition of LOC150587 (Accession XP_097917.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC150587.

[38789] LOC151057 (Accession XP_097998.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC151057 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151057, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151057 BINDING SITE, designated SEQ ID:5519, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38790] Another function of GAM1338 is therefore inhibition of LOC151057 (Accession XP_097998.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151057.

[38791] LOC151124 (Accession XP_098006.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC151124 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151124, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151124 BINDING SITE, designated SEQ ID:13932, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38792] Another function of GAM1338 is therefore inhibition of LOC151124 (Accession XP_098006.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151124.

[38793] LOC151196 (Accession XP_098019.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC151196 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151196, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151196 BINDING SITE, designated SEQ ID:12600, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38794] Another function of GAM1338 is therefore inhibition of

LOC151196 (Accession XP_098019.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151196.

[38795] LOC151201 (Accession XP_098021.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC151201 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE, designated SEQ ID:11934, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38796] Another function of GAM1338 is therefore inhibition of LOC151201 (Accession XP_098021.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151201.

[38797] LOC151475 (Accession XP_098063.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC151475 BINDING SITE1 and LOC151475 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC151475, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151475 BINDING SITE1 and LOC151475 BINDING SITE2, designated SEQ ID:7086 and SEQ ID:15680 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38798] Another function of GAM1338 is therefore inhibition of LOC151475 (Accession XP_098063.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151475.

[38799] LOC151636 (Accession NP_612144.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC151636 BINDING SITE1 through LOC151636 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC151636, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151636 BINDING SITE1 through LOC151636 BINDING SITE3, des-

ignated SEQ ID:19982, SEQ ID:896 and SEQ ID:2479 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38800] Another function of GAM1338 is therefore inhibition of LOC151636 (Accession NP_612144.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151636.

[38801] LOC151979 (Accession XP_087354.5) is another GAM1338 target gene, herein designated TARGET GENE. LOC151979 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151979, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151979 BINDING SITE, designated SEQ ID:2865, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38802] Another function of GAM1338 is therefore inhibition of LOC151979 (Accession XP_087354.5) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC151979.

[38803] LOC152245 (Accession XP_098182.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC152245 BINDING SITE1 and LOC152245 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC152245, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152245 BINDING SITE1 and LOC152245 BINDING SITE2, designated SEQ ID:19257 and SEQ ID:1714 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38804] Another function of GAM1338 is therefore inhibition of LOC152245 (Accession XP_098182.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152245.

[38805] LOC152445 (Accession XP_098231.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC152445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152445, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE, designated SEQ ID:13905, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38806] Another function of GAM1338 is therefore inhibition of LOC152445 (Accession XP_098231.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152445.

[38807] LOC152620 (Accession XP_011108.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC152620 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152620, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152620 BINDING SITE, designated SEQ ID:13870, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38808] Another function of GAM1338 is therefore inhibition of

LOC152620 (Accession XP_011108.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152620.

[38809] LOC152719 (Accession XP_098257.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC152719 BINDING SITE1 and LOC152719 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC152719, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152719 BINDING SITE1 and LOC152719 BINDING SITE2, designated SEQ ID:1141 and SEQ ID:7621 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38810] Another function of GAM1338 is therefore inhibition of LOC152719 (Accession XP_098257.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152719.

[38811] LOC152794 (Accession XP_087525.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC152794 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152794, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152794 BINDING SITE, designated SEQ ID:3556, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38812] Another function of GAM1338 is therefore inhibition of LOC152794 (Accession XP_087525.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152794.

[38813] LOC152804 (Accession XP_098266.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC152804 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152804, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152804 BINDING SITE, designated SEQ ID:8155, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38814] Another function of GAM1338 is therefore inhibition of LOC152804 (Accession XP_098266.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152804.

[38815] LOC153077 (Accession XP_098307.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC153077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153077 BINDING SITE, designated SEQ ID:19370, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38816] Another function of GAM1338 is therefore inhibition of LOC153077 (Accession XP_098307.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153077.

[38817] LOC153811 (Accession XP_087779.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC153811 BINDING SITE1 through LOC153811 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC153811, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153811 BINDING SITE1 through LOC153811 BINDING SITE4, designated SEQ ID:15030, SEQ ID:10119, SEQ ID:6031 and SEQ ID:14281 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38818] Another function of GAM1338 is therefore inhibition of LOC153811 (Accession XP_087779.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153811.

[38819] LOC153883 (Accession XP_087798.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC153883 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153883, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153883 BINDING SITE, designated SEQ ID:3293, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38820] Another function of GAM1338 is therefore inhibition of LOC153883 (Accession XP_087798.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153883.

[38821] LOC153910 (Accession XP_087801.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC153910 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153910, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153910 BINDING SITE, designated SEQ ID:7292, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38822] Another function of GAM1338 is therefore inhibition of

LOC153910 (Accession XP_087801.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153910.

[38823] LOC154282 (Accession XP_098505.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC154282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154282 BINDING SITE, designated SEQ ID:14848, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38824] Another function of GAM1338 is therefore inhibition of LOC154282 (Accession XP_098505.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154282.

[38825] LOC154822 (Accession XP_098618.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC154822 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC154822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154822 BINDING SITE, designated SEQ ID:3008, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38826] Another function of GAM1338 is therefore inhibition of LOC154822 (Accession XP_098618.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154822.

[38827] LOC154877 (Accession XP_098626.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC154877 BINDING SITE1 through LOC154877 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC154877, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE1 through LOC154877 BINDING SITE4, designated SEQ ID:3038, SEQ ID:15947, SEQ ID:14342 and

SEQ ID:14885 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38828] Another function of GAM1338 is therefore inhibition of LOC154877 (Accession XP_098626.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877.

[38829] LOC155066 (Accession XP_088142.4) is another GAM1338 target gene, herein designated TARGET GENE. LOC155066 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC155066, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC155066 BINDING SITE, designated SEQ ID:13906, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38830] Another function of GAM1338 is therefore inhibition of LOC155066 (Accession XP_088142.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC155066.

[38831] LOC158014 (Accession XP_088442.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC158014 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158014, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158014 BINDING SITE, designated SEQ ID:12285, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38832] Another function of GAM1338 is therefore inhibition of LOC158014 (Accession XP_088442.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158014.

[38833] LOC158228 (Accession XP_098903.4) is another GAM1338 target gene, herein designated TARGET GENE. LOC158228 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158228, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158228 BINDING SITE, designated SEQ ID:8757, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38834] Another function of GAM1338 is therefore inhibition of LOC158228 (Accession XP_098903.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158228.

[38835] LOC158310 (Accession XP_098919.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC158310 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158310, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158310 BINDING SITE, designated SEQ ID:18175, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38836] Another function of GAM1338 is therefore inhibition of LOC158310 (Accession XP_098919.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158310.

[38837] LOC158402 (Accession XP_098936.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC158402 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158402, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158402 BINDING SITE, designated SEQ ID:1414, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38838] Another function of GAM1338 is therefore inhibition of LOC158402 (Accession XP_098936.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158402.

[38839] LOC158436 (Accession XP_098942.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC158436 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC158436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158436 BINDING SITE, designated SEQ ID:7071, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38840] Another function of GAM1338 is therefore inhibition of LOC158436 (Accession XP_098942.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158436.

[38841] LOC158476 (Accession XP_098955.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC158476 BINDING SITE1 and LOC158476 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC158476, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158476 BINDING SITE1 and LOC158476 BINDING SITE2, designated SEQ ID:1355 and SEQ ID:436 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38842] Another function of GAM1338 is therefore inhibition of LOC158476 (Accession XP_098955.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158476.

[38843] LOC158668 (Accession XP_045161.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC158668 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158668, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158668 BINDING SITE, designated SEQ ID:19124, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38844] Another function of GAM1338 is therefore inhibition of LOC158668 (Accession XP_045161.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158668.

[38845] LOC160897 (Accession XP_090573.3) is another

GAM1338 target gene, herein designated TARGET GENE. LOC160897 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC160897, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC160897 BINDING SITE, designated SEQ ID:14437, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38846] Another function of GAM1338 is therefore inhibition of LOC160897 (Accession XP_090573.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160897.

[38847] LOC162427 (Accession NP_835227.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC162427, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2, designated SEQ ID:1761 and SEQ ID:12386 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38848] Another function of GAM1338 is therefore inhibition of LOC162427 (Accession NP_835227.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162427.

[38849] LOC162427 (Accession XP_091549.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC162427, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2, designated SEQ ID:1761 and SEQ ID:12386 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38850] Another function of GAM1338 is therefore inhibition of LOC162427 (Accession XP_091549.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162427.

[38851] LOC162962 (Accession XP_091886.7) is another GAM1338 target gene, herein designated TARGET GENE. LOC162962 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC162962, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162962 BINDING SITE, designated SEQ ID:4276, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38852] Another function of GAM1338 is therefore inhibition of LOC162962 (Accession XP_091886.7) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162962.

[38853] LOC162967 (Accession XP_091890.6) is another GAM1338 target gene, herein designated TARGET GENE.

LOC162967 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC162967, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162967 BINDING SITE, designated SEQ ID:3050, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38854] Another function of GAM1338 is therefore inhibition of LOC162967 (Accession XP_091890.6) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162967.

[38855] LOC163227 (Accession NP_775802.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC163227, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2, desig-

nated SEQ ID:1413 and SEQ ID:9582 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38856] Another function of GAM1338 is therefore inhibition of LOC163227 (Accession NP_775802.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163227.

[38857] LOC163233 (Accession XP_290865.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC163233 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC163233, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163233 BINDING SITE, designated SEQ ID:12968, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38858] Another function of GAM1338 is therefore inhibition of LOC163233 (Accession XP_290865.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC163233.

[38859] LOC167454 (Accession XP_094496.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC167454 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC167454, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC167454 BINDING SITE, designated SEQ ID:10263, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38860] Another function of GAM1338 is therefore inhibition of LOC167454 (Accession XP_094496.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC167454.

[38861] LOC168451 (Accession XP_095114.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC168451 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC168451, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC168451 BINDING SITE, designated SEQ ID:7426, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38862] Another function of GAM1338 is therefore inhibition of LOC168451 (Accession XP_095114.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168451.

[38863] LOC196264 (Accession XP_113683.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC196264 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196264, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196264 BINDING SITE, designated SEQ ID:8574, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38864] Another function of GAM1338 is therefore inhibition of LOC196264 (Accession XP_113683.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196264.

[38865] LOC196337 (Accession XP_113696.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC196337 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196337, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196337 BINDING SITE, designated SEQ ID:6623, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38866] Another function of GAM1338 is therefore inhibition of LOC196337 (Accession XP_113696.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196337.

[38867] LOC196540 (Accession XP_116933.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC196540 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC196540, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196540 BINDING SITE, designated SEQ ID:12661, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38868] Another function of GAM1338 is therefore inhibition of LOC196540 (Accession XP_116933.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196540.

[38869] LOC197358 (Accession XP_113872.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC197358 BINDING SITE1 and LOC197358 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC197358, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC197358 BINDING SITE1 and LOC197358 BINDING SITE2, designated SEQ ID:3887 and SEQ ID:5402 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[38870] Another function of GAM1338 is therefore inhibition of LOC197358 (Accession XP_113872.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197358.

[38871] LOC199899 (Accession XP_117153.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC199899 BINDING SITE1 and LOC199899 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC199899, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199899 BINDING SITE1 and LOC199899 BINDING SITE2, designated SEQ ID:17148 and SEQ ID:5955 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38872] Another function of GAM1338 is therefore inhibition of LOC199899 (Accession XP_117153.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199899.

[38873] LOC199906 (Accession XP_114052.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC199906 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC199906, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199906 BINDING SITE, designated SEQ ID:11637, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38874] Another function of GAM1338 is therefore inhibition of LOC199906 (Accession XP_114052.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199906.

[38875] LOC200169 (Accession XP_117200.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC200169 BINDING SITE1 and LOC200169 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC200169, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200169 BINDING SITE1 and LOC200169 BINDING SITE2, designated SEQ ID:6517 and SEQ ID:5066 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38876] Another function of GAM1338 is therefore inhibition of LOC200169 (Accession XP_117200.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200169.

[38877] LOC200860 (Accession XP_117289.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC200860 BINDING SITE1 and LOC200860 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC200860, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200860 BINDING SITE1 and LOC200860 BINDING SITE2, designated SEQ ID:15491 and SEQ ID:18182 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38878] Another function of GAM1338 is therefore inhibition of LOC200860 (Accession XP_117289.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200860.

[38879] LOC200895 (Accession NP_789785.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC200895 BINDING SITE1 and LOC200895 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC200895, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200895 BINDING SITE1 and LOC200895 BINDING SITE2, designated SEQ ID:3376 and SEQ ID:17681 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38880] Another function of GAM1338 is therefore inhibition of LOC200895 (Accession NP_789785.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200895.

[38881] LOC200916 (Accession XP_114317.3) is another

GAM1338 target gene, herein designated TARGET GENE. LOC200916 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200916, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200916 BINDING SITE, designated SEQ ID:873, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38882] Another function of GAM1338 is therefore inhibition of LOC200916 (Accession XP_114317.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200916.

[38883] LOC201164 (Accession XP_290750.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC201164 BINDING SITE1 and LOC201164 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC201164, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC201164 BINDING SITE1 and LOC201164 BINDING SITE2, designated SEQ ID:13530 and SEQ ID:18118 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38884] Another function of GAM1338 is therefore inhibition of LOC201164 (Accession XP_290750.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201164.

[38885] LOC201292 (Accession NP_775818.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC201292 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201292, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201292 BINDING SITE, designated SEQ ID:19674, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38886] Another function of GAM1338 is therefore inhibition of LOC201292 (Accession NP_775818.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201292.

[38887] LOC201562 (Accession XP_114343.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC201562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201562 BINDING SITE, designated SEQ ID:9102, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38888] Another function of GAM1338 is therefore inhibition of LOC201562 (Accession XP_114343.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201562.

[38889] LOC201725 (Accession XP_114370.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC201725 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC201725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201725 BINDING SITE, designated SEQ ID:18941, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38890] Another function of GAM1338 is therefore inhibition of LOC201725 (Accession XP_114370.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201725.

[38891] LOC202400 (Accession XP_117397.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC202400 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC202400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202400 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38892] Another function of GAM1338 is therefore inhibition of LOC202400 (Accession XP_117397.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202400.

[38893] LOC202404 (Accession XP_114481.4) is another GAM1338 target gene, herein designated TARGET GENE. LOC202404 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC202404, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202404 BINDING SITE, designated SEQ ID:15206, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38894] Another function of GAM1338 is therefore inhibition of LOC202404 (Accession XP_114481.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202404.

[38895] LOC202460 (Accession XP_114493.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC202460 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC202460, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202460 BINDING SITE, designated SEQ ID:1278, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38896] Another function of GAM1338 is therefore inhibition of LOC202460 (Accession XP_114493.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202460.

[38897] LOC202934 (Accession XP_117486.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC202934 BINDING SITE1 and LOC202934 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC202934, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE1 and LOC202934 BINDING SITE2, desig-

nated SEQ ID:9097 and SEQ ID:6782 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38898] Another function of GAM1338 is therefore inhibition of LOC202934 (Accession XP_117486.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934.

[38899] LOC203076 (Accession XP_114621.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC203076 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC203076, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC203076 BINDING SITE, designated SEQ ID:8849, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38900] Another function of GAM1338 is therefore inhibition of LOC203076 (Accession XP_114621.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC203076.

[38901] LOC203547 (Accession XP_114719.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC203547 BINDING SITE1 and LOC203547 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC203547, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC203547 BINDING SITE1 and LOC203547 BINDING SITE2, designated SEQ ID:10631 and SEQ ID:2923 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38902] Another function of GAM1338 is therefore inhibition of LOC203547 (Accession XP_114719.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203547.

[38903] LOC219293 (Accession XP_166599.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC219293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219293, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219293 BINDING SITE, designated SEQ ID:12080, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38904] Another function of GAM1338 is therefore inhibition of LOC219293 (Accession XP_166599.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219293.

[38905] LOC219731 (Accession XP_167596.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC219731 BINDING SITE1 and LOC219731 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC219731, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219731 BINDING SITE1 and LOC219731 BINDING SITE2, designated SEQ ID:10264 and SEQ ID:3320 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38906] Another function of GAM1338 is therefore inhibition of LOC219731 (Accession XP_167596.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219731.

[38907] LOC219735 (Accession XP_167601.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC219735 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219735 BINDING SITE, designated SEQ ID:3675, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38908] Another function of GAM1338 is therefore inhibition of LOC219735 (Accession XP_167601.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219735.

[38909] LOC219894 (Accession XP_167782.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC219894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219894 BINDING SITE, designated SEQ ID:7138, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38910] Another function of GAM1338 is therefore inhibition of LOC219894 (Accession XP_167782.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219894.

[38911] LOC220074 (Accession NP_660352.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC220074 BINDING SITE1 through LOC220074 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC220074, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220074 BINDING SITE1 through LOC220074 BINDING SITE3, des-

ignated SEQ ID:1413, SEQ ID:4396 and SEQ ID:2086 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38912] Another function of GAM1338 is therefore inhibition of LOC220074 (Accession NP_660352.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220074.

[38913] LOC221362 (Accession XP_168093.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC221362 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221362, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221362 BINDING SITE, designated SEQ ID:15454, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38914] Another function of GAM1338 is therefore inhibition of LOC221362 (Accession XP_168093.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC221362.

[38915] LOC221663 (Accession XP_168131.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC221663 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221663 BINDING SITE, designated SEQ ID:10616, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38916] Another function of GAM1338 is therefore inhibition of LOC221663 (Accession XP_168131.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221663.

[38917] LOC221946 (Accession XP_168340.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC221946 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221946, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221946 BINDING SITE, designated SEQ ID:3294, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38918] Another function of GAM1338 is therefore inhibition of LOC221946 (Accession XP_168340.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221946.

[38919] LOC221964 (Accession XP_168342.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC221964 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221964, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221964 BINDING SITE, designated SEQ ID:5581, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38920] Another function of GAM1338 is therefore inhibition of LOC221964 (Accession XP_168342.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221964.

[38921] LOC222057 (Accession XP_166594.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC222057 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222057, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222057 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38922] Another function of GAM1338 is therefore inhibition of LOC222057 (Accession XP_166594.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222057.

[38923] LOC222159 (Accession XP_212100.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC222159 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of

mRNA encoded by LOC222159, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222159 BINDING SITE, designated SEQ ID:563, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38924] Another function of GAM1338 is therefore inhibition of LOC222159 (Accession XP_212100.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222159.

[38925] LOC253612 (Accession XP_172985.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC253612 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253612, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253612 BINDING SITE, designated SEQ ID:19268, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38926] Another function of GAM1338 is therefore inhibition of LOC253612 (Accession XP_172985.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253612.

[38927] LOC253805 (Accession XP_172854.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC253805 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC253805, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253805 BINDING SITE, designated SEQ ID:7275, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38928] Another function of GAM1338 is therefore inhibition of LOC253805 (Accession XP_172854.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253805.

[38929] LOC254875 (Accession XP_171170.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC254875 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC254875, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254875 BINDING SITE, designated SEQ ID:14560, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38930] Another function of GAM1338 is therefore inhibition of LOC254875 (Accession XP_171170.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254875.

[38931] LOC255031 (Accession XP_173187.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC255031 BINDING SITE1 and LOC255031 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC255031, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255031 BINDING SITE1 and LOC255031 BINDING SITE2, desig-

nated SEQ ID:11416 and SEQ ID:19099 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38932] Another function of GAM1338 is therefore inhibition of LOC255031 (Accession XP_173187.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255031.

[38933] LOC255177 (Accession XP_172941.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC255177 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC255177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255177 BINDING SITE, designated SEQ ID:2303, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38934] Another function of GAM1338 is therefore inhibition of LOC255177 (Accession XP_172941.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC255177.

[38935] LOC255458 (Accession XP_173150.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC255458 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255458, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255458 BINDING SITE, designated SEQ ID:9251, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38936] Another function of GAM1338 is therefore inhibition of LOC255458 (Accession XP_173150.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255458.

[38937] LOC255488 (Accession XP_172581.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC255488 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC255488, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255488 BINDING SITE, designated SEQ ID:18594, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38938] Another function of GAM1338 is therefore inhibition of LOC255488 (Accession XP_172581.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255488.

[38939] LOC255975 (Accession XP_171083.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC255975 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255975 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38940] Another function of GAM1338 is therefore inhibition of LOC255975 (Accession XP_171083.2) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255975.

[38941] LOC256401 (Accession XP_171149.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC256401 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC256401, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256401 BINDING SITE, designated SEQ ID:9741, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38942] Another function of GAM1338 is therefore inhibition of LOC256401 (Accession XP_171149.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256401.

[38943] LOC256614 (Accession XP_172864.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC256614 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC256614, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256614 BINDING SITE, designated SEQ ID:3106, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38944] Another function of GAM1338 is therefore inhibition of LOC256614 (Accession XP_172864.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256614.

[38945] LOC282972 (Accession XP_210837.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC282972 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282972 BINDING SITE, designated SEQ ID:1691, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38946] Another function of GAM1338 is therefore inhibition of LOC282972 (Accession XP_210837.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282972.

[38947] LOC282987 (Accession XP_210845.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC282987 BINDING SITE1 and LOC282987 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC282987, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282987 BINDING SITE1 and LOC282987 BINDING SITE2, designated SEQ ID:12386 and SEQ ID:10460 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38948] Another function of GAM1338 is therefore inhibition of LOC282987 (Accession XP_210845.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282987.

[38949] LOC282997 (Accession XP_208473.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC282997 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282997, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282997 BINDING SITE, designated SEQ ID:5482, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38950] Another function of GAM1338 is therefore inhibition of LOC282997 (Accession XP_208473.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282997.

[38951] LOC283061 (Accession XP_210875.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283061 BINDING SITE, desig-

nated SEQ ID:18916, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38952] Another function of GAM1338 is therefore inhibition of LOC283061 (Accession XP_210875.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283061.

[38953] LOC283087 (Accession XP_208509.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283087 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283087, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283087 BINDING SITE, designated SEQ ID:6936, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38954] Another function of GAM1338 is therefore inhibition of LOC283087 (Accession XP_208509.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283087.

[38955] LOC283089 (Accession XP_210885.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283089 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283089, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283089 BINDING SITE, designated SEQ ID:6866, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38956] Another function of GAM1338 is therefore inhibition of LOC283089 (Accession XP_210885.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283089.

[38957] LOC283119 (Accession XP_210895.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283119 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283119, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283119 BINDING SITE, designated SEQ ID:1505, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38958] Another function of GAM1338 is therefore inhibition of LOC283119 (Accession XP_210895.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283119.

[38959] LOC283130 (Accession XP_208525.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC283130 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283130, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283130 BINDING SITE, designated SEQ ID:469, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38960] Another function of GAM1338 is therefore inhibition of LOC283130 (Accession XP_208525.3) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283130.

[38961] LOC283140 (Accession XP_210911.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283140 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283140 BINDING SITE, designated SEQ ID:15581, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38962] Another function of GAM1338 is therefore inhibition of LOC283140 (Accession XP_210911.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283140.

[38963] LOC283143 (Accession XP_210920.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC283143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283143 BINDING SITE, designated SEQ ID:14843, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38964] Another function of GAM1338 is therefore inhibition of LOC283143 (Accession XP_210920.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283143.

[38965] LOC283152 (Accession XP_210917.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC283152 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283152, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283152 BINDING SITE, designated SEQ ID:17431, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38966] Another function of GAM1338 is therefore inhibition of LOC283152 (Accession XP_210917.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283152.

[38967] LOC283170 (Accession XP_208535.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283170 BINDING SITE, designated SEQ ID:19643, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38968] Another function of GAM1338 is therefore inhibition of LOC283170 (Accession XP_208535.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283170.

[38969] LOC283177 (Accession XP_210903.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC283177 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283177 BINDING SITE, designated SEQ ID:13142, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38970] Another function of GAM1338 is therefore inhibition of LOC283177 (Accession XP_210903.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283177.

[38971] LOC283215 (Accession XP_208555.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC283215 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283215, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283215 BINDING SITE, designated SEQ ID:15736, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38972] Another function of GAM1338 is therefore inhibition of LOC283215 (Accession XP_208555.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283215.

[38973] LOC283241 (Accession NP_787089.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283241 BINDING SITE, designated SEQ ID:10625, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38974] Another function of GAM1338 is therefore inhibition of LOC283241 (Accession NP_787089.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283241.

[38975] LOC283278 (Accession XP_210961.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283278 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283278, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283278 BINDING SITE, designated SEQ ID:13142, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38976] Another function of GAM1338 is therefore inhibition of LOC283278 (Accession XP_210961.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283278.

[38977] LOC283293 (Accession XP_210962.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC283293 BINDING SITE, designated SEQ ID:438, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38978] Another function of GAM1338 is therefore inhibition of LOC283293 (Accession XP_210962.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283293.

[38979] LOC283323 (Accession XP_210973.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283323 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283323 BINDING SITE, designated SEQ ID:2314, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38980] Another function of GAM1338 is therefore inhibition of LOC283323 (Accession XP_210973.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283323.

[38981] LOC283335 (Accession XP_210981.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283335 BINDING SITE1 and LOC283335 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283335, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283335 BINDING SITE1 and LOC283335 BINDING SITE2, designated SEQ ID:9238 and SEQ ID:10626 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38982] Another function of GAM1338 is therefore inhibition of LOC283335 (Accession XP_210981.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283335.

[38983] LOC283377 (Accession XP_208647.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283377 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC283377, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283377 BINDING SITE, designated SEQ ID:8862, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38984] Another function of GAM1338 is therefore inhibition of LOC283377 (Accession XP_208647.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283377.

[38985] LOC283387 (Accession XP_211007.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283387 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283387, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283387 BINDING SITE, designated SEQ ID:7011, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38986] Another function of GAM1338 is therefore inhibition of LOC283387 (Accession XP_211007.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283387.

[38987] LOC283394 (Accession XP_211021.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283394 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283394, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283394 BINDING SITE, designated SEQ ID:11655, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38988] Another function of GAM1338 is therefore inhibition of LOC283394 (Accession XP_211021.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283394.

[38989] LOC283395 (Accession XP_211020.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC283395 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283395, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283395 BINDING SITE, designated SEQ ID:13838, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38990] Another function of GAM1338 is therefore inhibition of LOC283395 (Accession XP_211020.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283395.

[38991] LOC283432 (Accession XP_211032.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283432 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283432, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283432 BINDING SITE, designated SEQ ID:6836, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38992] Another function of GAM1338 is therefore inhibition of LOC283432 (Accession XP_211032.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283432.

[38993] LOC283434 (Accession XP_211034.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283434 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283434, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283434 BINDING SITE, designated SEQ ID:16416, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38994] Another function of GAM1338 is therefore inhibition of LOC283434 (Accession XP_211034.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283434.

[38995] LOC283441 (Accession XP_211043.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283441 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283441, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283441 BINDING SITE, designated SEQ ID:5582, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38996] Another function of GAM1338 is therefore inhibition of LOC283441 (Accession XP_211043.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283441.

[38997] LOC283442 (Accession XP_211037.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283442 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC283442 BINDING SITE, designated SEQ ID:4817, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[38998] Another function of GAM1338 is therefore inhibition of LOC283442 (Accession XP_211037.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283442.

[38999] LOC283445 (Accession XP_211044.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283445 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283445 BINDING SITE, designated SEQ ID:9159, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39000] Another function of GAM1338 is therefore inhibition of LOC283445 (Accession XP_211044.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283445.

[39001] LOC283452 (Accession XP_208679.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283452 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283452 BINDING SITE, designated SEQ ID:3497, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39002] Another function of GAM1338 is therefore inhibition of LOC283452 (Accession XP_208679.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283452.

[39003] LOC283454 (Accession XP_211049.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283454 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283454, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283454 BINDING SITE, designated SEQ ID:12385, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39004] Another function of GAM1338 is therefore inhibition of LOC283454 (Accession XP_211049.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283454.

[39005] LOC283467 (Accession XP_211050.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283467 BINDING SITE, designated SEQ ID:3857, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39006] Another function of GAM1338 is therefore inhibition of

LOC283467 (Accession XP_211050.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283467.

[39007] LOC283475 (Accession XP_211056.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283475 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283475 BINDING SITE, designated SEQ ID:12806, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39008] Another function of GAM1338 is therefore inhibition of LOC283475 (Accession XP_211056.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283475.

[39009] LOC283507 (Accession XP_211075.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283507 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC283507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283507 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39010] Another function of GAM1338 is therefore inhibition of LOC283507 (Accession XP_211075.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283507.

[39011] LOC283514 (Accession XP_210264.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC283514 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283514, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283514 BINDING SITE, designated SEQ ID:6317, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39012] Another function of GAM1338 is therefore inhibition of LOC283514 (Accession XP_210264.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283514.

[39013] LOC283534 (Accession XP_211083.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283534 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283534, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283534 BINDING SITE, designated SEQ ID:13197, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39014] Another function of GAM1338 is therefore inhibition of LOC283534 (Accession XP_211083.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283534.

[39015] LOC283551 (Accession XP_211110.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC283551 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283551, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283551 BINDING SITE, designated SEQ ID:10790, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39016] Another function of GAM1338 is therefore inhibition of LOC283551 (Accession XP_211110.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283551.

[39017] LOC283575 (Accession XP_211095.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283575 BINDING SITE1 and LOC283575 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283575, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283575

BINDING SITE1 and LOC283575 BINDING SITE2, designated SEQ ID:8540 and SEQ ID:13153 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39018] Another function of GAM1338 is therefore inhibition of LOC283575 (Accession XP_211095.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283575.

[39019] LOC283588 (Accession NP_787093.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283588 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283588, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283588 BINDING SITE, designated SEQ ID:14938, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39020] Another function of GAM1338 is therefore inhibition of LOC283588 (Accession NP_787093.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283588.

[39021] LOC283624 (Accession XP_211126.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283624 BINDING SITE1 and LOC283624 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283624, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283624 BINDING SITE1 and LOC283624 BINDING SITE2, designated SEQ ID:13972 and SEQ ID:1137 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39022] Another function of GAM1338 is therefore inhibition of LOC283624 (Accession XP_211126.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283624.

[39023] LOC283637 (Accession XP_211134.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283637 BINDING SITE1 and LOC283637 BINDING SITE2 are target binding sites found in untranslated re-

gions of mRNA encoded by LOC283637, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283637 BINDING SITE1 and LOC283637 BINDING SITE2, designated SEQ ID:3786 and SEQ ID:12382 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39024] Another function of GAM1338 is therefore inhibition of LOC283637 (Accession XP_211134.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283637.

[39025] LOC283641 (Accession XP_208764.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283641 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283641, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283641 BINDING SITE, designated SEQ ID:435, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39026] Another function of GAM1338 is therefore inhibition of LOC283641 (Accession XP_208764.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283641.

[39027] LOC283672 (Accession XP_211152.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283672 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283672, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283672 BINDING SITE, designated SEQ ID:11655, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39028] Another function of GAM1338 is therefore inhibition of LOC283672 (Accession XP_211152.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283672.

[39029] LOC283693 (Accession XP_208788.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC283693 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283693, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283693 BINDING SITE, designated SEQ ID:16069, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39030] Another function of GAM1338 is therefore inhibition of LOC283693 (Accession XP_208788.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283693.

[39031] LOC283701 (Accession XP_211170.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC283701 BINDING SITE1 and LOC283701 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283701, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283701

BINDING SITE1 and LOC283701 BINDING SITE2, designated SEQ ID:777 and SEQ ID:6491 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39032] Another function of GAM1338 is therefore inhibition of LOC283701 (Accession XP_211170.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283701.

[39033] LOC283741 (Accession XP_208115.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283741 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283741, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283741 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39034] Another function of GAM1338 is therefore inhibition of LOC283741 (Accession XP_208115.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283741.

[39035] LOC283767 (Accession XP_208835.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283767 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283767, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283767 BINDING SITE, designated SEQ ID:3888, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39036] Another function of GAM1338 is therefore inhibition of LOC283767 (Accession XP_208835.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283767.

[39037] LOC283778 (Accession XP_211199.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283778 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283778, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283778 BINDING SITE, designated SEQ ID:15679, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39038] Another function of GAM1338 is therefore inhibition of LOC283778 (Accession XP_211199.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283778.

[39039] LOC283801 (Accession XP_208122.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283801 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283801, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283801 BINDING SITE, designated SEQ ID:11237, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39040] Another function of GAM1338 is therefore inhibition of

LOC283801 (Accession XP_208122.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283801.

[39041] LOC283802 (Accession XP_208850.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283802 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283802, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283802 BINDING SITE, designated SEQ ID:16635, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39042] Another function of GAM1338 is therefore inhibition of LOC283802 (Accession XP_208850.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283802.

[39043] LOC283818 (Accession XP_211218.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283818 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC283818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283818 BINDING SITE, designated SEQ ID:3834, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39044] Another function of GAM1338 is therefore inhibition of LOC283818 (Accession XP_211218.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283818.

[39045] LOC283849 (Accession XP_208870.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283849 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC283849, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283849 BINDING SITE, designated SEQ ID:2515, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA,

also designated SEQ ID:360.

[39046] Another function of GAM1338 is therefore inhibition of LOC283849 (Accession XP_208870.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283849.

[39047] LOC283849 (Accession NP_848611.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283849 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC283849, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283849 BINDING SITE, designated SEQ ID:2515, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39048] Another function of GAM1338 is therefore inhibition of LOC283849 (Accession NP_848611.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283849.

[39049] LOC283851 (Accession XP_211229.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC283851 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283851, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283851 BINDING SITE, designated SEQ ID:12708, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39050] Another function of GAM1338 is therefore inhibition of LOC283851 (Accession XP_211229.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283851.

[39051] LOC283856 (Accession XP_211233.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283856 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283856 BINDING SITE, desig-

nated SEQ ID:11601, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39052] Another function of GAM1338 is therefore inhibition of LOC283856 (Accession XP_211233.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283856.

[39053] LOC283861 (Accession NP_787095.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283861 BINDING SITE1 and LOC283861 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283861, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283861 BINDING SITE1 and LOC283861 BINDING SITE2, designated SEQ ID:8996 and SEQ ID:10879 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39054] Another function of GAM1338 is therefore inhibition of LOC283861 (Accession NP_787095.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283861.

[39055] LOC283863 (Accession XP_208875.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283863 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283863, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283863 BINDING SITE, designated SEQ ID:14614, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39056] Another function of GAM1338 is therefore inhibition of LOC283863 (Accession XP_208875.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283863.

[39057] LOC283887 (Accession XP_211248.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC283887 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283887, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283887 BINDING SITE, designated SEQ ID:9775, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39058] Another function of GAM1338 is therefore inhibition of LOC283887 (Accession XP_211248.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283887.

[39059] LOC283888 (Accession XP_211249.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283888 BINDING SITE1 and LOC283888 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283888, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283888 BINDING SITE1 and LOC283888 BINDING SITE2, designated SEQ ID:2692 and SEQ ID:5011 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39060] Another function of GAM1338 is therefore inhibition of LOC283888 (Accession XP_211249.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283888.

[39061] LOC283889 (Accession XP_208899.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC283889 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283889, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283889 BINDING SITE, designated SEQ ID:13686, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39062] Another function of GAM1338 is therefore inhibition of LOC283889 (Accession XP_208899.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283889.

[39063] LOC283928 (Accession XP_208909.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC283928 BINDING SITE1 and LOC283928 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283928, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283928 BINDING SITE1 and LOC283928 BINDING SITE2, designated SEQ ID:13293 and SEQ ID:3604 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39064] Another function of GAM1338 is therefore inhibition of LOC283928 (Accession XP_208909.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283928.

[39065] LOC283929 (Accession XP_208905.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC283929 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283929, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283929 BINDING SITE, desig-

nated SEQ ID:10232, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39066] Another function of GAM1338 is therefore inhibition of LOC283929 (Accession XP_208905.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283929.

[39067] LOC283964 (Accession XP_208145.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC283964 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283964, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283964 BINDING SITE, designated SEQ ID:1384, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39068] Another function of GAM1338 is therefore inhibition of LOC283964 (Accession XP_208145.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283964.

[39069] LOC284016 (Accession XP_211298.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284016 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284016, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284016 BINDING SITE, designated SEQ ID:795, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39070] Another function of GAM1338 is therefore inhibition of LOC284016 (Accession XP_211298.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284016.

[39071] LOC284017 (Accession XP_208961.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284017 BINDING SITE, designated SEQ ID:3858, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39072] Another function of GAM1338 is therefore inhibition of LOC284017 (Accession XP_208961.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284017.

[39073] LOC284019 (Accession XP_211302.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284019 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284019, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284019 BINDING SITE, designated SEQ ID:19482, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39074] Another function of GAM1338 is therefore inhibition of LOC284019 (Accession XP_211302.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284019.

[39075] LOC284023 (Accession XP_208983.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC284023 BINDING SITE1 and LOC284023 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284023, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284023 BINDING SITE1 and LOC284023 BINDING SITE2, designated SEQ ID:5520 and SEQ ID:429 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39076] Another function of GAM1338 is therefore inhibition of LOC284023 (Accession XP_208983.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284023.

[39077] LOC284048 (Accession XP_208152.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284048 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC284048, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284048 BINDING SITE, designated SEQ ID:17222, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39078] Another function of GAM1338 is therefore inhibition of LOC284048 (Accession XP_208152.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284048.

[39079] LOC284063 (Accession XP_208992.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284063 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284063, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284063 BINDING SITE, designated SEQ ID:17713, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39080] Another function of GAM1338 is therefore inhibition of LOC284063 (Accession XP_208992.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284063.

[39081] LOC284074 (Accession XP_211321.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284074 BINDING SITE1 and LOC284074 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284074, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284074 BINDING SITE1 and LOC284074 BINDING SITE2, designated SEQ ID:18547 and SEQ ID:5751 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39082] Another function of GAM1338 is therefore inhibition of LOC284074 (Accession XP_211321.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284074.

[39083] LOC284082 (Accession XP_211323.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284082 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284082, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284082 BINDING SITE, designated SEQ ID:18527, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39084] Another function of GAM1338 is therefore inhibition of LOC284082 (Accession XP_211323.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284082.

[39085] LOC284095 (Accession XP_211324.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284095 BINDING SITE1 through LOC284095 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284095, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC284095 BINDING SITE1 through LOC284095 BINDING SITE3, designated SEQ ID:18259, SEQ ID:19595 and SEQ ID:16884 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39086] Another function of GAM1338 is therefore inhibition of LOC284095 (Accession XP_211324.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284095.

[39087] LOC284098 (Accession XP_209008.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC284098 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284098, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284098 BINDING SITE, designated SEQ ID:18178, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39088] Another function of GAM1338 is therefore inhibition of

LOC284098 (Accession XP_209008.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284098.

[39089] LOC284100 (Accession XP_209015.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284100 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284100, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284100 BINDING SITE, designated SEQ ID:11656, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39090] Another function of GAM1338 is therefore inhibition of LOC284100 (Accession XP_209015.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284100.

[39091] LOC284101 (Accession XP_209019.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284101 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC284101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284101 BINDING SITE, designated SEQ ID:4581, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39092] Another function of GAM1338 is therefore inhibition of LOC284101 (Accession XP_209019.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284101.

[39093] LOC284102 (Accession XP_211327.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC284102 BINDING SITE1 through LOC284102 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284102, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284102 BINDING SITE1 through LOC284102 BINDING SITE3, designated SEQ ID:8270, SEQ ID:17111 and SEQ ID:6349 re-

spectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39094] Another function of GAM1338 is therefore inhibition of LOC284102 (Accession XP_211327.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284102.

[39095] LOC284117 (Accession XP_209024.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284117 BINDING SITE, designated SEQ ID:11347, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39096] Another function of GAM1338 is therefore inhibition of LOC284117 (Accession XP_209024.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284117.

[39097] LOC284128 (Accession XP_211342.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284128 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284128 BINDING SITE, designated SEQ ID:17271, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39098] Another function of GAM1338 is therefore inhibition of LOC284128 (Accession XP_211342.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284128.

[39099] LOC284135 (Accession XP_209032.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284135 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284135 BINDING SITE, designated SEQ ID:5319, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39100] Another function of GAM1338 is therefore inhibition of LOC284135 (Accession XP_209032.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284135.

[39101] LOC284183 (Accession XP_209059.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284183 BINDING SITE1 and LOC284183 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284183, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284183 BINDING SITE1 and LOC284183 BINDING SITE2, designated SEQ ID:8524 and SEQ ID:11460 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39102] Another function of GAM1338 is therefore inhibition of LOC284183 (Accession XP_209059.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284183.

[39103] LOC284186 (Accession XP_209060.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC284186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284186 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39104] Another function of GAM1338 is therefore inhibition of LOC284186 (Accession XP_209060.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284186.

[39105] LOC284286 (Accession XP_211419.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284286 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC284286, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284286 BINDING SITE, designated SEQ ID:5521, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39106] Another function of GAM1338 is therefore inhibition of LOC284286 (Accession XP_211419.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284286.

[39107] LOC284289 (Accession XP_209105.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284289 BINDING SITE, designated SEQ ID:7635, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39108] Another function of GAM1338 is therefore inhibition of LOC284289 (Accession XP_209105.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284289.

[39109] LOC284304 (Accession XP_211426.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284304 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284304, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284304 BINDING SITE, designated SEQ ID:16163, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39110] Another function of GAM1338 is therefore inhibition of LOC284304 (Accession XP_211426.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284304.

[39111] LOC284317 (Accession XP_209162.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC284317 BINDING SITE1 and LOC284317 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284317, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284317 BINDING SITE1 and LOC284317 BINDING SITE2, designated SEQ ID:5320 and SEQ ID:11486 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39112] Another function of GAM1338 is therefore inhibition of LOC284317 (Accession XP_209162.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284317.

[39113] LOC284325 (Accession XP_209143.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284325 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284325, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284325 BINDING SITE, desig-

nated SEQ ID:11657, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39114] Another function of GAM1338 is therefore inhibition of LOC284325 (Accession XP_209143.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284325.

[39115] LOC284362 (Accession XP_211435.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284362 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284362, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284362 BINDING SITE, designated SEQ ID:10666, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39116] Another function of GAM1338 is therefore inhibition of LOC284362 (Accession XP_211435.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284362.

[39117] LOC284373 (Accession XP_211439.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284373 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284373, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284373 BINDING SITE, designated SEQ ID:3968, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39118] Another function of GAM1338 is therefore inhibition of LOC284373 (Accession XP_211439.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284373.

[39119] LOC284375 (Accession XP_209154.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284375 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284375, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284375 BINDING SITE, designated SEQ ID:13618, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39120] Another function of GAM1338 is therefore inhibition of LOC284375 (Accession XP_209154.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284375.

[39121] LOC284376 (Accession XP_209157.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284376 BINDING SITE1 and LOC284376 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284376, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284376 BINDING SITE1 and LOC284376 BINDING SITE2, designated SEQ ID:3410 and SEQ ID:9328 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39122] Another function of GAM1338 is therefore inhibition of

LOC284376 (Accession XP_209157.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284376.

[39123] LOC284379 (Accession XP_209163.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284379 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284379, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284379 BINDING SITE, designated SEQ ID:2198, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39124] Another function of GAM1338 is therefore inhibition of LOC284379 (Accession XP_209163.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284379.

[39125] LOC284396 (Accession XP_211452.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284396 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC284396, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284396 BINDING SITE, designated SEQ ID:2360, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39126] Another function of GAM1338 is therefore inhibition of LOC284396 (Accession XP_211452.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284396.

[39127] LOC284408 (Accession XP_211443.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284408 BINDING SITE, designated SEQ ID:10732, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39128] Another function of GAM1338 is therefore inhibition of LOC284408 (Accession XP_211443.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284408.

[39129] LOC284410 (Accession XP_211449.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284410 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284410, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284410 BINDING SITE, designated SEQ ID:7072, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39130] Another function of GAM1338 is therefore inhibition of LOC284410 (Accession XP_211449.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284410.

[39131] LOC284421 (Accession XP_209200.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC284421 BINDING SITE1 through LOC284421 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284421, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284421 BINDING SITE1 through LOC284421 BINDING SITE3, designated SEQ ID:15524, SEQ ID:3295 and SEQ ID:2985 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39132] Another function of GAM1338 is therefore inhibition of LOC284421 (Accession XP_209200.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284421.

[39133] LOC284421 (Accession XP_209200.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284421 BINDING SITE1 through LOC284421 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284421, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC284421 BINDING SITE1 through LOC284421 BINDING SITE3, designated SEQ ID:3295, SEQ ID:932 and SEQ ID:19419 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39134] Another function of GAM1338 is therefore inhibition of LOC284421 (Accession XP_209200.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284421.

[39135] LOC284436 (Accession XP_290862.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284436 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284436 BINDING SITE, designated SEQ ID:6140, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39136] Another function of GAM1338 is therefore inhibition of LOC284436 (Accession XP_290862.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284436.

[39137] LOC284440 (Accession XP_209210.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284440 BINDING SITE, designated SEQ ID:12050, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39138] Another function of GAM1338 is therefore inhibition of LOC284440 (Accession XP_209210.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284440.

[39139] LOC284454 (Accession XP_209216.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284454 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC284454, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284454 BINDING SITE, designated SEQ ID:18896, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39140] Another function of GAM1338 is therefore inhibition of LOC284454 (Accession XP_209216.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284454.

[39141] LOC284456 (Accession XP_211470.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284456 BINDING SITE1 and LOC284456 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284456, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284456 BINDING SITE1 and LOC284456 BINDING SITE2, designated SEQ ID:10594 and SEQ ID:6643 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[39142] Another function of GAM1338 is therefore inhibition of LOC284456 (Accession XP_211470.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284456.

[39143] LOC284471 (Accession XP_209225.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284471 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284471, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284471 BINDING SITE, designated SEQ ID:4926, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39144] Another function of GAM1338 is therefore inhibition of LOC284471 (Accession XP_209225.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284471.

[39145] LOC284475 (Accession XP_211478.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC284475 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284475 BINDING SITE, designated SEQ ID:17171, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39146] Another function of GAM1338 is therefore inhibition of LOC284475 (Accession XP_211478.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284475.

[39147] LOC284512 (Accession XP_211500.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284512 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284512, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284512 BINDING SITE, desig-

nated SEQ ID:16234, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39148] Another function of GAM1338 is therefore inhibition of LOC284512 (Accession XP_211500.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284512.

[39149] LOC284513 (Accession XP_211502.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284513 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284513, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284513 BINDING SITE, designated SEQ ID:19066, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39150] Another function of GAM1338 is therefore inhibition of LOC284513 (Accession XP_211502.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284513.

[39151] LOC284531 (Accession XP_211513.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284531 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284531, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284531 BINDING SITE, designated SEQ ID:2846, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39152] Another function of GAM1338 is therefore inhibition of LOC284531 (Accession XP_211513.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284531.

[39153] LOC284551 (Accession XP_211515.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284551 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284551, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284551 BINDING SITE, designated SEQ ID:17959, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39154] Another function of GAM1338 is therefore inhibition of LOC284551 (Accession XP_211515.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284551.

[39155] LOC284577 (Accession XP_211522.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284577 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284577, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284577 BINDING SITE, designated SEQ ID:11682, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39156] Another function of GAM1338 is therefore inhibition of LOC284577 (Accession XP_211522.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284577.

[39157] LOC284587 (Accession XP_209278.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC284587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284587 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39158] Another function of GAM1338 is therefore inhibition of LOC284587 (Accession XP_209278.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284587.

[39159] LOC284611 (Accession XP_211552.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284611 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC284611, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284611 BINDING SITE, designated SEQ ID:11652, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39160] Another function of GAM1338 is therefore inhibition of LOC284611 (Accession XP_211552.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284611.

[39161] LOC284628 (Accession XP_211561.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284628 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284628, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284628 BINDING SITE, designated SEQ ID:20050, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39162] Another function of GAM1338 is therefore inhibition of LOC284628 (Accession XP_211561.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284628.

[39163] LOC284668 (Accession XP_211583.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284668 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284668, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284668 BINDING SITE, designated SEQ ID:19894, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39164] Another function of GAM1338 is therefore inhibition of LOC284668 (Accession XP_211583.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284668.

[39165] LOC284675 (Accession XP_209319.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC284675 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284675, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284675 BINDING SITE, designated SEQ ID:8487, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39166] Another function of GAM1338 is therefore inhibition of LOC284675 (Accession XP_209319.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284675.

[39167] LOC284701 (Accession XP_294994.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284701 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284701, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284701 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39168] Another function of GAM1338 is therefore inhibition of LOC284701 (Accession XP_294994.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284701.

[39169] LOC284708 (Accession XP_209332.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284708 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284708 BINDING SITE, designated SEQ ID:12721, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39170] Another function of GAM1338 is therefore inhibition of LOC284708 (Accession XP_209332.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284708.

[39171] LOC284723 (Accession XP_211602.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284723 BINDING SITE1 and LOC284723 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284723, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284723 BINDING SITE1 and LOC284723 BINDING SITE2, designated SEQ ID:6492 and SEQ ID:17106 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39172] Another function of GAM1338 is therefore inhibition of LOC284723 (Accession XP_211602.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284723.

[39173] LOC284805 (Accession XP_209371.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284805 BINDING SITE1 through LOC284805 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284805, corresponding to target binding sites such as BINDING SITE I, BINDING SITE

II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284805 BINDING SITE1 through LOC284805 BINDING SITE3, designated SEQ ID:18781, SEQ ID:11447 and SEQ ID:17164 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39174] Another function of GAM1338 is therefore inhibition of LOC284805 (Accession XP_209371.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284805.

[39175] LOC284839 (Accession XP_211661.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284839 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284839, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284839 BINDING SITE, designated SEQ ID:4527, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39176] Another function of GAM1338 is therefore inhibition of LOC284839 (Accession XP_211661.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284839.

[39177] LOC284865 (Accession XP_211672.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284865 BINDING SITE, designated SEQ ID:1299, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39178] Another function of GAM1338 is therefore inhibition of LOC284865 (Accession XP_211672.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284865.

[39179] LOC284874 (Accession XP_209394.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC284874 BINDING SITE1 and LOC284874 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284874, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284874 BINDING SITE1 and LOC284874 BINDING SITE2, designated SEQ ID:14015 and SEQ ID:2751 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39180] Another function of GAM1338 is therefore inhibition of LOC284874 (Accession XP_209394.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284874.

[39181] LOC284934 (Accession XP_211696.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284934 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284934, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284934 BINDING SITE, desig-

nated SEQ ID:17477, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39182] Another function of GAM1338 is therefore inhibition of LOC284934 (Accession XP_211696.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284934.

[39183] LOC284947 (Accession XP_211705.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284947 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284947, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284947 BINDING SITE, designated SEQ ID:5006, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39184] Another function of GAM1338 is therefore inhibition of LOC284947 (Accession XP_211705.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284947.

[39185] LOC284950 (Accession XP_211703.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284950 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284950, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284950 BINDING SITE, designated SEQ ID:6753, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39186] Another function of GAM1338 is therefore inhibition of LOC284950 (Accession XP_211703.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284950.

[39187] LOC284960 (Accession XP_211715.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC284960 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284960, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284960 BINDING SITE, designated SEQ ID:8699, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39188] Another function of GAM1338 is therefore inhibition of LOC284960 (Accession XP_211715.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284960.

[39189] LOC285026 (Accession XP_209440.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285026 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285026, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285026 BINDING SITE, designated SEQ ID:14276, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39190] Another function of GAM1338 is therefore inhibition of LOC285026 (Accession XP_209440.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285026.

[39191] LOC285032 (Accession XP_211740.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285032 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285032, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285032 BINDING SITE, designated SEQ ID:5725, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39192] Another function of GAM1338 is therefore inhibition of LOC285032 (Accession XP_211740.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285032.

[39193] LOC285083 (Accession XP_209464.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285083 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC285083, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285083 BINDING SITE, designated SEQ ID:18085, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39194] Another function of GAM1338 is therefore inhibition of LOC285083 (Accession XP_209464.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285083.

[39195] LOC285088 (Accession XP_209465.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285088 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285088, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285088 BINDING SITE, designated SEQ ID:20100, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39196] Another function of GAM1338 is therefore inhibition of LOC285088 (Accession XP_209465.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285088.

[39197] LOC285123 (Accession XP_211773.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285123 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285123 BINDING SITE, designated SEQ ID:4218, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39198] Another function of GAM1338 is therefore inhibition of LOC285123 (Accession XP_211773.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285123.

[39199] LOC285127 (Accession XP_211771.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC285127 BINDING SITE1 and LOC285127 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285127, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285127 BINDING SITE1 and LOC285127 BINDING SITE2, designated SEQ ID:19204 and SEQ ID:3106 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39200] Another function of GAM1338 is therefore inhibition of LOC285127 (Accession XP_211771.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285127.

[39201] LOC285166 (Accession XP_211791.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285166 BINDING SITE, desig-

nated SEQ ID:19378, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39202] Another function of GAM1338 is therefore inhibition of LOC285166 (Accession XP_211791.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285166.

[39203] LOC285176 (Accession XP_209500.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285176 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285176, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285176 BINDING SITE, designated SEQ ID:12167, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39204] Another function of GAM1338 is therefore inhibition of LOC285176 (Accession XP_209500.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285176.

[39205] LOC285193 (Accession XP_209509.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285193, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285193 BINDING SITE, designated SEQ ID:13870, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39206] Another function of GAM1338 is therefore inhibition of LOC285193 (Accession XP_209509.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285193.

[39207] LOC285221 (Accession XP_209521.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285221 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285221, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285221 BINDING SITE, designated SEQ ID:15365, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39208] Another function of GAM1338 is therefore inhibition of LOC285221 (Accession XP_209521.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285221.

[39209] LOC285231 (Accession XP_211813.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285231 BINDING SITE1 and LOC285231 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285231, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285231 BINDING SITE1 and LOC285231 BINDING SITE2, designated SEQ ID:11238 and SEQ ID:13069 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39210] Another function of GAM1338 is therefore inhibition of

LOC285231 (Accession XP_211813.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285231.

[39211] LOC285281 (Accession XP_211829.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285281 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285281, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285281 BINDING SITE, designated SEQ ID:7766, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39212] Another function of GAM1338 is therefore inhibition of LOC285281 (Accession XP_211829.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285281.

[39213] LOC285299 (Accession XP_209554.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285299 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC285299, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285299 BINDING SITE, designated SEQ ID:15961, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39214] Another function of GAM1338 is therefore inhibition of LOC285299 (Accession XP_209554.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285299.

[39215] LOC285334 (Accession XP_211844.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285334 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285334 BINDING SITE, designated SEQ ID:17006, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39216] Another function of GAM1338 is therefore inhibition of LOC285334 (Accession XP_211844.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285334.

[39217] LOC285345 (Accession XP_211854.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285345 BINDING SITE1 and LOC285345 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285345, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285345 BINDING SITE1 and LOC285345 BINDING SITE2, designated SEQ ID:11821 and SEQ ID:13276 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39218] Another function of GAM1338 is therefore inhibition of LOC285345 (Accession XP_211854.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285345.

[39219] LOC285366 (Accession XP_209581.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285366 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285366, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285366 BINDING SITE, designated SEQ ID:4019, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39220] Another function of GAM1338 is therefore inhibition of LOC285366 (Accession XP_209581.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285366.

[39221] LOC285369 (Accession XP_211861.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC285369 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285369, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC285369 BINDING SITE, designated SEQ ID:19816, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39222] Another function of GAM1338 is therefore inhibition of LOC285369 (Accession XP_211861.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285369.

[39223] LOC285389 (Accession XP_211873.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285389 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285389, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285389 BINDING SITE, designated SEQ ID:7025, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39224] Another function of GAM1338 is therefore inhibition of LOC285389 (Accession XP_211873.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285389.

[39225] LOC285392 (Accession XP_211879.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285392 BINDING SITE1 and LOC285392 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285392, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285392 BINDING SITE1 and LOC285392 BINDING SITE2, designated SEQ ID:6034 and SEQ ID:436 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39226] Another function of GAM1338 is therefore inhibition of LOC285392 (Accession XP_211879.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285392.

[39227] LOC285398 (Accession XP_209593.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285398 BINDING SITE1 and LOC285398 BINDING SITE2 are target binding sites found in untranslated re-

gions of mRNA encoded by LOC285398, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285398 BINDING SITE1 and LOC285398 BINDING SITE2, designated SEQ ID:4020 and SEQ ID:3701 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39228] Another function of GAM1338 is therefore inhibition of LOC285398 (Accession XP_209593.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285398.

[39229] LOC285429 (Accession XP_209607.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC285429 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285429, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285429 BINDING SITE, designated SEQ ID:4870, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39230] Another function of GAM1338 is therefore inhibition of LOC285429 (Accession XP_209607.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285429.

[39231] LOC285488 (Accession XP_211914.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285488 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285488, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285488 BINDING SITE, designated SEQ ID:11093, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39232] Another function of GAM1338 is therefore inhibition of LOC285488 (Accession XP_211914.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285488.

[39233] LOC285491 (Accession XP_211917.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC285491 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285491, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285491 BINDING SITE, designated SEQ ID:8951, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39234] Another function of GAM1338 is therefore inhibition of LOC285491 (Accession XP_211917.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285491.

[39235] LOC285509 (Accession XP_211923.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285509 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285509, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285509 BINDING SITE, desig-

nated SEQ ID:11997, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39236] Another function of GAM1338 is therefore inhibition of LOC285509 (Accession XP_211923.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285509.

[39237] LOC285540 (Accession XP_209654.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285540 BINDING SITE1 and LOC285540 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285540, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285540 BINDING SITE1 and LOC285540 BINDING SITE2, designated SEQ ID:5384 and SEQ ID:19426 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39238] Another function of GAM1338 is therefore inhibition of LOC285540 (Accession XP_209654.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285540.

[39239] LOC285560 (Accession XP_209660.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285560 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285560, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285560 BINDING SITE, designated SEQ ID:7821, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39240] Another function of GAM1338 is therefore inhibition of LOC285560 (Accession XP_209660.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285560.

[39241] LOC285589 (Accession XP_209671.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285589 BINDING SITE1 and LOC285589 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285589, corresponding to

target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285589 BINDING SITE1 and LOC285589 BINDING SITE2, designated SEQ ID:3782 and SEQ ID:14069 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39242] Another function of GAM1338 is therefore inhibition of LOC285589 (Accession XP_209671.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285589.

[39243] LOC285626 (Accession XP_211959.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285626 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285626, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285626 BINDING SITE, designated SEQ ID:16288, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39244] Another function of GAM1338 is therefore inhibition of LOC285626 (Accession XP_211959.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285626.

[39245] LOC285638 (Accession XP_209693.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285638 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285638, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285638 BINDING SITE, designated SEQ ID:13619, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39246] Another function of GAM1338 is therefore inhibition of LOC285638 (Accession XP_209693.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285638.

[39247] LOC285678 (Accession XP_209717.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC285678 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285678, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285678 BINDING SITE, designated SEQ ID:16507, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39248] Another function of GAM1338 is therefore inhibition of LOC285678 (Accession XP_209717.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285678.

[39249] LOC285679 (Accession XP_209719.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC285679 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285679, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285679 BINDING SITE, designated SEQ ID:15031, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39250] Another function of GAM1338 is therefore inhibition of LOC285679 (Accession XP_209719.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285679.

[39251] LOC285683 (Accession XP_211980.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285683 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285683, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285683 BINDING SITE, designated SEQ ID:5151, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39252] Another function of GAM1338 is therefore inhibition of LOC285683 (Accession XP_211980.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285683.

[39253] LOC285687 (Accession XP_211985.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285687 BINDING SITE, designated SEQ ID:10580, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39254] Another function of GAM1338 is therefore inhibition of LOC285687 (Accession XP_211985.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285687.

[39255] LOC285689 (Accession XP_209724.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285689 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285689, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC285689 BINDING SITE, designated SEQ ID:4452, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39256] Another function of GAM1338 is therefore inhibition of LOC285689 (Accession XP_209724.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285689.

[39257] LOC285693 (Accession XP_211981.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285693 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285693, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285693 BINDING SITE, designated SEQ ID:7946, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39258] Another function of GAM1338 is therefore inhibition of LOC285693 (Accession XP_211981.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285693.

[39259] LOC285713 (Accession XP_211992.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285713 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285713, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285713 BINDING SITE, designated SEQ ID:6411, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39260] Another function of GAM1338 is therefore inhibition of LOC285713 (Accession XP_211992.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285713.

[39261] LOC285722 (Accession XP_211997.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285722 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285722, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285722 BINDING SITE, designated SEQ ID:19494, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39262] Another function of GAM1338 is therefore inhibition of LOC285722 (Accession XP_211997.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285722.

[39263] LOC285744 (Accession XP_209743.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285744 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285744, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285744 BINDING SITE, designated SEQ ID:11603, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39264] Another function of GAM1338 is therefore inhibition of

LOC285744 (Accession XP_209743.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285744.

[39265] LOC285747 (Accession XP_209742.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285747 BINDING SITE1 and LOC285747 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285747, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285747 BINDING SITE1 and LOC285747 BINDING SITE2, designated SEQ ID:13800 and SEQ ID:9553 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39266] Another function of GAM1338 is therefore inhibition of LOC285747 (Accession XP_209742.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285747.

[39267] LOC285760 (Accession XP_209750.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC285760 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285760, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285760 BINDING SITE, designated SEQ ID:13064, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39268] Another function of GAM1338 is therefore inhibition of LOC285760 (Accession XP_209750.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285760.

[39269] LOC285813 (Accession XP_212036.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285813 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285813 BINDING SITE, designated SEQ ID:17617, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39270] Another function of GAM1338 is therefore inhibition of LOC285813 (Accession XP_212036.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285813.

[39271] LOC285822 (Accession XP_209777.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285822 BINDING SITE1 and LOC285822 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285822, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285822 BINDING SITE1 and LOC285822 BINDING SITE2, designated SEQ ID:6178 and SEQ ID:6011 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39272] Another function of GAM1338 is therefore inhibition of LOC285822 (Accession XP_209777.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285822.

[39273] LOC285843 (Accession XP_212034.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285843 BINDING SITE1 and LOC285843 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285843, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285843 BINDING SITE1 and LOC285843 BINDING SITE2, designated SEQ ID:1414 and SEQ ID:11782 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39274] Another function of GAM1338 is therefore inhibition of LOC285843 (Accession XP_212034.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285843.

[39275] LOC285847 (Accession XP_212045.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285847 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285847, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285847 BINDING SITE, designated SEQ ID:7212, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39276] Another function of GAM1338 is therefore inhibition of LOC285847 (Accession XP_212045.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285847.

[39277] LOC285872 (Accession XP_212061.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285872 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285872, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285872 BINDING SITE, designated SEQ ID:7986, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39278] Another function of GAM1338 is therefore inhibition of

LOC285872 (Accession XP_212061.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285872.

[39279] LOC285896 (Accession XP_209806.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285896 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285896, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285896 BINDING SITE, designated SEQ ID:4795, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39280] Another function of GAM1338 is therefore inhibition of LOC285896 (Accession XP_209806.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285896.

[39281] LOC285899 (Accession XP_209807.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285899 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC285899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285899 BINDING SITE, designated SEQ ID:10004, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39282] Another function of GAM1338 is therefore inhibition of LOC285899 (Accession XP_209807.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285899.

[39283] LOC285914 (Accession XP_209810.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285914 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285914, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285914 BINDING SITE, designated SEQ ID:14560, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39284] Another function of GAM1338 is therefore inhibition of LOC285914 (Accession XP_209810.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285914.

[39285] LOC285922 (Accession XP_209822.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285922 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285922 BINDING SITE, designated SEQ ID:4795, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39286] Another function of GAM1338 is therefore inhibition of LOC285922 (Accession XP_209822.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285922.

[39287] LOC285923 (Accession XP_212104.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC285923 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285923, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285923 BINDING SITE, designated SEQ ID:16934, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39288] Another function of GAM1338 is therefore inhibition of LOC285923 (Accession XP_212104.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285923.

[39289] LOC285945 (Accession XP_212092.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285945 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285945, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285945 BINDING SITE, desig-

nated SEQ ID:12385, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39290] Another function of GAM1338 is therefore inhibition of LOC285945 (Accession XP_212092.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285945.

[39291] LOC285950 (Accession XP_212089.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285950 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285950, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285950 BINDING SITE, designated SEQ ID:11638, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39292] Another function of GAM1338 is therefore inhibition of LOC285950 (Accession XP_212089.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285950.

[39293] LOC285952 (Accession XP_209821.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285952 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285952, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285952 BINDING SITE, designated SEQ ID:2758, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39294] Another function of GAM1338 is therefore inhibition of LOC285952 (Accession XP_209821.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285952.

[39295] LOC285961 (Accession XP_209833.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285961 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285961, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285961 BINDING SITE, designated SEQ ID:11621, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39296] Another function of GAM1338 is therefore inhibition of LOC285961 (Accession XP_209833.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285961.

[39297] LOC285972 (Accession XP_212105.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285972 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285972 BINDING SITE, designated SEQ ID:8156, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39298] Another function of GAM1338 is therefore inhibition of LOC285972 (Accession XP_212105.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285972.

[39299] LOC285979 (Accession XP_212117.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285979 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285979, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285979 BINDING SITE, designated SEQ ID:13228, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39300] Another function of GAM1338 is therefore inhibition of LOC285979 (Accession XP_212117.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285979.

[39301] LOC285989 (Accession XP_212111.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285989 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC285989, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285989 BINDING SITE, designated SEQ ID:19067, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39302] Another function of GAM1338 is therefore inhibition of LOC285989 (Accession XP_212111.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285989.

[39303] LOC285999 (Accession XP_212120.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC285999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285999 BINDING SITE, designated SEQ ID:18120, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39304] Another function of GAM1338 is therefore inhibition of LOC285999 (Accession XP_212120.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285999.

[39305] LOC286030 (Accession XP_209868.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286030 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286030, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286030 BINDING SITE, designated SEQ ID:10050, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39306] Another function of GAM1338 is therefore inhibition of LOC286030 (Accession XP_209868.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286030.

[39307] LOC286032 (Accession XP_209867.2) is another GAM1338 target gene, herein designated TARGET GENE.

LOC286032 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286032, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286032 BINDING SITE, designated SEQ ID:1208, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39308] Another function of GAM1338 is therefore inhibition of LOC286032 (Accession XP_209867.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286032.

[39309] LOC286039 (Accession XP_209873.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286039 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286039, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286039 BINDING SITE, designated SEQ ID:17647, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39310] Another function of GAM1338 is therefore inhibition of LOC286039 (Accession XP_209873.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286039.

[39311] LOC286052 (Accession XP_212152.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286052 BINDING SITE, designated SEQ ID:14748, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39312] Another function of GAM1338 is therefore inhibition of LOC286052 (Accession XP_212152.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286052.

[39313] LOC286075 (Accession NP_776192.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286075 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286075, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286075 BINDING SITE, designated SEQ ID:1410, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39314] Another function of GAM1338 is therefore inhibition of LOC286075 (Accession NP_776192.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286075.

[39315] LOC286077 (Accession XP_209892.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC286077 BINDING SITE, designated SEQ ID:3388, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39316] Another function of GAM1338 is therefore inhibition of LOC286077 (Accession XP_209892.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286077.

[39317] LOC286078 (Accession XP_212163.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286078 BINDING SITE1 through LOC286078 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC286078, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286078 BINDING SITE1 through LOC286078 BINDING SITE4, designated SEQ ID:13798, SEQ ID:12045, SEQ ID:8139 and SEQ ID:9300 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39318] Another function of GAM1338 is therefore inhibition of

LOC286078 (Accession XP_212163.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286078.

[39319] LOC286103 (Accession NP_848630.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286103 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC286103, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286103 BINDING SITE, designated SEQ ID:15670, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39320] Another function of GAM1338 is therefore inhibition of LOC286103 (Accession NP_848630.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286103.

[39321] LOC286103 (Accession XP_209897.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286103 BINDING SITE is a target binding site found in

the 3` untranslated region of multiple transcripts of mRNA encoded by LOC286103, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286103 BINDING SITE, designated SEQ ID:15670, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39322] Another function of GAM1338 is therefore inhibition of LOC286103 (Accession XP_209897.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286103.

[39323] LOC286121 (Accession XP_212184.3) is another GAM1338 target gene, herein designated TARGET GENE. LOC286121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286121 BINDING SITE, designated SEQ ID:663, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39324] Another function of GAM1338 is therefore inhibition of LOC286121 (Accession XP_212184.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286121.

[39325] LOC286126 (Accession XP_212185.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286126 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286126, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286126 BINDING SITE, designated SEQ ID:8950, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39326] Another function of GAM1338 is therefore inhibition of LOC286126 (Accession XP_212185.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286126.

[39327] LOC286132 (Accession XP_212194.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC286132 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286132 BINDING SITE, designated SEQ ID:2266, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39328] Another function of GAM1338 is therefore inhibition of LOC286132 (Accession XP_212194.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286132.

[39329] LOC286166 (Accession XP_209925.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286166 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286166 BINDING SITE, desig-

nated SEQ ID:1529, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39330] Another function of GAM1338 is therefore inhibition of LOC286166 (Accession XP_209925.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286166.

[39331] LOC286170 (Accession XP_212211.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286170 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286170 BINDING SITE, designated SEQ ID:14196, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39332] Another function of GAM1338 is therefore inhibition of LOC286170 (Accession XP_212211.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC286170.

[39333] LOC286186 (Accession XP_212219.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286186 BINDING SITE1 and LOC286186 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC286186, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286186 BINDING SITE1 and LOC286186 BINDING SITE2, designated SEQ ID:15317 and SEQ ID:13117 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39334] Another function of GAM1338 is therefore inhibition of LOC286186 (Accession XP_212219.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286186.

[39335] LOC286206 (Accession XP_209953.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286206 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286206, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286206 BINDING SITE, designated SEQ ID:19418, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39336] Another function of GAM1338 is therefore inhibition of LOC286206 (Accession XP_209953.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286206.

[39337] LOC286207 (Accession XP_209941.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286207 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286207, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286207 BINDING SITE, designated SEQ ID:16987, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39338] Another function of GAM1338 is therefore inhibition of

LOC286207 (Accession XP_209941.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286207.

[39339] LOC286208 (Accession XP_212230.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286208 BINDING SITE1 through LOC286208 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC286208, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286208 BINDING SITE1 through LOC286208 BINDING SITE3, designated SEQ ID:16222, SEQ ID:12039 and SEQ ID:14347 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39340] Another function of GAM1338 is therefore inhibition of LOC286208 (Accession XP_212230.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286208.

[39341] LOC286223 (Accession XP_209956.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC286223 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286223, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286223 BINDING SITE, designated SEQ ID:13388, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39342] Another function of GAM1338 is therefore inhibition of LOC286223 (Accession XP_209956.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286223.

[39343] LOC286245 (Accession XP_212244.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286245 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286245, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286245 BINDING SITE, desig-

nated SEQ ID:18995, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39344] Another function of GAM1338 is therefore inhibition of LOC286245 (Accession XP_212244.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286245.

[39345] LOC286341 (Accession XP_212278.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286341 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286341, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286341 BINDING SITE, designated SEQ ID:14403, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39346] Another function of GAM1338 is therefore inhibition of LOC286341 (Accession XP_212278.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC286341.

[39347] LOC286354 (Accession XP_212286.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286354 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286354, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286354 BINDING SITE, designated SEQ ID:20172, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39348] Another function of GAM1338 is therefore inhibition of LOC286354 (Accession XP_212286.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286354.

[39349] LOC286356 (Accession XP_212290.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286356 BINDING SITE1 and LOC286356 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC286356, corresponding to target binding sites such as BINDING SITE I, BINDING SITE

II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286356 BINDING SITE1 and LOC286356 BINDING SITE2, designated SEQ ID:13800 and SEQ ID:3910 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39350] Another function of GAM1338 is therefore inhibition of LOC286356 (Accession XP_212290.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286356.

[39351] LOC286357 (Accession XP_212285.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286357 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286357, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286357 BINDING SITE, designated SEQ ID:13894, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39352] Another function of GAM1338 is therefore inhibition of

LOC286357 (Accession XP_212285.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286357.

[39353] LOC286395 (Accession XP_212308.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286395 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286395, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286395 BINDING SITE, designated SEQ ID:18548, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39354] Another function of GAM1338 is therefore inhibition of LOC286395 (Accession XP_212308.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286395.

[39355] LOC286404 (Accession XP_210036.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286404 BINDING SITE is a target binding site found in

the 3` untranslated region of multiple transcripts of mRNA encoded by LOC286404, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286404 BINDING SITE, designated SEQ ID:16900, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39356] Another function of GAM1338 is therefore inhibition of LOC286404 (Accession XP_210036.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286404.

[39357] LOC286441 (Accession XP_212319.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286441 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286441, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286441 BINDING SITE, designated SEQ ID:643, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39358] Another function of GAM1338 is therefore inhibition of LOC286441 (Accession XP_212319.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286441.

[39359] LOC286467 (Accession XP_210063.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286467 BINDING SITE, designated SEQ ID:12807, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39360] Another function of GAM1338 is therefore inhibition of LOC286467 (Accession XP_210063.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286467.

[39361] LOC286553 (Accession XP_212340.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC286553 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286553, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286553 BINDING SITE, designated SEQ ID:17107, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39362] Another function of GAM1338 is therefore inhibition of LOC286553 (Accession XP_212340.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286553.

[39363] LOC286558 (Accession XP_210106.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286558 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286558, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286558 BINDING SITE, desig-

nated SEQ ID:14505, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39364] Another function of GAM1338 is therefore inhibition of LOC286558 (Accession XP_210106.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286558.

[39365] LOC286564 (Accession XP_210108.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC286564 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286564, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286564 BINDING SITE, designated SEQ ID:14505, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39366] Another function of GAM1338 is therefore inhibition of LOC286564 (Accession XP_210108.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC286564.

[39367] LOC338562 (Accession XP_294654.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC338562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338562 BINDING SITE, designated SEQ ID:17586, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39368] Another function of GAM1338 is therefore inhibition of LOC338562 (Accession XP_294654.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338562.

[39369] LOC338565 (Accession XP_294653.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC338565 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338565, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338565 BINDING SITE, designated SEQ ID:12519, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39370] Another function of GAM1338 is therefore inhibition of LOC338565 (Accession XP_294653.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338565.

[39371] LOC338645 (Accession XP_290494.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC338645 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338645, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338645 BINDING SITE, designated SEQ ID:6141, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39372] Another function of GAM1338 is therefore inhibition of LOC338645 (Accession XP_290494.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338645.

[39373] LOC338709 (Accession XP_211595.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC338709 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338709, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338709 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39374] Another function of GAM1338 is therefore inhibition of LOC338709 (Accession XP_211595.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338709.

[39375] LOC338739 (Accession XP_294690.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC338739 BINDING SITE1 and LOC338739 BINDING SITE2 are target binding sites found in untranslated re-

gions of mRNA encoded by LOC338739, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338739 BINDING SITE1 and LOC338739 BINDING SITE2, designated SEQ ID:17520 and SEQ ID:11661 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39376] Another function of GAM1338 is therefore inhibition of LOC338739 (Accession XP_294690.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338739.

[39377] LOC338773 (Accession XP_290570.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC338773 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338773, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338773 BINDING SITE, designated SEQ ID:17388, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39378] Another function of GAM1338 is therefore inhibition of LOC338773 (Accession XP_290570.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338773.

[39379] LOC338817 (Accession XP_290588.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC338817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338817 BINDING SITE, designated SEQ ID:11448, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39380] Another function of GAM1338 is therefore inhibition of LOC338817 (Accession XP_290588.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338817.

[39381] LOC338923 (Accession XP_294742.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC338923 BINDING SITE1 and LOC338923 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC338923, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338923 BINDING SITE1 and LOC338923 BINDING SITE2, designated SEQ ID:14847 and SEQ ID:3243 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39382] Another function of GAM1338 is therefore inhibition of LOC338923 (Accession XP_294742.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338923.

[39383] LOC338991 (Accession XP_290663.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC338991 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338991, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC338991 BINDING SITE, designated SEQ ID:3888, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39384] Another function of GAM1338 is therefore inhibition of LOC338991 (Accession XP_290663.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338991.

[39385] LOC338999 (Accession XP_290659.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC338999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338999 BINDING SITE, designated SEQ ID:3888, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39386] Another function of GAM1338 is therefore inhibition of LOC338999 (Accession XP_290659.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC338999.

[39387] LOC339044 (Accession XP_294781.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339044 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339044, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339044 BINDING SITE, designated SEQ ID:11283, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39388] Another function of GAM1338 is therefore inhibition of LOC339044 (Accession XP_294781.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339044.

[39389] LOC339078 (Accession XP_290692.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339078 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339078, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339078 BINDING SITE, designated SEQ ID:19426, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39390] Another function of GAM1338 is therefore inhibition of LOC339078 (Accession XP_290692.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339078.

[39391] LOC339146 (Accession XP_294825.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339146 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339146 BINDING SITE, designated SEQ ID:822, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39392] Another function of GAM1338 is therefore inhibition of

LOC339146 (Accession XP_294825.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339146.

[39393] LOC339192 (Accession XP_294848.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339192 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339192, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339192 BINDING SITE, designated SEQ ID:4453, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39394] Another function of GAM1338 is therefore inhibition of LOC339192 (Accession XP_294848.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339192.

[39395] LOC339201 (Accession XP_290756.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339201 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC339201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339201 BINDING SITE, designated SEQ ID:11830, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39396] Another function of GAM1338 is therefore inhibition of LOC339201 (Accession XP_290756.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339201.

[39397] LOC339216 (Accession XP_290762.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC339216 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339216, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339216 BINDING SITE, designated SEQ ID:4581, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39398] Another function of GAM1338 is therefore inhibition of LOC339216 (Accession XP_290762.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339216.

[39399] LOC339282 (Accession XP_294900.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC339282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339282 BINDING SITE, designated SEQ ID:4581, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39400] Another function of GAM1338 is therefore inhibition of LOC339282 (Accession XP_294900.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339282.

[39401] LOC339283 (Accession XP_294899.2) is another

GAM1338 target gene, herein designated TARGET GENE. LOC339283 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339283, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339283 BINDING SITE, designated SEQ ID:15442, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39402] Another function of GAM1338 is therefore inhibition of LOC339283 (Accession XP_294899.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339283.

[39403] LOC339324 (Accession XP_290838.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339324 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339324, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339324 BINDING SITE, desig-

nated SEQ ID:11623, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39404] Another function of GAM1338 is therefore inhibition of LOC339324 (Accession XP_290838.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339324.

[39405] LOC339325 (Accession XP_290830.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339325 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339325, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339325 BINDING SITE, designated SEQ ID:7946, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39406] Another function of GAM1338 is therefore inhibition of LOC339325 (Accession XP_290830.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC339325.

[39407] LOC339400 (Accession XP_294926.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339400 BINDING SITE1 and LOC339400 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339400, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339400 BINDING SITE1 and LOC339400 BINDING SITE2, designated SEQ ID:14822 and SEQ ID:17314 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39408] Another function of GAM1338 is therefore inhibition of LOC339400 (Accession XP_294926.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339400.

[39409] LOC339417 (Accession XP_294944.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339417 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339417, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339417 BINDING SITE, designated SEQ ID:4497, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39410] Another function of GAM1338 is therefore inhibition of LOC339417 (Accession XP_294944.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339417.

[39411] LOC339458 (Accession XP_290911.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339458 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339458, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339458 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39412] Another function of GAM1338 is therefore inhibition of

LOC339458 (Accession XP_290911.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339458.

[39413] LOC339459 (Accession XP_290907.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC339459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339459 BINDING SITE, designated SEQ ID:13345, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39414] Another function of GAM1338 is therefore inhibition of LOC339459 (Accession XP_290907.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339459.

[39415] LOC339492 (Accession XP_290919.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339492 BINDING SITE1 and LOC339492 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339492, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339492 BINDING SITE1 and LOC339492 BINDING SITE2, designated SEQ ID:13601 and SEQ ID:19744 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39416] Another function of GAM1338 is therefore inhibition of LOC339492 (Accession XP_290919.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339492.

[39417] LOC339577 (Accession XP_295005.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339577 BINDING SITE1 and LOC339577 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339577, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339577 BINDING SITE1 and LOC339577 BINDING SITE2, desig-

nated SEQ ID:18182 and SEQ ID:9239 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39418] Another function of GAM1338 is therefore inhibition of LOC339577 (Accession XP_295005.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339577.

[39419] LOC339600 (Accession XP_295014.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339600 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339600, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339600 BINDING SITE, designated SEQ ID:15466, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39420] Another function of GAM1338 is therefore inhibition of LOC339600 (Accession XP_295014.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC339600.

[39421] LOC339659 (Accession XP_290981.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339659 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339659, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339659 BINDING SITE, designated SEQ ID:18371, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39422] Another function of GAM1338 is therefore inhibition of LOC339659 (Accession XP_290981.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339659.

[39423] LOC339685 (Accession XP_295032.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339685 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339685, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339685 BINDING SITE, designated SEQ ID:7793, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39424] Another function of GAM1338 is therefore inhibition of LOC339685 (Accession XP_295032.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339685.

[39425] LOC339711 (Accession XP_295038.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339711 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339711, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339711 BINDING SITE, designated SEQ ID:3106, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39426] Another function of GAM1338 is therefore inhibition of LOC339711 (Accession XP_295038.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339711.

[39427] LOC339720 (Accession XP_295041.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339720 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339720, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339720 BINDING SITE, designated SEQ ID:7943, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39428] Another function of GAM1338 is therefore inhibition of LOC339720 (Accession XP_295041.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339720.

[39429] LOC339803 (Accession XP_295072.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC339803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339803 BINDING SITE, designated SEQ ID:2943, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39430] Another function of GAM1338 is therefore inhibition of LOC339803 (Accession XP_295072.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339803.

[39431] LOC339809 (Accession XP_291020.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339809 BINDING SITE1 and LOC339809 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339809, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339809 BINDING SITE1 and LOC339809 BINDING SITE2, designated SEQ ID:8744 and SEQ ID:9098 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[39432] Another function of GAM1338 is therefore inhibition of LOC339809 (Accession XP_291020.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339809.

[39433] LOC339833 (Accession XP_291031.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339833 BINDING SITE1 and LOC339833 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339833, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339833 BINDING SITE1 and LOC339833 BINDING SITE2, designated SEQ ID:8180 and SEQ ID:10061 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39434] Another function of GAM1338 is therefore inhibition of LOC339833 (Accession XP_291031.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339833.

[39435] LOC339834 (Accession XP_291033.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339834 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC339834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339834 BINDING SITE, designated SEQ ID:2474, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39436] Another function of GAM1338 is therefore inhibition of LOC339834 (Accession XP_291033.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339834.

[39437] LOC339834 (Accession NP_835467.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339834 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC339834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of LOC339834 BINDING SITE, designated SEQ ID:2474, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39438] Another function of GAM1338 is therefore inhibition of LOC339834 (Accession NP_835467.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339834.

[39439] LOC339872 (Accession XP_291050.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339872 BINDING SITE1 through LOC339872 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC339872, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339872 BINDING SITE1 through LOC339872 BINDING SITE3, designated SEQ ID:15990, SEQ ID:6179 and SEQ ID:10908 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39440] Another function of GAM1338 is therefore inhibition of LOC339872 (Accession XP_291050.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339872.

[39441] LOC339894 (Accession XP_295095.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339894 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339894 BINDING SITE, designated SEQ ID:11426, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39442] Another function of GAM1338 is therefore inhibition of LOC339894 (Accession XP_295095.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339894.

[39443] LOC339896 (Accession XP_291059.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339896 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC339896, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339896 BINDING SITE, designated SEQ ID:11602, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39444] Another function of GAM1338 is therefore inhibition of LOC339896 (Accession XP_291059.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339896.

[39445] LOC339907 (Accession XP_291065.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339907 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339907, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339907 BINDING SITE, designated SEQ ID:1531, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39446] Another function of GAM1338 is therefore inhibition of LOC339907 (Accession XP_291065.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339907.

[39447] LOC339909 (Accession XP_291069.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339909 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339909, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339909 BINDING SITE, designated SEQ ID:9102, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39448] Another function of GAM1338 is therefore inhibition of LOC339909 (Accession XP_291069.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339909.

[39449] LOC339942 (Accession XP_295107.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC339942 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339942, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339942 BINDING SITE, designated SEQ ID:11079, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39450] Another function of GAM1338 is therefore inhibition of LOC339942 (Accession XP_295107.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339942.

[39451] LOC339970 (Accession XP_291095.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC339970 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339970, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339970 BINDING SITE, designated SEQ ID:8858, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39452] Another function of GAM1338 is therefore inhibition of LOC339970 (Accession XP_291095.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339970.

[39453] LOC340037 (Accession XP_295137.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC340037 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340037, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340037 BINDING SITE, designated SEQ ID:664, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39454] Another function of GAM1338 is therefore inhibition of LOC340037 (Accession XP_295137.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340037.

[39455] LOC340125 (Accession XP_291150.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC340125 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340125, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340125 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39456] Another function of GAM1338 is therefore inhibition of LOC340125 (Accession XP_291150.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340125.

[39457] LOC340156 (Accession XP_291158.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC340156 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340156, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC340156 BINDING SITE, designated SEQ ID:8575, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39458] Another function of GAM1338 is therefore inhibition of LOC340156 (Accession XP_291158.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340156.

[39459] LOC340227 (Accession XP_291203.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC340227 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340227, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340227 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39460] Another function of GAM1338 is therefore inhibition of LOC340227 (Accession XP_291203.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC340227.

[39461] LOC340290 (Accession XP_291214.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC340290 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340290, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340290 BINDING SITE, designated SEQ ID:15164, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39462] Another function of GAM1338 is therefore inhibition of LOC340290 (Accession XP_291214.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340290.

[39463] LOC340390 (Accession XP_291269.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC340390 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340390, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340390 BINDING SITE, designated SEQ ID:3427, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39464] Another function of GAM1338 is therefore inhibition of LOC340390 (Accession XP_291269.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340390.

[39465] LOC340408 (Accession XP_291274.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC340408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340408 BINDING SITE, designated SEQ ID:564, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39466] Another function of GAM1338 is therefore inhibition of

LOC340408 (Accession XP_291274.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340408.

[39467] LOC340414 (Accession XP_295240.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC340414 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340414, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340414 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39468] Another function of GAM1338 is therefore inhibition of LOC340414 (Accession XP_295240.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340414.

[39469] LOC340450 (Accession XP_295252.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC340450 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC340450, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340450 BINDING SITE, designated SEQ ID:4971, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39470] Another function of GAM1338 is therefore inhibition of LOC340450 (Accession XP_295252.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340450.

[39471] LOC342926 (Accession XP_292790.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC342926 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC342926, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC342926 BINDING SITE, designated SEQ ID:1413, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39472] Another function of GAM1338 is therefore inhibition of LOC342926 (Accession XP_292790.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC342926.

[39473] LOC345275 (Accession NP_835236.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC345275 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC345275, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC345275 BINDING SITE, designated SEQ ID:14511, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39474] Another function of GAM1338 is therefore inhibition of LOC345275 (Accession NP_835236.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC345275.

[39475] LOC346653 (Accession XP_294357.2) is another

GAM1338 target gene, herein designated TARGET GENE. LOC346653 BINDING SITE1 and LOC346653 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC346653, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC346653 BINDING SITE1 and LOC346653 BINDING SITE2, designated SEQ ID:4277 and SEQ ID:14945 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39476] Another function of GAM1338 is therefore inhibition of LOC346653 (Accession XP_294357.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC346653.

[39477] LOC347918 (Accession XP_300565.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC347918 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347918, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC347918 BINDING SITE, designated SEQ ID:983, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39478] Another function of GAM1338 is therefore inhibition of LOC347918 (Accession XP_300565.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347918.

[39479] LOC348075 (Accession XP_302653.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348075 BINDING SITE1 and LOC348075 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348075, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348075 BINDING SITE1 and LOC348075 BINDING SITE2, designated SEQ ID:6491 and SEQ ID:777 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39480] Another function of GAM1338 is therefore inhibition of LOC348075 (Accession XP_302653.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348075.

[39481] LOC348113 (Accession XP_300623.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348113 BINDING SITE, designated SEQ ID:3888, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39482] Another function of GAM1338 is therefore inhibition of LOC348113 (Accession XP_300623.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348113.

[39483] LOC348115 (Accession XP_300626.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348115 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC348115, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348115 BINDING SITE, designated SEQ ID:12601, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39484] Another function of GAM1338 is therefore inhibition of LOC348115 (Accession XP_300626.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348115.

[39485] LOC348137 (Accession XP_300635.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348137 BINDING SITE, designated SEQ ID:3888, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39486] Another function of GAM1338 is therefore inhibition of LOC348137 (Accession XP_300635.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348137.

[39487] LOC348142 (Accession XP_300636.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348142 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348142 BINDING SITE, designated SEQ ID:3888, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39488] Another function of GAM1338 is therefore inhibition of LOC348142 (Accession XP_300636.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348142.

[39489] LOC348161 (Accession XP_208864.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC348161 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348161, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348161 BINDING SITE, designated SEQ ID:8803, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39490] Another function of GAM1338 is therefore inhibition of LOC348161 (Accession XP_208864.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348161.

[39491] LOC348235 (Accession XP_300670.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348235 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348235 BINDING SITE, designated SEQ ID:11248, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39492] Another function of GAM1338 is therefore inhibition of LOC348235 (Accession XP_300670.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348235.

[39493] LOC348262 (Accession XP_300683.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348262 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348262 BINDING SITE, designated SEQ ID:7914, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39494] Another function of GAM1338 is therefore inhibition of LOC348262 (Accession XP_300683.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348262.

[39495] LOC348314 (Accession XP_302716.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348314 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348314, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348314 BINDING SITE, designated SEQ ID:9161, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39496] Another function of GAM1338 is therefore inhibition of LOC348314 (Accession XP_302716.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348314.

[39497] LOC348326 (Accession XP_300696.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348326 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348326, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC348326 BINDING SITE, designated SEQ ID:1995, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39498] Another function of GAM1338 is therefore inhibition of LOC348326 (Accession XP_300696.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348326.

[39499] LOC348393 (Accession XP_302741.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348393 BINDING SITE1 and LOC348393 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348393, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348393 BINDING SITE1 and LOC348393 BINDING SITE2, designated SEQ ID:16960 and SEQ ID:20185 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39500] Another function of GAM1338 is therefore inhibition of LOC348393 (Accession XP_302741.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348393.

[39501] LOC348396 (Accession XP_300729.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348396 BINDING SITE1 and LOC348396 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348396, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348396 BINDING SITE1 and LOC348396 BINDING SITE2, designated SEQ ID:1615 and SEQ ID:10631 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39502] Another function of GAM1338 is therefore inhibition of LOC348396 (Accession XP_300729.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348396.

[39503] LOC348402 (Accession XP_300730.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348402 BINDING SITE1 and LOC348402 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348402, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348402 BINDING SITE1 and LOC348402 BINDING SITE2, designated SEQ ID:13601 and SEQ ID:19744 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39504] Another function of GAM1338 is therefore inhibition of LOC348402 (Accession XP_300730.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348402.

[39505] LOC348445 (Accession XP_300738.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348445 BINDING SITE, designated SEQ ID:1995, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39506] Another function of GAM1338 is therefore inhibition of LOC348445 (Accession XP_300738.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348445.

[39507] LOC348455 (Accession XP_302760.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348455 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348455, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348455 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39508] Another function of GAM1338 is therefore inhibition of LOC348455 (Accession XP_302760.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348455.

[39509] LOC348460 (Accession XP_300743.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348460 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348460, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348460 BINDING SITE, designated SEQ ID:8756, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39510] Another function of GAM1338 is therefore inhibition of LOC348460 (Accession XP_300743.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348460.

[39511] LOC348474 (Accession XP_209299.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC348474 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348474, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC348474 BINDING SITE, designated SEQ ID:6597, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39512] Another function of GAM1338 is therefore inhibition of LOC348474 (Accession XP_209299.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348474.

[39513] LOC348503 (Accession XP_300762.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348503 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348503, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348503 BINDING SITE, designated SEQ ID:12080, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39514] Another function of GAM1338 is therefore inhibition of LOC348503 (Accession XP_300762.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348503.

[39515] LOC348508 (Accession XP_302806.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348508 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348508, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348508 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39516] Another function of GAM1338 is therefore inhibition of LOC348508 (Accession XP_302806.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348508.

[39517] LOC348525 (Accession XP_300778.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348525 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348525, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348525 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39518] Another function of GAM1338 is therefore inhibition of LOC348525 (Accession XP_300778.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348525.

[39519] LOC348532 (Accession XP_302818.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348532 BINDING SITE1 and LOC348532 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348532, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348532 BINDING SITE1 and LOC348532 BINDING SITE2, designated SEQ ID:16960 and SEQ ID:20185 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39520] Another function of GAM1338 is therefore inhibition of LOC348532 (Accession XP_302818.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348532.

[39521] LOC348702 (Accession XP_300808.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348702 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348702, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348702 BINDING SITE, designated SEQ ID:3103, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39522] Another function of GAM1338 is therefore inhibition of LOC348702 (Accession XP_300808.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348702.

[39523] LOC348790 (Accession XP_300843.1) is another GAM1338 target gene, herein designated TARGET GENE.

LOC348790 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348790, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348790 BINDING SITE, designated SEQ ID:11124, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39524] Another function of GAM1338 is therefore inhibition of LOC348790 (Accession XP_300843.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348790.

[39525] LOC348797 (Accession XP_302888.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348797 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348797, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348797 BINDING SITE, designated SEQ ID:4796, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39526] Another function of GAM1338 is therefore inhibition of LOC348797 (Accession XP_302888.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348797.

[39527] LOC348798 (Accession XP_300845.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348798 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348798, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348798 BINDING SITE, designated SEQ ID:5915, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39528] Another function of GAM1338 is therefore inhibition of LOC348798 (Accession XP_300845.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348798.

[39529] LOC348825 (Accession XP_300853.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348825 BINDING SITE1 and LOC348825 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348825, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348825 BINDING SITE1 and LOC348825 BINDING SITE2, designated SEQ ID:2639 and SEQ ID:10307 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39530] Another function of GAM1338 is therefore inhibition of LOC348825 (Accession XP_300853.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348825.

[39531] LOC348842 (Accession XP_300861.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348842 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348842 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39532] Another function of GAM1338 is therefore inhibition of LOC348842 (Accession XP_300861.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348842.

[39533] LOC348995 (Accession XP_300434.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC348995 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348995, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348995 BINDING SITE, designated SEQ ID:9379, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39534] Another function of GAM1338 is therefore inhibition of LOC348995 (Accession XP_300434.1) . Accordingly, utili-

ties of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348995.

[39535] LOC349024 (Accession XP_300250.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC349024 BINDING SITE1 and LOC349024 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC349024, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349024 BINDING SITE1 and LOC349024 BINDING SITE2, designated SEQ ID:4753 and SEQ ID:11653 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39536] Another function of GAM1338 is therefore inhibition of LOC349024 (Accession XP_300250.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349024.

[39537] LOC349075 (Accession XP_300932.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC349075 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC349075, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349075 BINDING SITE, designated SEQ ID:9465, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39538] Another function of GAM1338 is therefore inhibition of LOC349075 (Accession XP_300932.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349075.

[39539] LOC349096 (Accession XP_300937.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC349096 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349096, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349096 BINDING SITE, designated SEQ ID:14560, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39540] Another function of GAM1338 is therefore inhibition of LOC349096 (Accession XP_300937.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349096.

[39541] LOC349114 (Accession XP_302960.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC349114 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349114 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39542] Another function of GAM1338 is therefore inhibition of LOC349114 (Accession XP_302960.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349114.

[39543] LOC349170 (Accession XP_300969.1) is another

GAM1338 target gene, herein designated TARGET GENE. LOC349170 BINDING SITE1 through LOC349170 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC349170, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349170 BINDING SITE1 through LOC349170 BINDING SITE3, designated SEQ ID:19429, SEQ ID:4197 and SEQ ID:13839 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39544] Another function of GAM1338 is therefore inhibition of LOC349170 (Accession XP_300969.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349170.

[39545] LOC349360 (Accession XP_088528.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC349360 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349360, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC349360 BINDING SITE, designated SEQ ID:13307, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39546] Another function of GAM1338 is therefore inhibition of LOC349360 (Accession XP_088528.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349360.

[39547] LOC349408 (Accession XP_303044.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC349408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349408 BINDING SITE, designated SEQ ID:12395, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39548] Another function of GAM1338 is therefore inhibition of LOC349408 (Accession XP_303044.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC349408.

[39549] LOC349440 (Accession XP_300513.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC349440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349440 BINDING SITE, designated SEQ ID:19505, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39550] Another function of GAM1338 is therefore inhibition of LOC349440 (Accession XP_300513.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349440.

[39551] LOC349613 (Accession XP_303409.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC349613 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349613, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349613 BINDING SITE, designated SEQ ID:17346, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39552] Another function of GAM1338 is therefore inhibition of LOC349613 (Accession XP_303409.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349613.

[39553] LOC350106 (Accession XP_303810.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC350106 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC350106, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC350106 BINDING SITE, designated SEQ ID:20158, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39554] Another function of GAM1338 is therefore inhibition of

LOC350106 (Accession XP_303810.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC350106.

[39555] LOC51193 (Accession NP_057415.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC51193 BINDING SITE1 and LOC51193 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC51193, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51193 BINDING SITE1 and LOC51193 BINDING SITE2, designated SEQ ID:6858 and SEQ ID:6812 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39556] Another function of GAM1338 is therefore inhibition of LOC51193 (Accession NP_057415.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51193.

[39557] LOC51257 (Accession NP_057580.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC51257

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC51257, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51257 BINDING SITE, designated SEQ ID:18183, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39558] Another function of GAM1338 is therefore inhibition of LOC51257 (Accession NP_057580.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51257.

[39559] LOC51334 (Accession NP_057728.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC51334 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC51334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51334 BINDING SITE, designated SEQ ID:7944, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39560] Another function of GAM1338 is therefore inhibition of LOC51334 (Accession NP_057728.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51334.

[39561] LOC51336 (Accession NP_057730.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC51336 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51336 BINDING SITE, designated SEQ ID:18609, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39562] Another function of GAM1338 is therefore inhibition of LOC51336 (Accession NP_057730.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51336.

[39563] LOC55954 (Accession NP_061976.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC55954 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by LOC55954, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC55954 BINDING SITE, designated SEQ ID:17853, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39564] Another function of GAM1338 is therefore inhibition of LOC55954 (Accession NP_061976.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC55954.

[39565] LOC56902 (Accession NP_064528.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC56902 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC56902, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC56902 BINDING SITE, designated SEQ ID:8077, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39566] Another function of GAM1338 is therefore inhibition of

LOC56902 (Accession NP_064528.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56902.

[39567] LOC57107 (Accession NP_065114.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC57107 BINDING SITE1 and LOC57107 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC57107, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC57107 BINDING SITE1 and LOC57107 BINDING SITE2, designated SEQ ID:19749 and SEQ ID:12670 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39568] Another function of GAM1338 is therefore inhibition of LOC57107 (Accession NP_065114.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57107.

[39569] LOC57146 (Accession NP_065155.2) is another GAM1338 target gene, herein designated TARGET GENE. LOC57146

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC57146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC57146 BINDING SITE, designated SEQ ID:17648, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39570] Another function of GAM1338 is therefore inhibition of LOC57146 (Accession NP_065155.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57146.

[39571] LOC90408 (Accession XP_031517.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC90408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC90408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90408 BINDING SITE, designated SEQ ID:2729, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39572] Another function of GAM1338 is therefore inhibition of LOC90408 (Accession XP_031517.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90408.

[39573] LOC90485 (Accession XP_032059.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC90485 BINDING SITE1 and LOC90485 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC90485, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90485 BINDING SITE1 and LOC90485 BINDING SITE2, designated SEQ ID:15525 and SEQ ID:10103 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39574] Another function of GAM1338 is therefore inhibition of LOC90485 (Accession XP_032059.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90485.

[39575] LOC90999 (Accession XP_035410.1) is another GAM1338

target gene, herein designated TARGET GENE. LOC90999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90999 BINDING SITE, designated SEQ ID:11655, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39576] Another function of GAM1338 is therefore inhibition of LOC90999 (Accession XP_035410.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90999.

[39577] LOC91115 (Accession XP_036218.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC91115 BINDING SITE1 and LOC91115 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC91115, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91115 BINDING SITE1 and LOC91115 BINDING SITE2, designated SEQ ID:17070

and SEQ ID:18042 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39578] Another function of GAM1338 is therefore inhibition of LOC91115 (Accession XP_036218.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91115.

[39579] LOC91170 (Accession XP_036612.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC91170 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91170 BINDING SITE, designated SEQ ID:3969, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39580] Another function of GAM1338 is therefore inhibition of LOC91170 (Accession XP_036612.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91170.

[39581] LOC91266 (Accession XP_037268.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC91266 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91266, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91266 BINDING SITE, designated SEQ ID:9160, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39582] Another function of GAM1338 is therefore inhibition of LOC91266 (Accession XP_037268.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91266.

[39583] LOC91373 (Accession XP_038063.5) is another GAM1338 target gene, herein designated TARGET GENE. LOC91373 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91373, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91373 BINDING SITE, designated SEQ ID:5516, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39584] Another function of GAM1338 is therefore inhibition of LOC91373 (Accession XP_038063.5) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91373.

[39585] LOC91663 (Accession NP_612382.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC91663 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91663 BINDING SITE, designated SEQ ID:13779, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39586] Another function of GAM1338 is therefore inhibition of LOC91663 (Accession NP_612382.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91663.

[39587] LOC91893 (Accession XP_041340.1) is another GAM1338

target gene, herein designated TARGET GENE. LOC91893 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91893, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91893 BINDING SITE, designated SEQ ID:9129, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39588] Another function of GAM1338 is therefore inhibition of LOC91893 (Accession XP_041340.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91893.

[39589] LOC92148 (Accession XP_043160.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC92148 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC92148, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92148 BINDING SITE, designated SEQ ID:16536, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[39590] Another function of GAM1338 is therefore inhibition of LOC92148 (Accession XP_043160.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92148.

[39591] LOC92597 (Accession NP_775739.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC92597 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92597, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92597 BINDING SITE, designated SEQ ID:19028, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39592] Another function of GAM1338 is therefore inhibition of LOC92597 (Accession NP_775739.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92597.

[39593] LOC93132 (Accession XP_049396.1) is another GAM1338 target gene, herein designated TARGET GENE. LOC93132

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC93132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC93132 BINDING SITE, designated SEQ ID:14290, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39594] Another function of GAM1338 is therefore inhibition of LOC93132 (Accession XP_049396.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93132.

[39595] Leukotriene b4 receptor (LTB4R, Accession NP_000743.1) is another GAM1338 target gene, herein designated TARGET GENE. LTB4R BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LTB4R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LTB4R BINDING SITE, designated SEQ ID:19595, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ

ID:360.

[39596] Another function of GAM1338 is therefore inhibition of Leukotriene b4 receptor (LTB4R, Accession NP_000743.1), a gene which may be the cardiac p2y receptor involved in the regulation of cardiac muscle contraction through modulation of l- type calcium currents. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LTB4R.

[39597] The function of LTB4R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Lymphocyte antigen 75 (LY75, Accession NP_002340.1) is another GAM1338 target gene, herein designated TARGET GENE. LY75 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LY75, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LY75 BINDING SITE, designated SEQ ID:4451, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39598] Another function of GAM1338 is therefore inhibition of Lymphocyte antigen 75 (LY75, Accession NP_002340.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LY75.

[39599] Lysozyme (renal amyloidosis) (LYZ, Accession NP_000230.1) is another GAM1338 target gene, herein designated TARGET GENE. LYZ BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LYZ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LYZ BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39600] Another function of GAM1338 is therefore inhibition of Lysozyme (renal amyloidosis) (LYZ, Accession NP_000230.1), a gene which a bacteriolytic enzyme. and therefore may be associated with Renal amyloidosis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Renal amyloidosis, and of other diseases and clinical conditions associated with LYZ.

[39601] The function of LYZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Leucine zipper, putative tumor suppressor 1 (LZTS1, Accession NP_066300.1) is another GAM1338 target gene, herein designated TARGET GENE. LZTS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LZTS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LZTS1 BINDING SITE, designated SEQ ID:13405, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39602] Another function of GAM1338 is therefore inhibition of Leucine zipper, putative tumor suppressor 1 (LZTS1, Accession NP_066300.1), a gene which is an essential component of the nucleoskeleton. potential role in crosslinking filaments or anchoring other molecules. it is essential for growth. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTS1.

[39603] The function of LZTS1 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.MAC30 (Accession XP_031536.2) is another GAM1338 target gene, herein designated TARGET GENE. MAC30 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAC30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAC30 BINDING SITE, designated SEQ ID:13959, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39604] Another function of GAM1338 is therefore inhibition of MAC30 (Accession XP_031536.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAC30.

[39605] Male germ cell-associated kinase (MAK, Accession NP_005897.1) is another GAM1338 target gene, herein designated TARGET GENE. MAK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of MAK BINDING SITE, designated SEQ ID:11208, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39606] Another function of GAM1338 is therefore inhibition of Male germ cell-associated kinase (MAK, Accession NP_005897.1), a gene which plays an important role in spermatogenesis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAK.

[39607] The function of MAK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Mastermind-like 1 (drosophila) (MAML1, Accession NP_055572.1) is another GAM1338 target gene, herein designated TARGET GENE. MAML1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAML1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAML1 BINDING SITE, designated SEQ ID:5648, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also des-

ignated SEQ ID:360.

[39608] Another function of GAM1338 is therefore inhibition of Mastermind-like 1 (drosophila) (MAML1, Accession NP_055572.1), a gene which MAML1 functions as a transcriptional coactivator for Notch signaling. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAML1.

[39609] The function of MAML1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.Microtubule-associated protein, rp/eb family, member 1 (MAPRE1, Accession NP_036457.1) is another GAM1338 target gene, herein designated TARGET GENE. MAPRE1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAPRE1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPRE1 BINDING SITE, designated SEQ ID:6409, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39610] Another function of GAM1338 is therefore inhibition of

Microtubule-associated protein, rp/eb family, member 1 (MAPRE1, Accession NP_036457.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPRE1.

[39611] MCLC (Accession NP_055942.1) is another GAM1338 target gene, herein designated TARGET GENE. MCLC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MCLC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCLC BINDING SITE, designated SEQ ID:4526, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39612] Another function of GAM1338 is therefore inhibition of MCLC (Accession NP_055942.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCLC.

[39613] Mcm10 minichromosome maintenance deficient 10 (s. cerevisiae) (MCM10, Accession NP_060988.2) is another GAM1338 target gene, herein designated TARGET GENE. MCM10 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by MCM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCM10 BINDING SITE, designated SEQ ID:4821, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39614] Another function of GAM1338 is therefore inhibition of Mcm10 minichromosome maintenance deficient 10 (s. cerevisiae) (MCM10, Accession NP_060988.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCM10.

[39615] Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_002383.1) is another GAM1338 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39616] Another function of GAM1338 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_002383.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[39617] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006872.1) is another GAM1338 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39618] Another function of GAM1338 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006872.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[39619] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006869.1) is another GAM1338 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39620] Another function of GAM1338 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006869.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[39621] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute

2, p53 binding protein (mouse) (MDM2, Accession NP_006871.1) is another GAM1338 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39622] Another function of GAM1338 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006871.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[39623] The function of MDM2 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006873.1) is another GAM1338 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39624] Another function of GAM1338 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006873.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas

and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[39625] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006870.1) is another GAM1338 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39626] Another function of GAM1338 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006870.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarco-

mas, osteosarcomas and gliomas). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[39627] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm4, transformed 3t3 cell double minute 4, p53 binding protein (mouse) (MDM4, Accession NP_002384.1) is another GAM1338 target gene, herein designated TARGET GENE. MDM4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MDM4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM4 BINDING SITE, designated SEQ ID:19527, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39628] Another function of GAM1338 is therefore inhibition of Mdm4, transformed 3t3 cell double minute 4, p53 binding protein (mouse) (MDM4, Accession NP_002384.1), a gene

which Strongly similar to murine Mdm4; may interact with p53. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDM4.

[39629] The function of MDM4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mediterranean fever (MEFV, Accession NP_000234.1) is another GAM1338 target gene, herein designated TARGET GENE. MEFV BINDING SITE1 and MEFV BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MEFV, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MEFV BINDING SITE1 and MEFV BINDING SITE2, designated SEQ ID:12284 and SEQ ID:17376 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39630] Another function of GAM1338 is therefore inhibition of Mediterranean fever (MEFV, Accession NP_000234.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with MEFV.

[39631] Mesoderm development candidate 2 (MESDC2, Accession XP_051854.1) is another GAM1338 target gene, herein designated TARGET GENE. MESDC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MESDC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MESDC2 BINDING SITE, designated SEQ ID:17209, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39632] Another function of GAM1338 is therefore inhibition of Mesoderm development candidate 2 (MESDC2, Accession XP_051854.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MESDC2.

[39633] MFTC (Accession NP_110407.2) is another GAM1338 target gene, herein designated TARGET GENE. MFTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MFTC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of MFTC BINDING SITE, designated SEQ ID:10459, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39634] Another function of GAM1338 is therefore inhibition of MFTC (Accession NP_110407.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MFTC.

[39635] Mannosyl (alpha-1,6-)-glycoprotein beta-1,2-n-acetylglucosaminyltransferase (MGAT2, Accession NP_079374.1) is another GAM1338 target gene, herein designated TARGET GENE. MGAT2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MGAT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGAT2 BINDING SITE, designated SEQ ID:18270, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39636] Another function of GAM1338 is therefore inhibition of Mannosyl (alpha-1,6-)-glycoprotein beta-1,2-n-acetylglucosaminyltransferase (MGAT2, Accession

NP_079374.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAT2.

[39637] MGC10200 (Accession NP_659497.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC10200 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10200, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10200 BINDING SITE, designated SEQ ID:13048, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39638] Another function of GAM1338 is therefore inhibition of MGC10200 (Accession NP_659497.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10200.

[39639] MGC11102 (Accession NP_115701.2) is another GAM1338 target gene, herein designated TARGET GENE. MGC11102 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC11102, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC11102 BINDING SITE, designated SEQ ID:14977, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39640] Another function of GAM1338 is therefore inhibition of MGC11102 (Accession NP_115701.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11102.

[39641] MGC11115 (Accession NP_115686.2) is another GAM1338 target gene, herein designated TARGET GENE. MGC11115 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC11115, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC11115 BINDING SITE, designated SEQ ID:5608, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39642] Another function of GAM1338 is therefore inhibition of MGC11115 (Accession NP_115686.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC11115.

[39643] MGC12262 (Accession NP_116085.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC12262 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC12262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC12262 BINDING SITE, designated SEQ ID:6361, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39644] Another function of GAM1338 is therefore inhibition of MGC12262 (Accession NP_116085.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12262.

[39645] MGC12518 (Accession NP_291026.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC12518 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC12518, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC12518 BINDING SITE, designated SEQ ID:18251, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39646] Another function of GAM1338 is therefore inhibition of MGC12518 (Accession NP_291026.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12518.

[39647] MGC12760 (Accession NP_116112.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC12760 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC12760, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC12760 BINDING SITE, designated SEQ ID:5586, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39648] Another function of GAM1338 is therefore inhibition of MGC12760 (Accession NP_116112.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC12760.

[39649] MGC13017 (Accession NP_542387.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC13017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13017 BINDING SITE, designated SEQ ID:18970, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39650] Another function of GAM1338 is therefore inhibition of MGC13017 (Accession NP_542387.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13017.

[39651] MGC13024 (Accession NP_689501.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC13024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC13024 BINDING SITE, designated SEQ ID:15630, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39652] Another function of GAM1338 is therefore inhibition of MGC13024 (Accession NP_689501.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13024.

[39653] MGC13138 (Accession NP_219363.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC13138 BINDING SITE1 and MGC13138 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC13138, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13138 BINDING SITE1 and MGC13138 BINDING SITE2, designated SEQ ID:19426 and SEQ ID:14027 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39654] Another function of GAM1338 is therefore inhibition of MGC13138 (Accession NP_219363.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC13138.

[39655] MGC13170 (Accession NP_116101.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC13170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13170 BINDING SITE, designated SEQ ID:12394, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39656] Another function of GAM1338 is therefore inhibition of MGC13170 (Accession NP_116101.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13170.

[39657] MGC13204 (Accession NP_113653.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC13204 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13204, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC13204 BINDING SITE, designated SEQ ID:17963, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39658] Another function of GAM1338 is therefore inhibition of MGC13204 (Accession NP_113653.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13204.

[39659] MGC14289 (Accession NP_542391.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC14289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14289 BINDING SITE, designated SEQ ID:1959, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39660] Another function of GAM1338 is therefore inhibition of MGC14289 (Accession NP_542391.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC14289.

[39661] MGC14836 (Accession NP_219480.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC14836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14836 BINDING SITE, designated SEQ ID:9102, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39662] Another function of GAM1338 is therefore inhibition of MGC14836 (Accession NP_219480.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14836.

[39663] MGC15606 (Accession NP_659474.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC15606 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC15606, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC15606 BINDING SITE, designated SEQ ID:6622, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39664] Another function of GAM1338 is therefore inhibition of MGC15606 (Accession NP_659474.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15606.

[39665] MGC15668 (Accession NP_116145.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC15668 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC15668, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15668 BINDING SITE, designated SEQ ID:15177, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39666] Another function of GAM1338 is therefore inhibition of MGC15668 (Accession NP_116145.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15668.

[39667] MGC15705 (Accession NP_116146.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC15705 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC15705, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15705 BINDING SITE, designated SEQ ID:6734, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39668] Another function of GAM1338 is therefore inhibition of MGC15705 (Accession NP_116146.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15705.

[39669] MGC15873 (Accession NP_116309.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC15873 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC15873, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15873 BINDING SITE, designated SEQ ID:9079, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39670] Another function of GAM1338 is therefore inhibition of MGC15873 (Accession NP_116309.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15873.

[39671] MGC17839 (Accession NP_777586.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC17839 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC17839, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC17839 BINDING SITE, designated SEQ ID:18441, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39672] Another function of GAM1338 is therefore inhibition of MGC17839 (Accession NP_777586.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC17839.

[39673] MGC17919 (Accession NP_653222.2) is another GAM1338

target gene, herein designated TARGET GENE. MGC17919 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC17919, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC17919 BINDING SITE, designated SEQ ID:1588, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39674] Another function of GAM1338 is therefore inhibition of MGC17919 (Accession NP_653222.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC17919.

[39675] MGC1842 (Accession XP_037797.2) is another GAM1338 target gene, herein designated TARGET GENE. MGC1842 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC1842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC1842 BINDING SITE, designated SEQ ID:11658, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[39676] Another function of GAM1338 is therefore inhibition of MGC1842 (Accession XP_037797.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC1842.

[39677] MGC21675 (Accession NP_443093.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC21675 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC21675, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC21675 BINDING SITE, designated SEQ ID:19749, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39678] Another function of GAM1338 is therefore inhibition of MGC21675 (Accession NP_443093.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21675.

[39679] MGC2474 (Accession NP_076420.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC2474

BINDING SITE1 and MGC2474 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC2474, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2474 BINDING SITE1 and MGC2474 BINDING SITE2, designated SEQ ID:18119 and SEQ ID:19749 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39680] Another function of GAM1338 is therefore inhibition of MGC2474 (Accession NP_076420.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2474.

[39681] MGC2477 (Accession NP_077004.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC2477 BINDING SITE1 through MGC2477 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by MGC2477, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2477 BINDING SITE1

through MGC2477 BINDING SITE3, designated SEQ ID:12048, SEQ ID:19729 and SEQ ID:3973 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39682] Another function of GAM1338 is therefore inhibition of MGC2477 (Accession NP_077004.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2477.

[39683] MGC2603 (Accession NP_076942.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC2603 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2603 BINDING SITE, designated SEQ ID:17763, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39684] Another function of GAM1338 is therefore inhibition of MGC2603 (Accession NP_076942.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC2603.

[39685] MGC26484 (Accession NP_689840.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC26484 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC26484, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC26484 BINDING SITE, designated SEQ ID:9741, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39686] Another function of GAM1338 is therefore inhibition of MGC26484 (Accession NP_689840.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC26484.

[39687] MGC26989 (Accession NP_689976.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC26989 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC26989, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC26989 BINDING SITE, designated SEQ ID:14418, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39688] Another function of GAM1338 is therefore inhibition of MGC26989 (Accession NP_689976.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC26989.

[39689] MGC27345 (Accession XP_300964.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC27345 BINDING SITE1 and MGC27345 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MGC27345, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC27345 BINDING SITE1 and MGC27345 BINDING SITE2, designated SEQ ID:7706 and SEQ ID:18352 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39690] Another function of GAM1338 is therefore inhibition of MGC27345 (Accession XP_300964.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC27345.

[39691] MGC29891 (Accession NP_653219.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC29891 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC29891, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC29891 BINDING SITE, designated SEQ ID:18179, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39692] Another function of GAM1338 is therefore inhibition of MGC29891 (Accession NP_653219.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29891.

[39693] MGC29898 (Accession NP_659485.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC29898 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC29898, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC29898 BINDING SITE, designated SEQ ID:9164, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39694] Another function of GAM1338 is therefore inhibition of MGC29898 (Accession NP_659485.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29898.

[39695] MGC3113 (Accession NP_076940.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC3113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3113 BINDING SITE, designated SEQ ID:15946, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39696] Another function of GAM1338 is therefore inhibition of MGC3113 (Accession NP_076940.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC3113.

[39697] MGC3195 (Accession NP_114111.2) is another GAM1338 target gene, herein designated TARGET GENE. MGC3195 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC3195, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3195 BINDING SITE, designated SEQ ID:15735, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39698] Another function of GAM1338 is therefore inhibition of MGC3195 (Accession NP_114111.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3195.

[39699] MGC3207 (Accession NP_115661.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC3207 BINDING SITE1 and MGC3207 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC3207, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of MGC3207 BINDING SITE1 and MGC3207 BINDING SITE2, designated SEQ ID:12382 and SEQ ID:14723 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39700] Another function of GAM1338 is therefore inhibition of MGC3207 (Accession NP_115661.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3207.

[39701] MGC3329 (Accession NP_076991.2) is another GAM1338 target gene, herein designated TARGET GENE. MGC3329 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3329 BINDING SITE, designated SEQ ID:4873, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39702] Another function of GAM1338 is therefore inhibition of MGC3329 (Accession NP_076991.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MGC3329.

[39703] MGC33637 (Accession NP_689809.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC33637 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC33637, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC33637 BINDING SITE, designated SEQ ID:12383, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39704] Another function of GAM1338 is therefore inhibition of MGC33637 (Accession NP_689809.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33637.

[39705] MGC34034 (Accession NP_694956.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC34034 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC34034, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC34034 BINDING SITE, designated SEQ ID:9789, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39706] Another function of GAM1338 is therefore inhibition of MGC34034 (Accession NP_694956.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34034.

[39707] MGC34079 (Accession NP_689688.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC34079 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC34079, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34079 BINDING SITE, designated SEQ ID:19879, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39708] Another function of GAM1338 is therefore inhibition of MGC34079 (Accession NP_689688.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC34079.

[39709] MGC34132 (Accession XP_291029.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC34132 BINDING SITE1 and MGC34132 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC34132, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34132 BINDING SITE1 and MGC34132 BINDING SITE2, designated SEQ ID:9188 and SEQ ID:8862 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39710] Another function of GAM1338 is therefore inhibition of MGC34132 (Accession XP_291029.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34132.

[39711] MGC35440 (Accession NP_694952.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC35440 BINDING SITE1 and MGC35440 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC35440, corresponding to target binding

sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35440 BINDING SITE1 and MGC35440 BINDING SITE2, designated SEQ ID:15523 and SEQ ID:13796 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39712] Another function of GAM1338 is therefore inhibition of MGC35440 (Accession NP_694952.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35440.

[39713] MGC35468 (Accession NP_694976.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC35468 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35468, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35468 BINDING SITE, designated SEQ ID:15490, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39714] Another function of GAM1338 is therefore inhibition of

MGC35468 (Accession NP_694976.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35468.

[39715] MGC39320 (Accession NP_689642.2) is another GAM1338 target gene, herein designated TARGET GENE. MGC39320 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC39320, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC39320 BINDING SITE, designated SEQ ID:2691, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39716] Another function of GAM1338 is therefore inhibition of MGC39320 (Accession NP_689642.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC39320.

[39717] MGC40157 (Accession NP_689563.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC40157 BINDING SITE1 and MGC40157 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by MGC40157, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40157 BINDING SITE1 and MGC40157 BINDING SITE2, designated SEQ ID:865 and SEQ ID:13547 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39718] Another function of GAM1338 is therefore inhibition of MGC40157 (Accession NP_689563.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40157.

[39719] MGC40168 (Accession NP_714920.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC40168 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC40168, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40168 BINDING SITE, designated SEQ ID:3717, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39720] Another function of GAM1338 is therefore inhibition of MGC40168 (Accession NP_714920.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40168.

[39721] MGC40579 (Accession NP_689989.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC40579 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC40579, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40579 BINDING SITE, designated SEQ ID:516, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39722] Another function of GAM1338 is therefore inhibition of MGC40579 (Accession NP_689989.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40579.

[39723] MGC4248 (Accession NP_115709.2) is another GAM1338 target gene, herein designated TARGET GENE. MGC4248 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC4248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4248 BINDING SITE, designated SEQ ID:8539, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39724] Another function of GAM1338 is therefore inhibition of MGC4248 (Accession NP_115709.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4248.

[39725] MGC50452 (Accession NP_775733.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC50452 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC50452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC50452 BINDING SITE, designated SEQ ID:8458, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39726] Another function of GAM1338 is therefore inhibition of

MGC50452 (Accession NP_775733.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC50452.

[39727] MGC50559 (Accession NP_776163.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC50559 BINDING SITE1 and MGC50559 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC50559, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC50559 BINDING SITE1 and MGC50559 BINDING SITE2, designated SEQ ID:7831 and SEQ ID:5794 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39728] Another function of GAM1338 is therefore inhibition of MGC50559 (Accession NP_776163.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC50559.

[39729] MGC5149 (Accession XP_051200.2) is another GAM1338 target gene, herein designated TARGET GENE. MGC5149

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC5149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC5149 BINDING SITE, designated SEQ ID:17590, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39730] Another function of GAM1338 is therefore inhibition of MGC5149 (Accession XP_051200.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5149.

[39731] MGC9912 (Accession NP_542395.1) is another GAM1338 target gene, herein designated TARGET GENE. MGC9912 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC9912, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC9912 BINDING SITE, designated SEQ ID:11391, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39732] Another function of GAM1338 is therefore inhibition of MGC9912 (Accession NP_542395.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC9912.

[39733] MGRN1 (Accession XP_048119.4) is another GAM1338 target gene, herein designated TARGET GENE. MGRN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGRN1 BINDING SITE, designated SEQ ID:13807, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39734] Another function of GAM1338 is therefore inhibition of MGRN1 (Accession XP_048119.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGRN1.

[39735] Mhc class ii transactivator (MHC2TA, Accession NP_000237.1) is another GAM1338 target gene, herein designated TARGET GENE. MHC2TA BINDING SITE1 through MHC2TA BINDING SITE3 are target binding sites

found in untranslated regions of mRNA encoded by MHC2TA, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MHC2TA BINDING SITE1 through MHC2TA BINDING SITE3, designated SEQ ID:4816, SEQ ID:6437 and SEQ ID:9987 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39736] Another function of GAM1338 is therefore inhibition of Mhc class ii transactivator (MHC2TA, Accession NP_000237.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MHC2TA.

[39737] MIRAB13 (Accession XP_039236.6) is another GAM1338 target gene, herein designated TARGET GENE. MIRAB13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MIRAB13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIRAB13 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM1338

RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39738] Another function of GAM1338 is therefore inhibition of MIRAB13 (Accession XP_039236.6) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIRAB13.

[39739] MIRAB13 (Accession NP_203744.1) is another GAM1338 target gene, herein designated TARGET GENE. MIRAB13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MIRAB13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIRAB13 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39740] Another function of GAM1338 is therefore inhibition of MIRAB13 (Accession NP_203744.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIRAB13.

[39741] Makorin, ring finger protein, 4 (MKRN4, Accession NP_110384.1) is another GAM1338 target gene, herein designated TARGET GENE. MKRN4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MKRN4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MKRN4 BINDING SITE, designated SEQ ID:12385, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39742] Another function of GAM1338 is therefore inhibition of Makorin, ring finger protein, 4 (MKRN4, Accession NP_110384.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKRN4.

[39743] Melan-a (MLANA, Accession NP_005502.1) is another GAM1338 target gene, herein designated TARGET GENE. MLANA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MLANA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of MLANA BINDING SITE, designated SEQ ID:17276, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39744] Another function of GAM1338 is therefore inhibition of Melan-a (MLANA, Accession NP_005502.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLANA.

[39745] Melanoma-derived leucine zipper, extra-nuclear factor (MLZE, Accession NP_113603.1) is another GAM1338 target gene, herein designated TARGET GENE. MLZE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MLZE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLZE BINDING SITE, designated SEQ ID:11404, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39746] Another function of GAM1338 is therefore inhibition of Melanoma-derived leucine zipper, extra-nuclear factor (MLZE, Accession NP_113603.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with MLZE.

[39747] MMAB (Accession NP_443077.1) is another GAM1338 target gene, herein designated TARGET GENE. MMAB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MMAB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MMAB BINDING SITE, designated SEQ ID:11037, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39748] Another function of GAM1338 is therefore inhibition of MMAB (Accession NP_443077.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMAB.

[39749] MO25 (Accession NP_057373.1) is another GAM1338 target gene, herein designated TARGET GENE. MO25 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MO25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MO25 BINDING SITE, designated SEQ ID:6709, to the nucleotide se-

quence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39750] Another function of GAM1338 is therefore inhibition of MO25 (Accession NP_057373.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MO25.

[39751] Modulator of apoptosis 1 (MOAP1, Accession NP_071434.2) is another GAM1338 target gene, herein designated TARGET GENE. MOAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MOAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MOAP1 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39752] Another function of GAM1338 is therefore inhibition of Modulator of apoptosis 1 (MOAP1, Accession NP_071434.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOAP1.

[39753] moblak (Accession NP_570719.1) is another GAM1338

target gene, herein designated TARGET GENE. moblak BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by moblak, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of moblak BINDING SITE, designated SEQ ID:2270, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39754] Another function of GAM1338 is therefore inhibition of moblak (Accession NP_570719.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with moblak.

[39755] Molybdenum cofactor synthesis 3 (MOCS3, Accession NP_055299.1) is another GAM1338 target gene, herein designated TARGET GENE. MOCS3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MOCS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MOCS3 BINDING SITE, designated SEQ ID:6108, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ

ID:360.

[39756] Another function of GAM1338 is therefore inhibition of Molybdenum cofactor synthesis 3 (MOCS3, Accession NP_055299.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOCS3.

[39757] Myeloproliferative leukemia virus oncogene (MPL, Accession NP_005364.1) is another GAM1338 target gene, herein designated TARGET GENE. MPL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPL BINDING SITE, designated SEQ ID:11909, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39758] Another function of GAM1338 is therefore inhibition of Myeloproliferative leukemia virus oncogene (MPL, Accession NP_005364.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPL.

[39759] Mitochondrial ribosomal protein l10 (MRPL10, Accession

NP_683685.1) is another GAM1338 target gene, herein designated TARGET GENE. MRPL10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MRPL10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL10 BINDING SITE, designated SEQ ID:3339, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39760] Another function of GAM1338 is therefore inhibition of Mitochondrial ribosomal protein l10 (MRPL10, Accession NP_683685.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL10.

[39761] Mitochondrial ribosomal protein l35 (MRPL35, Accession NP_057706.2) is another GAM1338 target gene, herein designated TARGET GENE. MRPL35 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL35, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MRPL35 BINDING SITE, designated SEQ ID:10631, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39762] Another function of GAM1338 is therefore inhibition of Mitochondrial ribosomal protein l35 (MRPL35, Accession NP_057706.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL35.

[39763] Mitochondrial ribosomal protein l44 (MRPL44, Accession NP_075066.1) is another GAM1338 target gene, herein designated TARGET GENE. MRPL44 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPL44, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL44 BINDING SITE, designated SEQ ID:6410, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39764] Another function of GAM1338 is therefore inhibition of Mitochondrial ribosomal protein l44 (MRPL44, Accession NP_075066.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL44.

[39765] Mitochondrial ribosomal protein l49 (MRPL49, Accession NP_004918.1) is another GAM1338 target gene, herein

designated TARGET GENE. MRPL49 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPL49, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL49 BINDING SITE, designated SEQ ID:13534, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39766] Another function of GAM1338 is therefore inhibition of Mitochondrial ribosomal protein l49 (MRPL49, Accession NP_004918.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL49.

[39767] Mitochondrial ribosomal protein s27 (MRPS27, Accession NP_055899.1) is another GAM1338 target gene, herein designated TARGET GENE. MRPS27 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPS27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPS27 BINDING SITE, designated SEQ ID:13372, to the nucleotide se-

quence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39768] Another function of GAM1338 is therefore inhibition of Mitochondrial ribosomal protein s27 (MRPS27, Accession NP_055899.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS27.

[39769] Male-specific lethal 3-like 1 (drosophila) (MSL3L1, Accession NP_523353.1) is another GAM1338 target gene, herein designated TARGET GENE. MSL3L1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MSL3L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MSL3L1 BINDING SITE, designated SEQ ID:1303, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39770] Another function of GAM1338 is therefore inhibition of Male-specific lethal 3-like 1 (drosophila) (MSL3L1, Accession NP_523353.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSL3L1.

[39771] Male-specific lethal 3-like 1 (drosophila) (MSL3L1, Accession NP_523354.1) is another GAM1338 target gene, herein designated TARGET GENE. MSL3L1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MSL3L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MSL3L1 BINDING SITE, designated SEQ ID:1303, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39772] Another function of GAM1338 is therefore inhibition of Male-specific lethal 3-like 1 (drosophila) (MSL3L1, Accession NP_523354.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSL3L1.

[39773] Male-specific lethal 3-like 1 (drosophila) (MSL3L1, Accession NP_006791.2) is another GAM1338 target gene, herein designated TARGET GENE. MSL3L1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MSL3L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of MSL3L1 BINDING SITE, designated SEQ ID:1303, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39774] Another function of GAM1338 is therefore inhibition of Male-specific lethal 3-like 1 (drosophila) (MSL3L1, Accession NP_006791.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSL3L1.

[39775] MSTP028 (Accession NP_114160.1) is another GAM1338 target gene, herein designated TARGET GENE. MSTP028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MSTP028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MSTP028 BINDING SITE, designated SEQ ID:11359, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39776] Another function of GAM1338 is therefore inhibition of MSTP028 (Accession NP_114160.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MSTP028.

[39777] MTH2 (Accession NP_060753.1) is another GAM1338 target gene, herein designated TARGET GENE. MTH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTH2 BINDING SITE, designated SEQ ID:12462, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39778] Another function of GAM1338 is therefore inhibition of MTH2 (Accession NP_060753.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTH2.

[39779] 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR, Accession NP_000245.1) is another GAM1338 target gene, herein designated TARGET GENE. MTR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MTR BINDING SITE, designated SEQ ID:13325, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39780] Another function of GAM1338 is therefore inhibition of 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR, Accession NP_000245.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTR.

[39781] Myosin id (MYO1D, Accession XP_050041.4) is another GAM1338 target gene, herein designated TARGET GENE. MYO1D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYO1D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYO1D BINDING SITE, designated SEQ ID:2339, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39782] Another function of GAM1338 is therefore inhibition of Myosin id (MYO1D, Accession XP_050041.4), a gene which is an unconventional myosin. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with MYO1D.

[39783] The function of MYO1D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM227.1.Myosin 5c (MYO5C, Accession NP_061198.1) is another GAM1338 target gene, herein designated TARGET GENE. MYO5C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYO5C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYO5C BINDING SITE, designated SEQ ID:14846, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39784] Another function of GAM1338 is therefore inhibition of Myosin 5c (MYO5C, Accession NP_061198.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYO5C.

[39785] Nanog (Accession NP_079141.1) is another GAM1338 target gene, herein designated TARGET GENE. Nanog BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by Nanog, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Nanog BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39786] Another function of GAM1338 is therefore inhibition of Nanog (Accession NP_079141.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Nanog.

[39787] NCAG1 (Accession NP_115536.1) is another GAM1338 target gene, herein designated TARGET GENE. NCAG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCAG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCAG1 BINDING SITE, designated SEQ ID:11436, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39788] Another function of GAM1338 is therefore inhibition of NCAG1 (Accession NP_115536.1) . Accordingly, utilities of

GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCAG1.

[39789] Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1) is another GAM1338 target gene, herein designated TARGET GENE. NCOA6 BINDING SITE1 and NCOA6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCOA6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE1 and NCOA6 BINDING SITE2, designated SEQ ID:6181 and SEQ ID:5484 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39790] Another function of GAM1338 is therefore inhibition of Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1), a gene which activates gene transcription through ligand- dependent association with coactivators. and therefore may be associated with Breast cancer. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Breast cancer., and of other diseases and clinical conditions associated with NCOA6.

[39791] The function of NCOA6 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NP_079107.5) is another GAM1338 target gene, herein designated TARGET GENE. NCOA6IP BINDING SITE1 and NCOA6IP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCOA6IP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6IP BINDING SITE1 and NCOA6IP BINDING SITE2, designated SEQ ID:13249 and SEQ ID:3026 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39792] Another function of GAM1338 is therefore inhibition of Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NP_079107.5) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6IP.

[39793] Ndrg family member 3 (NDRG3, Accession NP_114402.1) is another GAM1338 target gene, herein designated TAR-

GET GENE. NDRG3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NDRG3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDRG3 BINDING SITE, designated SEQ ID:20109, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39794] Another function of GAM1338 is therefore inhibition of Ndrg family member 3 (NDRG3, Accession NP_114402.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG3.

[39795] Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) is another GAM1338 target gene, herein designated TARGET GENE. NDUFC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDUFC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDUFC2 BINDING SITE, designated

SEQ ID:15362, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39796] Another function of GAM1338 is therefore inhibition of Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDUFC2.

[39797] Nadh dehydrogenase (ubiquinone) fe-s protein 1, 75kda (nadh-coenzyme q reductase) (NDUFS1, Accession NP_004997.3) is another GAM1338 target gene, herein designated TARGET GENE. NDUFS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDUFS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDUFS1 BINDING SITE, designated SEQ ID:6109, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39798] Another function of GAM1338 is therefore inhibition of Nadh dehydrogenase (ubiquinone) fe-s protein 1, 75kda

(nadh-coenzyme q reductase) (NDUFS1, Accession NP_004997.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDUFS1.

[39799] Sialidase 3 (membrane sialidase) (NEU3, Accession NP_006647.2) is another GAM1338 target gene, herein designated TARGET GENE. NEU3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NEU3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEU3 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39800] Another function of GAM1338 is therefore inhibition of Sialidase 3 (membrane sialidase) (NEU3, Accession NP_006647.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEU3.

[39801] Nucleolar protein 3 (apoptosis repressor with card domain) (NOL3, Accession NP_003937.1) is another GAM1338 target gene, herein designated TARGET GENE.

NOL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOL3 BINDING SITE, designated SEQ ID:18676, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39802] Another function of GAM1338 is therefore inhibition of Nucleolar protein 3 (apoptosis repressor with card domain) (NOL3, Accession NP_003937.1), a gene which inhibits CASP2 and CASP8 and interacts with splicing factors. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOL3.

[39803] The function of NOL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Non-pou domain containing, octamer-binding (NONO, Accession NP_031389.2) is another GAM1338 target gene, herein designated TARGET GENE. NONO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NONO, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NONO BINDING SITE, designated SEQ ID:1412, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39804] Another function of GAM1338 is therefore inhibition of Non-pou domain containing, octamer-binding (NONO, Accession NP_031389.2), a gene which is a nuclear protein which contains RNA recognition motifs. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NONO.

[39805] The function of NONO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.NOSIP (Accession NP_057037.1) is another GAM1338 target gene, herein designated TARGET GENE. NOSIP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NOSIP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

NOSIP BINDING SITE, designated SEQ ID:8269, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39806] Another function of GAM1338 is therefore inhibition of NOSIP (Accession NP_057037.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOSIP.

[39807] Nadph oxidase, ef hand calcium-binding domain 5 (NOX5, Accession NP_078781.2) is another GAM1338 target gene, herein designated TARGET GENE. NOX5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NOX5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOX5 BINDING SITE, designated SEQ ID:7634, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39808] Another function of GAM1338 is therefore inhibition of Nadph oxidase, ef hand calcium-binding domain 5 (NOX5, Accession NP_078781.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOX5.

[39809] Neuronal pentraxin receptor (NPTXR, Accession NP_478058.1) is another GAM1338 target gene, herein designated TARGET GENE. NPTXR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NPTXR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE, designated SEQ ID:17176, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39810] Another function of GAM1338 is therefore inhibition of Neuronal pentraxin receptor (NPTXR, Accession NP_478058.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR.

[39811] Neuronal pentraxin receptor (NPTXR, Accession NP_055108.2) is another GAM1338 target gene, herein designated TARGET GENE. NPTXR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NPTXR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates

the complementarity of the nucleotide sequences of NPTXR BINDING SITE, designated SEQ ID:17176, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39812] Another function of GAM1338 is therefore inhibition of Neuronal pentraxin receptor (NPTXR, Accession NP_055108.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR.

[39813] Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1) is another GAM1338 target gene, herein designated TARGET GENE. NQO1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NQO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NQO1 BINDING SITE, designated SEQ ID:18183, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39814] Another function of GAM1338 is therefore inhibition of Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1), a gene which is cytochrome b5 reductase

which reduces redox dyes and quinones. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NQO1.

[39815] The function of NQO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.NRLN1 (Accession NP_660277.1) is another GAM1338 target gene, herein designated TARGET GENE. NRLN1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NRLN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRLN1 BINDING SITE, designated SEQ ID:15192, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39816] Another function of GAM1338 is therefore inhibition of NRLN1 (Accession NP_660277.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRLN1.

[39817] 5'-nucleotidase, cytosolic ii (NT5C2, Accession NP_036361.1) is another GAM1338 target gene, herein

designated TARGET GENE. NT5C2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NT5C2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NT5C2 BINDING SITE, designated SEQ ID:15388, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39818] Another function of GAM1338 is therefore inhibition of 5'-nucleotidase, cytosolic ii (NT5C2, Accession NP_036361.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NT5C2.

[39819] NUP43 (Accession NP_078923.2) is another GAM1338 target gene, herein designated TARGET GENE. NUP43 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NUP43, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUP43 BINDING SITE, designated SEQ ID:9379, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA,

also designated SEQ ID:360.

[39820] Another function of GAM1338 is therefore inhibition of NUP43 (Accession NP_078923.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUP43.

[39821] Nucleoredoxin (NXN, Accession NP_071908.1) is another GAM1338 target gene, herein designated TARGET GENE. NXN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NXN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NXN BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39822] Another function of GAM1338 is therefore inhibition of Nucleoredoxin (NXN, Accession NP_071908.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXN.

[39823] OIP106 (Accession NP_055780.1) is another GAM1338 target gene, herein designated TARGET GENE. OIP106 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by OIP106, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OIP106 BINDING SITE, designated SEQ ID:10262, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39824] Another function of GAM1338 is therefore inhibition of OIP106 (Accession NP_055780.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OIP106.

[39825] Olfactory receptor, family 51, subfamily e, member 2 (OR51E2, Accession NP_110401.1) is another GAM1338 target gene, herein designated TARGET GENE. OR51E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OR51E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OR51E2 BINDING SITE, designated SEQ ID:8690, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39826] Another function of GAM1338 is therefore inhibition of

Olfactory receptor, family 51, subfamily e, member 2 (OR51E2, Accession NP_110401.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OR51E2.

[39827] Origin recognition complex, subunit 1-like (yeast) (ORC1L, Accession NP_004144.1) is another GAM1338 target gene, herein designated TARGET GENE. ORC1L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ORC1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ORC1L BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39828] Another function of GAM1338 is therefore inhibition of Origin recognition complex, subunit 1-like (yeast) (ORC1L, Accession NP_004144.1), a gene which may be required for initiation of DNA replication. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ORC1L.

[39829] The function of ORC1L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Oxysterol binding protein-like 2 (OSBPL2, Accession NP_055650.1) is another GAM1338 target gene, herein designated TARGET GENE. OSBPL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL2 BINDING SITE, designated SEQ ID:18258, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39830] Another function of GAM1338 is therefore inhibition of Oxysterol binding protein-like 2 (OSBPL2, Accession NP_055650.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL2.

[39831] Oxysterol binding protein-like 2 (OSBPL2, Accession NP_653081.1) is another GAM1338 target gene, herein designated TARGET GENE. OSBPL2 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by OSBPL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL2 BINDING SITE, designated SEQ ID:18258, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39832] Another function of GAM1338 is therefore inhibition of Oxysterol binding protein-like 2 (OSBPL2, Accession NP_653081.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL2.

[39833] Otoancorin (OTOA, Accession NP_733764.1) is another GAM1338 target gene, herein designated TARGET GENE. OTOA BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by OTOA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OTOA BINDING SITE, designated SEQ ID:9822, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39834] Another function of GAM1338 is therefore inhibition of Otoancorin (OTOA, Accession NP_733764.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OTOA.

[39835] Purinergic receptor p2y, g-protein coupled, 11 (P2RY11, Accession NP_002557.2) is another GAM1338 target gene, herein designated TARGET GENE. P2RY11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P2RY11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P2RY11 BINDING SITE, designated SEQ ID:6710, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39836] Another function of GAM1338 is therefore inhibition of Purinergic receptor p2y, g-protein coupled, 11 (P2RY11, Accession NP_002557.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RY11.

[39837] Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase

(PAICS, Accession NP_006443.1) is another GAM1338 target gene, herein designated TARGET GENE. PAICS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PAICS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PAICS BINDING SITE, designated SEQ ID:11127, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39838] Another function of GAM1338 is therefore inhibition of Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS, Accession NP_006443.1), a gene which is required for purine biosynthesis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAICS.

[39839] The function of PAICS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Pantothenate kinase 3 (PANK3, Accession NP_078870.1) is another GAM1338 target gene, herein designated TARGET GENE. PANK3 BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by PANK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PANK3 BINDING SITE, designated SEQ ID:18008, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39840] Another function of GAM1338 is therefore inhibition of Pantothenate kinase 3 (PANK3, Accession NP_078870.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PANK3.

[39841] Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) is another GAM1338 target gene, herein designated TARGET GENE. PASK BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PASK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PASK BINDING SITE, designated SEQ ID:3230, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:360.

[39842] Another function of GAM1338 is therefore inhibition of Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PASK.

[39843] Protocadherin alpha 9 (PCDHA9, Accession NP_054724.1) is another GAM1338 target gene, herein designated TARGET GENE. PCDHA9 BINDING SITE1 and PCDHA9 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PCDHA9, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA9 BINDING SITE1 and PCDHA9 BINDING SITE2, designated SEQ ID:10631 and SEQ ID:11879 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39844] Another function of GAM1338 is therefore inhibition of Protocadherin alpha 9 (PCDHA9, Accession NP_054724.1), a gene which is a calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM1338 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with PCDHA9.

[39845] The function of PCDHA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Protocadherin beta 16 (PCDHB16, Accession NP_066008.1) is another GAM1338 target gene, herein designated TARGET GENE. PCDHB16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB16 BINDING SITE, designated SEQ ID:4753, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39846] Another function of GAM1338 is therefore inhibition of Protocadherin beta 16 (PCDHB16, Accession NP_066008.1), a gene which is a potential calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB16.

[39847] The function of PCDHB16 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Protocadherin beta 9 (PCDHB9, Accession NP_061992.2) is another GAM1338 target gene, herein designated TARGET GENE. PCDHB9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB9 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39848] Another function of GAM1338 is therefore inhibition of Protocadherin beta 9 (PCDHB9, Accession NP_061992.2), a gene which is a potential calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB9.

[39849] The function of PCDHB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Phosphodiesterase 6b, cgmp-specific, rod,

beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NP_000274.1) is another GAM1338 target gene, herein designated TARGET GENE. PDE6B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDE6B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDE6B BINDING SITE, designated SEQ ID:18070, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39850] Another function of GAM1338 is therefore inhibition of Phosphodiesterase 6b, cgmp-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NP_000274.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE6B.

[39851] Platelet derived growth factor c (PDGFC, Accession NP_057289.1) is another GAM1338 target gene, herein designated TARGET GENE. PDGFC BINDING SITE1 and PDGFC BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PDGFC, corre-

sponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDGFC BINDING SITE1 and PDGFC BINDING SITE2, designated SEQ ID:19767 and SEQ ID:3930 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39852] Another function of GAM1338 is therefore inhibition of Platelet derived growth factor c (PDGFC, Accession NP_057289.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFC.

[39853] Pdz and lim domain 2 (mystique) (PDLIM2, Accession NP_789847.1) is another GAM1338 target gene, herein designated TARGET GENE. PDLIM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PDLIM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDLIM2 BINDING SITE, designated SEQ ID:4874, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39854] Another function of GAM1338 is therefore inhibition of Pdz and lim domain 2 (mystique) (PDLIM2, Accession NP_789847.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDLIM2.

[39855] Pdz domain containing 1 (PDZK1, Accession NP_002605.2) is another GAM1338 target gene, herein designated TARGET GENE. PDZK1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PDZK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDZK1 BINDING SITE, designated SEQ ID:11598, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39856] Another function of GAM1338 is therefore inhibition of Pdz domain containing 1 (PDZK1, Accession NP_002605.2), a gene which is a contains PDZ interaction domains, interacts with MAP17, a protein involved in control of cell proliferation. and therefore may be associated with Autosomal dominant hypophosphatemic rickets. Accordingly, utilities of GAM1338 include diagnosis, preven-

tion and treatment of Autosomal dominant hypophosphatemic rickets, and of other diseases and clinical conditions associated with PDZK1.

[39857] The function of PDZK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.PDZRN1 (Accession NP_699202.1) is another GAM1338 target gene, herein designated TARGET GENE. PDZRN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDZRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDZRN1 BINDING SITE, designated SEQ ID:17567, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39858] Another function of GAM1338 is therefore inhibition of PDZRN1 (Accession NP_699202.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDZRN1.

[39859] Pellino homolog 1 (drosophila) (PELI1, Accession NP_065702.2) is another GAM1338 target gene, herein

designated TARGET GENE. PELI1 BINDING SITE1 through PELI1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PELI1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PELI1 BINDING SITE1 through PELI1 BINDING SITE3, designated SEQ ID:18182, SEQ ID:430 and SEQ ID:13801 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39860] Another function of GAM1338 is therefore inhibition of Pellino homolog 1 (drosophila) (PELI1, Accession NP_065702.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PELI1.

[39861] Period homolog 2 (drosophila) (PER2, Accession NP_073728.1) is another GAM1338 target gene, herein designated TARGET GENE. PER2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PER2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PER2

BINDING SITE, designated SEQ ID:6602, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39862] Another function of GAM1338 is therefore inhibition of Period homolog 2 (drosophila) (PER2, Accession NP_073728.1), a gene which Period homolog 2; putative circadian clock protein; has a PAS dimerization domain and therefore may be associated with Familial advanced sleep- phase syndrome. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Familial advanced sleep- phase syndrome, and of other diseases and clinical conditions associated with PER2.

[39863] The function of PER2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Peroxisome biogenesis factor 10 (PEX10, Accession NP_722540.1) is another GAM1338 target gene, herein designated TARGET GENE. PEX10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PEX10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

PEX10 BINDING SITE, designated SEQ ID:7262, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39864] Another function of GAM1338 is therefore inhibition of Peroxisome biogenesis factor 10 (PEX10, Accession NP_722540.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEX10.

[39865] Peroxisome biogenesis factor 10 (PEX10, Accession NP_002608.1) is another GAM1338 target gene, herein designated TARGET GENE. PEX10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PEX10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PEX10 BINDING SITE, designated SEQ ID:7262, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39866] Another function of GAM1338 is therefore inhibition of Peroxisome biogenesis factor 10 (PEX10, Accession NP_002608.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PEX10.

[39867] PHAX (Accession NP_115553.1) is another GAM1338 target gene, herein designated TARGET GENE. PHAX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PHAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PHAX BINDING SITE, designated SEQ ID:12387, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39868] Another function of GAM1338 is therefore inhibition of PHAX (Accession NP_115553.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHAX.

[39869] Polymeric immunoglobulin receptor (PIGR, Accession NP_002635.2) is another GAM1338 target gene, herein designated TARGET GENE. PIGR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIGR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIGR BINDING SITE, designated

SEQ ID:8350, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39870] Another function of GAM1338 is therefore inhibition of Polymeric immunoglobulin receptor (PIGR, Accession NP_002635.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGR.

[39871] Phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B, Accession NP_002637.2) is another GAM1338 target gene, herein designated TARGET GENE. PIK3C2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3C2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3C2B BINDING SITE, designated SEQ ID:15277, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39872] Another function of GAM1338 is therefore inhibition of Phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B, Accession NP_002637.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PIK3C2B.

[39873] Phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD, Accession NP_005017.2) is another GAM1338 target gene, herein designated TARGET GENE. PIK3CD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3CD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3CD BINDING SITE, designated SEQ ID:4771, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39874] Another function of GAM1338 is therefore inhibition of Phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD, Accession NP_005017.2), a gene which regulating cell growth. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3CD.

[39875] The function of PIK3CD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Pbx/knotted 1 homeobox 1 (PKNOX1, Ac-

cession NP_004562.2) is another GAM1338 target gene, herein designated TARGET GENE. PKNOX1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PKNOX1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PKNOX1 BINDING SITE, designated SEQ ID:11464, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39876] Another function of GAM1338 is therefore inhibition of Pbx/knotted 1 homeobox 1 (PKNOX1, Accession NP_004562.2), a gene which may regulate gene expression and control cell differentiation. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKNOX1.

[39877] The function of PKNOX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Pro-melanin-concentrating hormone-like 1 (PMCHL1, Accession NP_114093.1) is another GAM1338 target gene, herein designated TARGET GENE. PMCHL1

BINDING SITE1 and PMCHL1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PMCHL1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMCHL1 BINDING SITE1 and PMCHL1 BINDING SITE2, designated SEQ ID:12367 and SEQ ID:982 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39878] Another function of GAM1338 is therefore inhibition of Pro-melanin-concentrating hormone-like 1 (PMCHL1, Accession NP_114093.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMCHL1.

[39879] Pro-melanin-concentrating hormone-like 2 (PMCHL2, Accession NP_114094.1) is another GAM1338 target gene, herein designated TARGET GENE. PMCHL2 BINDING SITE1 and PMCHL2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PMCHL2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of PMCHL2 BINDING SITE1 and PMCHL2 BINDING SITE2, designated SEQ ID:12367 and SEQ ID:982 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39880] Another function of GAM1338 is therefore inhibition of Pro-melanin-concentrating hormone-like 2 (PMCHL2, Accession NP_114094.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMCHL2.

[39881] PMPCA (Accession NP_055975.1) is another GAM1338 target gene, herein designated TARGET GENE. PMPCA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMPCA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMPCA BINDING SITE, designated SEQ ID:7152, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39882] Another function of GAM1338 is therefore inhibition of PMPCA (Accession NP_055975.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMPCA.

[39883] Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) is another GAM1338 target gene, herein designated TARGET GENE. PNMA2 BINDING SITE1 and PNMA2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PNMA2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PNMA2 BINDING SITE1 and PNMA2 BINDING SITE2, designated SEQ ID:11236 and SEQ ID:11189 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39884] Another function of GAM1338 is therefore inhibition of Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNMA2.

[39885] Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) is another GAM1338 target gene, herein designated TARGET GENE. POFUT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by POFUT1, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POFUT1 BINDING SITE, designated SEQ ID:1760, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39886] Another function of GAM1338 is therefore inhibition of Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POFUT1.

[39887] Polymerase (dna directed), epsilon 3 (p17 subunit) (POLE3, Accession NP_059139.2) is another GAM1338 target gene, herein designated TARGET GENE. POLE3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLE3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLE3 BINDING SITE, designated SEQ ID:5665, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39888] Another function of GAM1338 is therefore inhibition of Polymerase (dna directed), epsilon 3 (p17 subunit) (POLE3,

Accession NP_059139.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLE3.

[39889] Polymerase (rna) ii (dna directed) polypeptide d (POLR2D, Accession NP_004796.1) is another GAM1338 target gene, herein designated TARGET GENE. POLR2D BINDING SITE1 and POLR2D BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by POLR2D, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLR2D BINDING SITE1 and POLR2D BINDING SITE2, designated SEQ ID:850 and SEQ ID:11282 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39890] Another function of GAM1338 is therefore inhibition of Polymerase (rna) ii (dna directed) polypeptide d (POLR2D, Accession NP_004796.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLR2D.

[39891] Paraoxonase 1 (PON1, Accession NP_000437.3) is another GAM1338 target gene, herein designated TARGET GENE. PON1 BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by PON1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PON1 BINDING SITE, designated SEQ ID:19429, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39892] Another function of GAM1338 is therefore inhibition of Paraoxonase 1 (PON1, Accession NP_000437.3), a gene which hydrolyzes the toxic metabolites of a variety of organophosphorus insecticides. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PON1.

[39893] The function of PON1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Pou domain, class 2, associating factor 1 (POU2AF1, Accession NP_006226.1) is another GAM1338 target gene, herein designated TARGET GENE. POU2AF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POU2AF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of POU2AF1 BINDING SITE, designated SEQ ID:4674, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39894] Another function of GAM1338 is therefore inhibition of Pou domain, class 2, associating factor 1 (POU2AF1, Accession NP_006226.1), a gene which is a transcriptional coactivator that specifically associates with either oct1 or oct2 and therefore may be associated with A form of b-cell leukemia. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of A form of b- cell leukemia, and of other diseases and clinical conditions associated with POU2AF1.

[39895] The function of POU2AF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Pou domain, class 2, transcription factor 3 (POU2F3, Accession NP_055167.1) is another GAM1338 target gene, herein designated TARGET GENE. POU2F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POU2F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of POU2F3 BINDING SITE, designated SEQ ID:7036, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39896] Another function of GAM1338 is therefore inhibition of Pou domain, class 2, transcription factor 3 (POU2F3, Accession NP_055167.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU2F3.

[39897] Pou domain, class 3, transcription factor 1 (POU3F1, Accession NP_002690.2) is another GAM1338 target gene, herein designated TARGET GENE. POU3F1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POU3F1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POU3F1 BINDING SITE, designated SEQ ID:7918, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39898] Another function of GAM1338 is therefore inhibition of Pou domain, class 3, transcription factor 1 (POU3F1, Accession NP_002690.2), a gene which involves in early em-

bryogenesis and neurogenesis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU3F1.

[39899] The function of POU3F1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM281.1.PP3856 (Accession NP_660202.1) is another GAM1338 target gene, herein designated TARGET GENE. PP3856 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PP3856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP3856 BINDING SITE, designated SEQ ID:6293, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39900] Another function of GAM1338 is therefore inhibition of PP3856 (Accession NP_660202.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP3856.

[39901] Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690911.1) is another GAM1338 target gene, herein designated TARGET GENE. PPEF2 BINDING

SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPEF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPEF2 BINDING SITE, designated SEQ ID:568, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39902] Another function of GAM1338 is therefore inhibition of Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690911.1), a gene which is a homolog of Drosophila rdgC. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPEF2.

[39903] The function of PPEF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690910.1) is another GAM1338 target gene, herein designated TARGET GENE. PPEF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPEF2, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPEF2 BINDING SITE, designated SEQ ID:568, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39904] Another function of GAM1338 is therefore inhibition of Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_690910.1), a gene which is a homolog of Drosophila rdgC. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPEF2.

[39905] The function of PPEF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_006230.2) is another GAM1338 target gene, herein designated TARGET GENE. PPEF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPEF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPEF2 BINDING SITE, designated

SEQ ID:568, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39906] Another function of GAM1338 is therefore inhibition of Protein phosphatase, ef hand calcium-binding domain 2 (PPEF2, Accession NP_006230.2), a gene which is a homolog of Drosophila rdgC. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPEF2.

[39907] The function of PPEF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Protein tyrosine phosphatase, receptor type, f polypeptide (ptprf), interacting protein (liprin), alpha 4 (PPFIA4, Accession XP_046751.3) is another GAM1338 target gene, herein designated TARGET GENE. PPFIA4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPFIA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPFIA4 BINDING SITE, designated SEQ ID:10102, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39908] Another function of GAM1338 is therefore inhibition of Protein tyrosine phosphatase, receptor type, f polypeptide (ptprf), interacting protein (liprin), alpha 4 (PPFIA4, Accession XP_046751.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPFIA4.

[39909] Ptprf interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1, Accession NP_003613.2) is another GAM1338 target gene, herein designated TARGET GENE. PPFIBP1 BINDING SITE1 and PPFIBP1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PPFIBP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPFIBP1 BINDING SITE1 and PPFIBP1 BINDING SITE2, designated SEQ ID:8861 and SEQ ID:5523 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39910] Another function of GAM1338 is therefore inhibition of Ptprf interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1, Accession NP_003613.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PP-FIBP1.

[39911] Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession NP_005029.1) is another GAM1338 target gene, herein designated TARGET GENE. PPID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPID BINDING SITE, designated SEQ ID:3110, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39912] Another function of GAM1338 is therefore inhibition of Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession NP_005029.1), a gene which catalyzes the cis- trans isomerization of proline imidic peptide bonds in oligopeptides. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPID.

[39913] The function of PPID and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM136.1.Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) is another GAM1338 target gene, herein designated TARGET GENE. PPIL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPIL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPIL2 BINDING SITE, designated SEQ ID:18677, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39914] Another function of GAM1338 is therefore inhibition of Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPIL2.

[39915] Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_115288.1) is another GAM1338 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE1 and PPP1R12B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to target binding sites such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE1 and PPP1R12B BINDING SITE2, designated SEQ ID:17555 and SEQ ID:14820 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39916] Another function of GAM1338 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_115288.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[39917] Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) is another GAM1338 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE1 and PPP1R12B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE1 and PPP1R12B BINDING SITE2, designated SEQ ID:17555 and SEQ ID:14820 respectively, to the nu-

cleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39918] Another function of GAM1338 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[39919] Primase, polypeptide 2a, 58kda (PRIM2A, Accession NP_000938.1) is another GAM1338 target gene, herein designated TARGET GENE. PRIM2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRIM2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRIM2A BINDING SITE, designated SEQ ID:12707, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39920] Another function of GAM1338 is therefore inhibition of Primase, polypeptide 2a, 58kda (PRIM2A, Accession NP_000938.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PRIM2A.

[39921] Protein kinase, interferon-inducible double stranded rna dependent (PRKR, Accession NP_002750.1) is another GAM1338 target gene, herein designated TARGET GENE. PRKR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKR BINDING SITE, designated SEQ ID:17566, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39922] Another function of GAM1338 is therefore inhibition of Protein kinase, interferon-inducible double stranded rna dependent (PRKR, Accession NP_002750.1), a gene which catalyze the phosphorylation of the alpha subunit of eif2. and therefore may be associated with Huntington's disease. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Huntington's disease, and of other diseases and clinical conditions associated with PRKR.

[39923] The function of PRKR and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM136.1.Protein kinase, lysine deficient 3 (PRKWNK3, Accession NP_065973.1) is another GAM1338 target gene, herein designated TARGET GENE. PRKWNK3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKWNK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKWNK3 BINDING SITE, designated SEQ ID:5524, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39924] Another function of GAM1338 is therefore inhibition of Protein kinase, lysine deficient 3 (PRKWNK3, Accession NP_065973.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKWNK3.

[39925] Prion protein 2 (dublet) (PRND, Accession NP_036541.1) is another GAM1338 target gene, herein designated TARGET GENE. PRND BINDING SITE1 and PRND BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PRND, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRND BINDING SITE1 and PRND BINDING SITE2, designated SEQ ID:5776 and SEQ ID:7084 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39926] Another function of GAM1338 is therefore inhibition of Prion protein 2 (dublet) (PRND, Accession NP_036541.1), a gene which is similar to prion protein PRNP. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRND.

[39927] The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.PRO0297 (Accession NP_054800.1) is another GAM1338 target gene, herein designated TARGET GENE. PRO0297 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0297, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0297 BINDING SITE, designated

SEQ ID:1504, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39928] Another function of GAM1338 is therefore inhibition of PRO0297 (Accession NP_054800.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0297.

[39929] PRO0365 (Accession NP_054845.1) is another GAM1338 target gene, herein designated TARGET GENE. PRO0365 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0365, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0365 BINDING SITE, designated SEQ ID:7958, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39930] Another function of GAM1338 is therefore inhibition of PRO0365 (Accession NP_054845.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0365.

[39931] PRO1048 (Accession NP_060967.1) is another GAM1338 target gene, herein designated TARGET GENE. PRO1048 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO1048, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO1048 BINDING SITE, designated SEQ ID:2738, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39932] Another function of GAM1338 is therefore inhibition of PRO1048 (Accession NP_060967.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1048.

[39933] PROM2 (Accession NP_653308.1) is another GAM1338 target gene, herein designated TARGET GENE. PROM2 BINDING SITE1 and PROM2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PROM2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PROM2 BINDING SITE1 and PROM2

BINDING SITE2, designated SEQ ID:19427 and SEQ ID:6958 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39934] Another function of GAM1338 is therefore inhibition of PROM2 (Accession NP_653308.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROM2.

[39935] Proteasome (prosome, macropain) 26s subunit, non-atpase, 9 (PSMD9, Accession NP_002804.2) is another GAM1338 target gene, herein designated TARGET GENE. PSMD9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSMD9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSMD9 BINDING SITE, designated SEQ ID:11654, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39936] Another function of GAM1338 is therefore inhibition of Proteasome (prosome, macropain) 26s subunit, non-atpase, 9 (PSMD9, Accession NP_002804.2), a gene which acts as a regulatory subunit of the 26 proteasome. Ac-

cordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSMD9.

[39937] The function of PSMD9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Phosphoserine phosphatase (PSPH, Accession NP_004568.1) is another GAM1338 target gene, herein designated TARGET GENE. PSPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSPH BINDING SITE, designated SEQ ID:9102, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39938] Another function of GAM1338 is therefore inhibition of Phosphoserine phosphatase (PSPH, Accession NP_004568.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSPH.

[39939] Proline-serine-threonine phosphatase interacting protein

2 (PSTPIP2, Accession NP_077748.2) is another GAM1338 target gene, herein designated TARGET GENE. PSTPIP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSTPIP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSTPIP2 BINDING SITE, designated SEQ ID:14086, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39940] Another function of GAM1338 is therefore inhibition of Proline-serine-threonine phosphatase interacting protein 2 (PSTPIP2, Accession NP_077748.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSTPIP2.

[39941] Prostaglandin e synthase (PTGES, Accession NP_004869.1) is another GAM1338 target gene, herein designated TARGET GENE. PTGES BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of PTGES BINDING SITE, designated SEQ ID:11575, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39942] Another function of GAM1338 is therefore inhibition of Prostaglandin e synthase (PTGES, Accession NP_004869.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGES.

[39943] Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1) is another GAM1338 target gene, herein designated TARGET GENE. PTGIS BINDING SITE1 and PTGIS BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PTGIS, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGIS BINDING SITE1 and PTGIS BINDING SITE2, designated SEQ ID:11917 and SEQ ID:13582 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39944] Another function of GAM1338 is therefore inhibition of Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession

NP_000952.1), a gene which catalyzes the isomerization of prostaglandin h2 to prostacyclin (= prostaglandin i2). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGIS.

[39945] The function of PTGIS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Ptk2 protein tyrosine kinase 2 (PTK2, Accession NP_005598.3) is another GAM1338 target gene, herein designated TARGET GENE. PTK2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PTK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTK2 BINDING SITE, designated SEQ ID:17374, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39946] Another function of GAM1338 is therefore inhibition of Ptk2 protein tyrosine kinase 2 (PTK2, Accession NP_005598.3), a gene which involves in intracellular signal transduction pathway and is a putative homolog of

chicken focal adhesion associated kinase. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTK2.

[39947] The function of PTK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.2.Phosphorylase, glycogen; muscle (mcardle syndrome, glycogen storage disease type v) (PYGM, Accession NP_005600.1) is another GAM1338 target gene, herein designated TARGET GENE. PYGM BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PYGM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PYGM BINDING SITE, designated SEQ ID:4024, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39948] Another function of GAM1338 is therefore inhibition of Phosphorylase, glycogen; muscle (mcardle syndrome, glycogen storage disease type v) (PYGM, Accession NP_005600.1) . Accordingly, utilities of GAM1338 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with PYGM.

[39949] RAB11-FIP4 (Accession NP_116321.2) is another GAM1338 target gene, herein designated TARGET GENE. RAB11-FIP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB11-FIP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB11-FIP4 BINDING SITE, designated SEQ ID:5406, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39950] Another function of GAM1338 is therefore inhibition of RAB11-FIP4 (Accession NP_116321.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB11-FIP4.

[39951] Rab31, member ras oncogene family (RAB31, Accession NP_006859.1) is another GAM1338 target gene, herein designated TARGET GENE. RAB31 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB31, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB31 BINDING SITE, designated SEQ ID:536, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39952] Another function of GAM1338 is therefore inhibition of Rab31, member ras oncogene family (RAB31, Accession NP_006859.1), a gene which is an GTP- binding protein of the RAB family. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB31.

[39953] The function of RAB31 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM145.1.Rab33b, member ras oncogene family (RAB33B, Accession NP_112586.1) is another GAM1338 target gene, herein designated TARGET GENE. RAB33B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB33B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB33B BINDING SITE, designated SEQ ID:15333, to the

nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39954] Another function of GAM1338 is therefore inhibition of Rab33b, member ras oncogene family (RAB33B, Accession NP_112586.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB33B.

[39955] Rab36, member ras oncogene family (RAB36, Accession NP_004905.1) is another GAM1338 target gene, herein designated TARGET GENE. RAB36 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB36, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB36 BINDING SITE, designated SEQ ID:15649, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39956] Another function of GAM1338 is therefore inhibition of Rab36, member ras oncogene family (RAB36, Accession NP_004905.1), a gene which is involved in protein transport. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with RAB36.

[39957] The function of RAB36 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Rab39, member ras oncogene family (RAB39, Accession XP_084662.1) is another GAM1338 target gene, herein designated TARGET GENE. RAB39 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB39, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB39 BINDING SITE, designated SEQ ID:2158, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39958] Another function of GAM1338 is therefore inhibition of Rab39, member ras oncogene family (RAB39, Accession XP_084662.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB39.

[39959] Rab, member of ras oncogene family-like 2a (RABL2A, Accession NP_038198.1) is another GAM1338 target gene, herein designated TARGET GENE. RABL2A BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RABL2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RABL2A BINDING SITE, designated SEQ ID:14847, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39960] Another function of GAM1338 is therefore inhibition of Rab, member of ras oncogene family-like 2a (RABL2A, Accession NP_038198.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2A.

[39961] Rab, member of ras oncogene family-like 2b (RABL2B, Accession NP_009012.1) is another GAM1338 target gene, herein designated TARGET GENE. RABL2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RABL2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RABL2B BINDING SITE, designated SEQ ID:14847, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA,

also designated SEQ ID:360.

[39962] Another function of GAM1338 is therefore inhibition of Rab, member of ras oncogene family-like 2b (RABL2B, Accession NP_009012.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2B.

[39963] RAI (Accession NP_006654.1) is another GAM1338 target gene, herein designated TARGET GENE. RAI BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI BINDING SITE, designated SEQ ID:17223, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39964] Another function of GAM1338 is therefore inhibition of RAI (Accession NP_006654.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI.

[39965] Retinoic acid induced 3 (RAI3, Accession NP_003970.1) is another GAM1338 target gene, herein designated TARGET GENE. RAI3 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by RAI3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI3 BINDING SITE, designated SEQ ID:16116, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39966] Another function of GAM1338 is therefore inhibition of Retinoic acid induced 3 (RAI3, Accession NP_003970.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI3.

[39967] RAP140 (Accession NP_056039.1) is another GAM1338 target gene, herein designated TARGET GENE. RAP140 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAP140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAP140 BINDING SITE, designated SEQ ID:9663, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39968] Another function of GAM1338 is therefore inhibition of

RAP140 (Accession NP_056039.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP140.

[39969] Retinoic acid receptor, gamma (RARG, Accession NP_000957.1) is another GAM1338 target gene, herein designated TARGET GENE. RARG BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RARG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RARG BINDING SITE, designated SEQ ID:18678, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39970] Another function of GAM1338 is therefore inhibition of Retinoic acid receptor, gamma (RARG, Accession NP_000957.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RARG.

[39971] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739579.1) is another GAM1338 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:7664, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39972] Another function of GAM1338 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739579.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[39973] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739580.1) is another GAM1338 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:7664, to the nucleotide sequence of GAM1338 RNA, herein designated

GAM RNA, also designated SEQ ID:360.

[39974] Another function of GAM1338 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739580.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[39975] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_055552.1) is another GAM1338 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:7664, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39976] Another function of GAM1338 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_055552.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[39977] Retinoblastoma binding protein 9 (RBBP9, Accession

NP_006597.2) is another GAM1338 target gene, herein designated TARGET GENE. RBBP9 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RBBP9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RBBP9 BINDING SITE, designated SEQ ID:2397, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39978] Another function of GAM1338 is therefore inhibition of Retinoblastoma binding protein 9 (RBBP9, Accession NP_006597.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP9.

[39979] RCBTB1 (Accession NP_060661.2) is another GAM1338 target gene, herein designated TARGET GENE. RCBTB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RCBTB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RCBTB1 BINDING SITE, designated SEQ ID:3049, to the nu-

cleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39980] Another function of GAM1338 is therefore inhibition of RCBTB1 (Accession NP_060661.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RCBTB1.

[39981] RDH13 (Accession NP_612421.1) is another GAM1338 target gene, herein designated TARGET GENE. RDH13 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RDH13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RDH13 BINDING SITE, designated SEQ ID:11485, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39982] Another function of GAM1338 is therefore inhibition of RDH13 (Accession NP_612421.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RDH13.

[39983] Arginine-glutamic acid dipeptide (re) repeats (RERE, Accession NP_036234.2) is another GAM1338 target gene,

herein designated TARGET GENE. RERE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RERE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RERE BINDING SITE, designated SEQ ID:8833, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39984] Another function of GAM1338 is therefore inhibition of Arginine-glutamic acid dipeptide (re) repeats (RERE, Accession NP_036234.2), a gene which binds DRPLA and locates in the nucleus and therefore may be associated with Dentatorubral- pallidoluysian atrophy. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Dentatorubral- pallidoluysian atrophy, and of other diseases and clinical conditions associated with RERE.

[39985] The function of RERE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Regulator of g-protein signalling 3 (RGS3, Accession NP_570613.1) is another GAM1338 target gene,

herein designated TARGET GENE. RGS3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by RGS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RGS3 BINDING SITE, designated SEQ ID:3826, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39986] Another function of GAM1338 is therefore inhibition of Regulator of g-protein signalling 3 (RGS3, Accession NP_570613.1), a gene which negatively regulates G protein- coupled receptor signalling. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS3.

[39987] The function of RGS3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM146.1.Rhesus blood group, d antigen (RHD, Accession NP_057208.2) is another GAM1338 target gene, herein designated TARGET GENE. RHD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RHD, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE, designated SEQ ID:8756, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39988] Another function of GAM1338 is therefore inhibition of Rhesus blood group, d antigen (RHD, Accession NP_057208.2), a gene which Major antigen of the RH system. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[39989] The function of RHD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Rhesus blood group, d antigen (RHD, Accession NP_057309.2) is another GAM1338 target gene, herein designated TARGET GENE. RHD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RHD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

RHD BINDING SITE, designated SEQ ID:8756, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39990] Another function of GAM1338 is therefore inhibition of Rhesus blood group, d antigen (RHD, Accession NP_057309.2), a gene which Major antigen of the RH system. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[39991] The function of RHD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.RHPN2 (Accession NP_149094.2) is another GAM1338 target gene, herein designated TARGET GENE. RHPN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RHPN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHPN2 BINDING SITE, designated SEQ ID:5481, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39992] Another function of GAM1338 is therefore inhibition of

RHPN2 (Accession NP_149094.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHPN2.

[39993] RNAC (Accession NP_005763.2) is another GAM1338 target gene, herein designated TARGET GENE. RNAC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNAC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNAC BINDING SITE, designated SEQ ID:18459, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39994] Another function of GAM1338 is therefore inhibition of RNAC (Accession NP_005763.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNAC.

[39995] RNF137 (Accession NP_060543.4) is another GAM1338 target gene, herein designated TARGET GENE. RNF137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of RNF137 BINDING SITE, designated SEQ ID:8861, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39996] Another function of GAM1338 is therefore inhibition of RNF137 (Accession NP_060543.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF137.

[39997] Ring finger protein (c3hc4 type) 8 (RNF8, Accession NP_003949.1) is another GAM1338 target gene, herein designated TARGET GENE. RNF8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF8 BINDING SITE, designated SEQ ID:14570, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[39998] Another function of GAM1338 is therefore inhibition of Ring finger protein (c3hc4 type) 8 (RNF8, Accession NP_003949.1) . Accordingly, utilities of GAM1338 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF8.

[39999] Retinitis pigmentosa 2 (x-linked recessive) (RP2, Accession NP_008846.1) is another GAM1338 target gene, herein designated TARGET GENE. RP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RP2 BINDING SITE, designated SEQ ID:6575, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40000] Another function of GAM1338 is therefore inhibition of Retinitis pigmentosa 2 (x-linked recessive) (RP2, Accession NP_008846.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RP2.

[40001] Rabphilin 3a-like (without c2 domains) (RPH3AL, Accession NP_008918.1) is another GAM1338 target gene, herein designated TARGET GENE. RPH3AL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RPH3AL, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RPH3AL BINDING SITE, designated SEQ ID:467, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40002] Another function of GAM1338 is therefore inhibition of Rabphilin 3a-like (without c2 domains) (RPH3AL, Accession NP_008918.1), a gene which is a protein transporter. could play a role in neurotransmitter release by regulating membrane flow in the nerve terminal. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPH3AL.

[40003] The function of RPH3AL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.RPP30 (Accession NP_006404.1) is another GAM1338 target gene, herein designated TARGET GENE. RPP30 BINDING SITE1 and RPP30 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by RPP30, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RPP30 BINDING SITE1 and RPP30 BINDING SITE2, designated SEQ ID:3259 and SEQ ID:13376 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40004] Another function of GAM1338 is therefore inhibition of RPP30 (Accession NP_006404.1), a gene which is a component of ribonuclease p that processes 5' ends of precursor tRNAs. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPP30.

[40005] The function of RPP30 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.S100A15 (Accession NP_789793.1) is another GAM1338 target gene, herein designated TARGET GENE. S100A15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100A15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of S100A15 BINDING SITE, designated

SEQ ID:18561, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40006] Another function of GAM1338 is therefore inhibition of S100A15 (Accession NP_789793.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with S100A15.

[40007] SARM1 (Accession NP_055892.1) is another GAM1338 target gene, herein designated TARGET GENE. SARM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SARM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SARM1 BINDING SITE, designated SEQ ID:16324, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40008] Another function of GAM1338 is therefore inhibition of SARM1 (Accession NP_055892.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SARM1.

[40009] Sarcoma amplified sequence (SAS, Accession

NP_005972.1) is another GAM1338 target gene, herein designated TARGET GENE. SAS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SAS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SAS BINDING SITE, designated SEQ ID:1301, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40010] Another function of GAM1338 is therefore inhibition of Sarcoma amplified sequence (SAS, Accession NP_005972.1), a gene which is a member of the trans-membrane 4 superfamily (TM4SF) and may be involved in growth- related cellular processes T. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SAS.

[40011] The function of SAS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM88.1.SBLF (Accession NP_006864.2) is another GAM1338 target gene, herein designated TARGET GENE. SBLF BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by SBLF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SBLF BINDING SITE, designated SEQ ID:14250, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40012] Another function of GAM1338 is therefore inhibition of SBLF (Accession NP_006864.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SBLF.

[40013] SCAMP-4 (Accession NP_524558.1) is another GAM1338 target gene, herein designated TARGET GENE. SCAMP-4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCAMP-4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAMP-4 BINDING SITE, designated SEQ ID:19434, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40014] Another function of GAM1338 is therefore inhibition of SCAMP-4 (Accession NP_524558.1) . Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP-4.

[40015] Scan domain containing 2 (SCAND2, Accession NP_071333.2) is another GAM1338 target gene, herein designated TARGET GENE. SCAND2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SCAND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAND2 BINDING SITE, designated SEQ ID:16790, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40016] Another function of GAM1338 is therefore inhibition of Scan domain containing 2 (SCAND2, Accession NP_071333.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAND2.

[40017] Scavenger receptor class f, member 1 (SCARF1, Accession NP_003684.1) is another GAM1338 target gene, herein designated TARGET GENE. SCARF1 BINDING SITE1 and SCARF1 BINDING SITE2 are target binding sites found in

untranslated regions of mRNA encoded by SCARF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCARF1 BINDING SITE1 and SCARF1 BINDING SITE2, designated SEQ ID:9540 and SEQ ID:12384 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40018] Another function of GAM1338 is therefore inhibition of Scavenger receptor class f, member 1 (SCARF1, Accession NP_003684.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCARF1.

[40019] SCMH1 (Accession NP_036368.1) is another GAM1338 target gene, herein designated TARGET GENE. SCMH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCMH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCMH1 BINDING SITE, designated SEQ ID:9755, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40020] Another function of GAM1338 is therefore inhibition of SCMH1 (Accession NP_036368.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCMH1.

[40021] Sex comb on midleg-like 2 (drosophila) (SCML2, Accession NP_006080.1) is another GAM1338 target gene, herein designated TARGET GENE. SCML2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCML2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCML2 BINDING SITE, designated SEQ ID:9058, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40022] Another function of GAM1338 is therefore inhibition of Sex comb on midleg-like 2 (drosophila) (SCML2, Accession NP_006080.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCML2.

[40023] SCN3B (Accession NP_060870.1) is another GAM1338 target gene, herein designated TARGET GENE. SCN3B BINDING SITE1 and SCN3B BINDING SITE2 are target binding

sites found in untranslated regions of mRNA encoded by SCN3B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCN3B BINDING SITE1 and SCN3B BINDING SITE2, designated SEQ ID:9932 and SEQ ID:1471 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40024] Another function of GAM1338 is therefore inhibition of SCN3B (Accession NP_060870.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN3B.

[40025] SDS-RS1 (Accession NP_612441.1) is another GAM1338 target gene, herein designated TARGET GENE. SDS-RS1 BINDING SITE1 and SDS-RS1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SDS-RS1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SDS-RS1 BINDING SITE1 and SDS-RS1 BINDING SITE2, designated SEQ ID:2100 and SEQ ID:6910 respectively, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40026] Another function of GAM1338 is therefore inhibition of SDS-RS1 (Accession NP_612441.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDS-RS1.

[40027] SDS3 (Accession XP_045014.1) is another GAM1338 target gene, herein designated TARGET GENE. SDS3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SDS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SDS3 BINDING SITE, designated SEQ ID:8869, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40028] Another function of GAM1338 is therefore inhibition of SDS3 (Accession XP_045014.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDS3.

[40029] Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1) is another GAM1338 target gene, herein

designated TARGET GENE. SEDL BINDING SITE1 through SEDL BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by SEDL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEDL BINDING SITE1 through SEDL BINDING SITE4, designated SEQ ID:13872, SEQ ID:16842, SEQ ID:7261 and SEQ ID:13400 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40030] Another function of GAM1338 is therefore inhibition of Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1), a gene which may play role in vesicular transport from endoplasmic reticulum to golgi. and therefore may be associated with Spondyloepiphyseal dysplasia. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Spondyloepiphyseal dysplasia, and of other diseases and clinical conditions associated with SEDL.

[40031] The function of SEDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM30.1.Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) is another GAM1338 target gene, herein designated TARGET GENE. SERF1A BINDING SITE1 and SERF1A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERF1A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1A BINDING SITE1 and SERF1A BINDING SITE2, designated SEQ ID:14767 and SEQ ID:11123 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40032] Another function of GAM1338 is therefore inhibition of Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1A.

[40033] Small edrk-rich factor 1b (centromeric) (SERF1B, Accession NP_075267.1) is another GAM1338 target gene, herein designated TARGET GENE. SERF1B BINDING SITE1 and SERF1B BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERF1B, corresponding to target binding sites such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1B BINDING SITE1 and SERF1B BINDING SITE2, designated SEQ ID:11123 and SEQ ID:14767 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40034] Another function of GAM1338 is therefore inhibition of Small edrk-rich factor 1b (centromeric) (SERF1B, Accession NP_075267.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1B.

[40035] Small edrk-rich factor 2 (SERF2, Accession NP_005761.2) is another GAM1338 target gene, herein designated TARGET GENE. SERF2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SERF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF2 BINDING SITE, designated SEQ ID:13138, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40036] Another function of GAM1338 is therefore inhibition of

Small edrk-rich factor 2 (SERF2, Accession NP_005761.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF2.

[40037] Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 9 (SERPINB9, Accession NP_004146.1) is another GAM1338 target gene, herein designated TARGET GENE. SERPINB9 BINDING SITE1 and SERPINB9 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERPINB9, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERPINB9 BINDING SITE1 and SERPINB9 BINDING SITE2, designated SEQ ID:4057 and SEQ ID:437 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40038] Another function of GAM1338 is therefore inhibition of Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 9 (SERPINB9, Accession NP_004146.1), a gene which may be a serpin serine protease inhibitor that interacts with granzyme B (GZMB). Accordingly, utilities of GAM1338 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with SERPINB9.

[40039] The function of SERPINB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM88.2.Sideroflexin 2 (SFXN2, Accession XP_058359.2) is another GAM1338 target gene, herein designated TARGET GENE. SFXN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SFXN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SFXN2 BINDING SITE, designated SEQ ID:1960, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40040] Another function of GAM1338 is therefore inhibition of Sideroflexin 2 (SFXN2, Accession XP_058359.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN2.

[40041] Sideroflexin 2 (SFXN2, Accession NP_849189.1) is another GAM1338 target gene, herein designated TARGET GENE.

SFXN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SFXN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SFXN2 BINDING SITE, designated SEQ ID:1960, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40042] Another function of GAM1338 is therefore inhibition of Sideroflexin 2 (SFXN2, Accession NP_849189.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN2.

[40043] Sideroflexin 4 (SFXN4, Accession NP_849198.1) is another GAM1338 target gene, herein designated TARGET GENE. SFXN4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SFXN4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SFXN4 BINDING SITE, designated SEQ ID:6466, to the nucleotide sequence of GAM1338

RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40044] Another function of GAM1338 is therefore inhibition of Sideroflexin 4 (SFXN4, Accession NP_849198.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN4.

[40045] Sideroflexin 4 (SFXN4, Accession XP_058406.1) is another GAM1338 target gene, herein designated TARGET GENE. SFXN4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SFXN4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SFXN4 BINDING SITE, designated SEQ ID:6466, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40046] Another function of GAM1338 is therefore inhibition of Sideroflexin 4 (SFXN4, Accession XP_058406.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN4.

[40047] Sh3-domain binding protein 2 (SH3BP2, Accession NP_003014.2) is another GAM1338 target gene, herein designated TARGET GENE. SH3BP2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SH3BP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SH3BP2 BINDING SITE, designated SEQ ID:18716, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40048] Another function of GAM1338 is therefore inhibition of Sh3-domain binding protein 2 (SH3BP2, Accession NP_003014.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BP2.

[40049] Short stature homeobox (SHOX, Accession NP_000442.1) is another GAM1338 target gene, herein designated TARGET GENE. SHOX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SHOX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of SHOX BINDING SITE, designated SEQ ID:3808, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40050] Another function of GAM1338 is therefore inhibition of Short stature homeobox (SHOX, Accession NP_000442.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHOX.

[40051] Sialic acid binding ig-like lectin 8 (SIGLEC8, Accession NP_055257.1) is another GAM1338 target gene, herein designated TARGET GENE. SIGLEC8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIGLEC8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIGLEC8 BINDING SITE, designated SEQ ID:3441, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40052] Another function of GAM1338 is therefore inhibition of Sialic acid binding ig-like lectin 8 (SIGLEC8, Accession NP_055257.1), a gene which is a cell adhesion molecule

for postnatal neural development. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIGLEC8.

[40053] The function of SIGLEC8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Src-like-adaptor 2 (SLA2, Accession NP_778252.1) is another GAM1338 target gene, herein designated TARGET GENE. SLA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLA2 BINDING SITE, designated SEQ ID:15357, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40054] Another function of GAM1338 is therefore inhibition of Src-like-adaptor 2 (SLA2, Accession NP_778252.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA2.

[40055] Src-like-adaptor 2 (SLA2, Accession NP_115590.1) is an-

other GAM1338 target gene, herein designated TARGET GENE. SLA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLA2 BINDING SITE, designated SEQ ID:15357, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40056] Another function of GAM1338 is therefore inhibition of Src-like-adaptor 2 (SLA2, Accession NP_115590.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA2.

[40057] Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (SLC11A2, Accession NP_000608.1) is another GAM1338 target gene, herein designated TARGET GENE. SLC11A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC11A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of SLC11A2 BINDING SITE, designated SEQ ID:16731, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40058] Another function of GAM1338 is therefore inhibition of Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (SLC11A2, Accession NP_000608.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC11A2.

[40059] Solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8, Accession NP_078904.1) is another GAM1338 target gene, herein designated TARGET GENE. SLC12A8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC12A8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC12A8 BINDING SITE, designated SEQ ID:18425, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40060] Another function of GAM1338 is therefore inhibition of Solute carrier family 12 (potassium/chloride transporters),

member 8 (SLC12A8, Accession NP_078904.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC12A8.

[40061] Solute carrier family 13 (sodium/sulfate symporters), member 1 (SLC13A1, Accession NP_071889.2) is another GAM1338 target gene, herein designated TARGET GENE. SLC13A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC13A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC13A1 BINDING SITE, designated SEQ ID:15679, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40062] Another function of GAM1338 is therefore inhibition of Solute carrier family 13 (sodium/sulfate symporters), member 1 (SLC13A1, Accession NP_071889.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC13A1.

[40063] Solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1, Accession NP_005064.1) is another

GAM1338 target gene, herein designated TARGET GENE. SLC15A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC15A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC15A1 BINDING SITE, designated SEQ ID:20019, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40064] Another function of GAM1338 is therefore inhibition of Solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1, Accession NP_005064.1), a gene which is a H(+)- coupled peptide transporter. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC15A1.

[40065] The function of SLC15A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Solute carrier family 16 (monocarboxylic acid transporters), member 4 (SLC16A4, Accession NP_004687.1) is another GAM1338 target gene, herein designated TARGET GENE. SLC16A4 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by SLC16A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A4 BINDING SITE, designated SEQ ID:20157, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40066] Another function of GAM1338 is therefore inhibition of Solute carrier family 16 (monocarboxylic acid transporters), member 4 (SLC16A4, Accession NP_004687.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A4.

[40067] Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) is another GAM1338 target gene, herein designated TARGET GENE. SLC16A6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC16A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A6 BINDING SITE, designated

SEQ ID:517, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40068] Another function of GAM1338 is therefore inhibition of Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A6.

[40069] Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1, Accession NP_004718.1) is another GAM1338 target gene, herein designated TARGET GENE. SLC24A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC24A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC24A1 BINDING SITE, designated SEQ ID:7931, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40070] Another function of GAM1338 is therefore inhibition of Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1, Accession NP_004718.1),

a gene which is a critical component of the visual transduction cascade, controlling the calcium concentration of outer segments during light and darkness. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC24A1.

[40071] The function of SLC24A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 (SLC25A10, Accession NP_036272.2) is another GAM1338 target gene, herein designated TARGET GENE. SLC25A10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC25A10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC25A10 BINDING SITE, designated SEQ ID:1937, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40072] Another function of GAM1338 is therefore inhibition of Solute carrier family 25 (mitochondrial carrier; dicarboxy-

late transporter), member 10 (SLC25A10, Accession NP_036272.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC25A10.

[40073] SLC30A5 (Accession NP_076960.1) is another GAM1338 target gene, herein designated TARGET GENE. SLC30A5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLC30A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC30A5 BINDING SITE, designated SEQ ID:1341, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40074] Another function of GAM1338 is therefore inhibition of SLC30A5 (Accession NP_076960.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC30A5.

[40075] SLC30A6 (Accession NP_060434.2) is another GAM1338 target gene, herein designated TARGET GENE. SLC30A6 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by SLC30A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC30A6 BINDING SITE, designated SEQ ID:11622, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40076] Another function of GAM1338 is therefore inhibition of SLC30A6 (Accession NP_060434.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC30A6.

[40077] SLC35E2 (Accession XP_049733.6) is another GAM1338 target gene, herein designated TARGET GENE. SLC35E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC35E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC35E2 BINDING SITE, designated SEQ ID:12300, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40078] Another function of GAM1338 is therefore inhibition of

SLC35E2 (Accession XP_049733.6) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35E2.

[40079] Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2) is another GAM1338 target gene, herein designated TARGET GENE. SLC39A1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC39A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC39A1 BINDING SITE, designated SEQ ID:19430, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40080] Another function of GAM1338 is therefore inhibition of Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2), a gene which is a divalent (zinc/iron) metal ion transporter. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC39A1.

[40081] The function of SLC39A1 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.1.Solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14, Accession NP_009162.1) is another GAM1338 target gene, herein designated TARGET GENE. SLC6A14 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC6A14 BINDING SITE, designated SEQ ID:16741, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40082] Another function of GAM1338 is therefore inhibition of Solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14, Accession NP_009162.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A14.

[40083] SMAC (Accession NP_620308.1) is another GAM1338 target gene, herein designated TARGET GENE. SMAC BINDING SITE1 and SMAC BINDING SITE2 are target binding sites

found in untranslated regions of multiple transcripts of mRNA encoded by SMAC, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMAC BINDING SITE1 and SMAC BINDING SITE2, designated SEQ ID:15275 and SEQ ID:1245 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40084] Another function of GAM1338 is therefore inhibition of SMAC (Accession NP_620308.1), a gene which promotes apoptosis via caspase activation. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMAC.

[40085] The function of SMAC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_003816.2) is another GAM1338 target gene, herein designated TARGET GENE. SNAP23 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNAP23, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP23 BINDING SITE, designated SEQ ID:14270, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40086] Another function of GAM1338 is therefore inhibition of Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_003816.2), a gene which is essential component of the high affinity receptor for the general membrane fusion machinery. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP23.

[40087] The function of SNAP23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_570710.1) is another GAM1338 target gene, herein designated TARGET GENE. SNAP23 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNAP23, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP23 BINDING SITE, designated SEQ ID:14270, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40088] Another function of GAM1338 is therefore inhibition of Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_570710.1), a gene which is essential component of the high affinity receptor for the general membrane fusion machinery. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP23.

[40089] The function of SNAP23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Syntaphilin (SNPH, Accession NP_055538.1) is another GAM1338 target gene, herein designated TARGET GENE. SNPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNPH BINDING SITE, designated SEQ ID:1354,

to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40090] Another function of GAM1338 is therefore inhibition of Syntaphilin (SNPH, Accession NP_055538.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNPH.

[40091] Sorting nexin 15 (SNX15, Accession NP_037438.2) is another GAM1338 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:2728, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40092] Another function of GAM1338 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NP_037438.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15.

[40093] Sorting nexin 15 (SNX15, Accession NP_680086.1) is another GAM1338 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:2728, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40094] Another function of GAM1338 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NP_680086.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15.

[40095] SNX22 (Accession NP_079074.1) is another GAM1338 target gene, herein designated TARGET GENE. SNX22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNX22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX22

BINDING SITE, designated SEQ ID:11205, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40096] Another function of GAM1338 is therefore inhibition of SNX22 (Accession NP_079074.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX22.

[40097] SNX27 (Accession NP_112180.4) is another GAM1338 target gene, herein designated TARGET GENE. SNX27 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNX27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX27 BINDING SITE, designated SEQ ID:8857, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40098] Another function of GAM1338 is therefore inhibition of SNX27 (Accession NP_112180.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX27.

[40099] Speckle-type poz protein (SPOP, Accession NP_003554.1) is another GAM1338 target gene, herein designated TAR-

GET GENE. SPOP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SPOP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPOP BINDING SITE, designated SEQ ID:7212, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40100] Another function of GAM1338 is therefore inhibition of Speckle-type poz protein (SPOP, Accession NP_003554.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPOP.

[40101] SQV7L (Accession XP_047287.1) is another GAM1338 target gene, herein designated TARGET GENE. SQV7L BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SQV7L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SQV7L BINDING SITE, designated SEQ ID:15016, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40102] Another function of GAM1338 is therefore inhibition of SQV7L (Accession XP_047287.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SQV7L.

[40103] SRISNF2L (Accession NP_055921.1) is another GAM1338 target gene, herein designated TARGET GENE. SRISNF2L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SRISNF2L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRISNF2L BINDING SITE, designated SEQ ID:9707, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40104] Another function of GAM1338 is therefore inhibition of SRISNF2L (Accession NP_055921.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRISNF2L.

[40105] Sarcalumenin (SRL, Accession XP_064152.3) is another GAM1338 target gene, herein designated TARGET GENE. SRL BINDING SITE1 and SRL BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by SRL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRL BINDING SITE1 and SRL BINDING SITE2, designated SEQ ID:7583 and SEQ ID:9910 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40106] Another function of GAM1338 is therefore inhibition of Sarcalumenin (SRL, Accession XP_064152.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRL.

[40107] Serine/arginine repetitive matrix 2 (SRRM2, Accession NP_057417.2) is another GAM1338 target gene, herein designated TARGET GENE. SRRM2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SRRM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRRM2 BINDING SITE, designated SEQ ID:18975, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40108] Another function of GAM1338 is therefore inhibition of Serine/arginine repetitive matrix 2 (SRRM2, Accession NP_057417.2), a gene which RELATED NUCLEAR MATRIX PROTEIN. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRRM2.

[40109] The function of SRRM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1) is another GAM1338 target gene, herein designated TARGET GENE. SS18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SS18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SS18 BINDING SITE, designated SEQ ID:10975, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40110] Another function of GAM1338 is therefore inhibition of Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1), a gene which is a putative tran-

scriptional activator. and therefore is associated with Human synovial sarcomas. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Human synovial sarcomas., and of other diseases and clinical conditions associated with SS18.

[40111] The function of SS18 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Signal transducing adaptor molecule (sh3 domain and itam motif) 2 (STAM2, Accession NP_005834.3) is another GAM1338 target gene, herein designated TARGET GENE. STAM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STAM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAM2 BINDING SITE, designated SEQ ID:5920, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40112] Another function of GAM1338 is therefore inhibition of Signal transducing adaptor molecule (sh3 domain and itam motif) 2 (STAM2, Accession NP_005834.3) . Accord-

ingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAM2.

[40113] Start domain containing 4, sterol regulated (STARD4, Accession NP_631903.1) is another GAM1338 target gene, herein designated TARGET GENE. STARD4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STARD4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STARD4 BINDING SITE, designated SEQ ID:14279, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40114] Another function of GAM1338 is therefore inhibition of Start domain containing 4, sterol regulated (STARD4, Accession NP_631903.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STARD4.

[40115] Staufen, rna binding protein (drosophila) (STAU, Accession NP_004593.1) is another GAM1338 target gene, herein designated TARGET GENE. STAU BINDING SITE is a target binding site found in the 5` untranslated region of multi-

ple transcripts of mRNA encoded by STAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAU BINDING SITE, designated SEQ ID:9365, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40116] Another function of GAM1338 is therefore inhibition of Staufen, rna binding protein (drosophila) (STAU, Accession NP_004593.1), a gene which may play a role in specific positioning of mrnas at given sites in the cell and in stimulating their translation at the site. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAU.

[40117] The function of STAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM37.1.Sulfotransferase, estrogen-preferring (STE, Accession NP_005411.1) is another GAM1338 target gene, herein designated TARGET GENE. STE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STE BINDING SITE, designated SEQ ID:13898, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40118] Another function of GAM1338 is therefore inhibition of Sulfotransferase, estrogen-preferring (STE, Accession NP_005411.1), a gene which sulfates estrone and dehydroepiandrosterone, but not dopamine. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STE.

[40119] The function of STE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Six transmembrane epithelial antigen of prostate 2 (STEAP2, Accession NP_694544.1) is another GAM1338 target gene, herein designated TARGET GENE. STEAP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STEAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of STEAP2 BINDING SITE, designated SEQ ID:1413, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40120] Another function of GAM1338 is therefore inhibition of Six transmembrane epithelial antigen of prostate 2 (STEAP2, Accession NP_694544.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STEAP2.

[40121] Stomatin (STOM, Accession NP_004090.3) is another GAM1338 target gene, herein designated TARGET GENE. STOM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STOM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STOM BINDING SITE, designated SEQ ID:4144, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40122] Another function of GAM1338 is therefore inhibition of Stomatin (STOM, Accession NP_004090.3) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with STOM.

[40123] Syntaxin binding protein 6 (amisyn) (STXBP6, Accession NP_054897.4) is another GAM1338 target gene, herein designated TARGET GENE. STXBP6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by STXBP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STXBP6 BINDING SITE, designated SEQ ID:11916, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40124] Another function of GAM1338 is therefore inhibition of Syntaxin binding protein 6 (amisyn) (STXBP6, Accession NP_054897.4) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STXBP6.

[40125] Synaptotagmin xi (SYT11, Accession NP_689493.2) is another GAM1338 target gene, herein designated TARGET GENE. SYT11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYT11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of SYT11 BINDING SITE, designated SEQ ID:1690, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40126] Another function of GAM1338 is therefore inhibition of Synaptotagmin xi (SYT11, Accession NP_689493.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT11.

[40127] Synaptotagmin xiii (SYT13, Accession NP_065877.1) is another GAM1338 target gene, herein designated TARGET GENE. SYT13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYT13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYT13 BINDING SITE, designated SEQ ID:19065, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40128] Another function of GAM1338 is therefore inhibition of Synaptotagmin xiii (SYT13, Accession NP_065877.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with SYT13.

[40129] TADA3L (Accession NP_597814.1) is another GAM1338 target gene, herein designated TARGET GENE. TADA3L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TADA3L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TADA3L BINDING SITE, designated SEQ ID:10415, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40130] Another function of GAM1338 is therefore inhibition of TADA3L (Accession NP_597814.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TADA3L.

[40131] T-cell acute lymphocytic leukemia 1 (TAL1, Accession NP_003180.1) is another GAM1338 target gene, herein designated TARGET GENE. TAL1 BINDING SITE1 and TAL1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TAL1, corresponding to target binding sites such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAL1 BINDING SITE1 and TAL1 BINDING SITE2, designated SEQ ID:7347 and SEQ ID:19155 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40132] Another function of GAM1338 is therefore inhibition of T-cell acute lymphocytic leukemia 1 (TAL1, Accession NP_003180.1), a gene which may help control cell growth and differentiation. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAL1.

[40133] The function of TAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tap binding protein (tapasin) (TAPBP, Accession NP_003181.3) is another GAM1338 target gene, herein designated TARGET GENE. TAPBP BINDING SITE1 through TAPBP BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TAPBP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of TAPBP BINDING SITE1 through TAPBP BINDING SITE3, designated SEQ ID:6086, SEQ ID:8861 and SEQ ID:3109 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40134] Another function of GAM1338 is therefore inhibition of Tap binding protein (tapasin) (TAPBP, Accession NP_003181.3), a gene which is involved in MHC class I-restricted antigen processing. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAPBP.

[40135] The function of TAPBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Tyrosine aminotransferase (TAT, Accession NP_000344.1) is another GAM1338 target gene, herein designated TARGET GENE. TAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAT BINDING SITE, designated SEQ ID:20161, to the nucleotide sequence of GAM1338

RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40136] Another function of GAM1338 is therefore inhibition of Tyrosine aminotransferase (TAT, Accession NP_000344.1), a gene which is tyrosine aminotransferase and strongly similar to rat Rn.9947, which plays a role in gluconeogenesis. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAT.

[40137] The function of TAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Tafazzin (cardiomyopathy, dilated 3a (x-linked); endocardial fibroelastosis 2; barth syndrome) (TAZ, Accession NP_851831.1) is another GAM1338 target gene, herein designated TARGET GENE. TAZ BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TAZ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAZ BINDING SITE, designated SEQ ID:14872, to the nucleotide sequence of GAM1338 RNA, herein des-

ignated GAM RNA, also designated SEQ ID:360.

[40138] Another function of GAM1338 is therefore inhibition of Tafazzin (cardiomyopathy, dilated 3a (x-linked); endocardial fibroelastosis 2; barth syndrome) (TAZ, Accession NP_851831.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAZ.

[40139] Tbc1 domain family, member 5 (TBC1D5, Accession NP_055559.1) is another GAM1338 target gene, herein designated TARGET GENE. TBC1D5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TBC1D5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TBC1D5 BINDING SITE, designated SEQ ID:12382, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40140] Another function of GAM1338 is therefore inhibition of Tbc1 domain family, member 5 (TBC1D5, Accession NP_055559.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBC1D5.

[40141] Titin-cap (telethonin) (TCAP, Accession NP_003664.1) is another GAM1338 target gene, herein designated TARGET GENE. TCAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TCAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCAP BINDING SITE, designated SEQ ID:19403, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40142] Another function of GAM1338 is therefore inhibition of Titin-cap (telethonin) (TCAP, Accession NP_003664.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCAP.

[40143] Transcription factor 2, hepatic; lf-b3; variant hepatic nuclear factor (TCF2, Accession NP_006472.1) is another GAM1338 target gene, herein designated TARGET GENE. TCF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TCF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of TCF2 BINDING SITE, designated SEQ ID:401, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40144] Another function of GAM1338 is therefore inhibition of Transcription factor 2, hepatic; lf-b3; variant hepatic nuclear factor (TCF2, Accession NP_006472.1), a gene which probably binds to the inverted palindrome 5'- gttaatnattaac- 3'. and therefore is associated with Maturity- onset diabetes of the young type 5 (mody5), familial hypoplastic glomerulocystic kidney disease (gckd). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Maturity- onset diabetes of the young type 5 (mody5), familial hypoplastic glomerulocystic kidney disease (gckd), and of other diseases and clinical conditions associated with TCF2.

[40145] The function of TCF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.T-cell, immune regulator 1, atpase, h+ transporting, lysosomal v0 protein a isoform 3 (TCIRG1, Accession NP_006010.2) is another GAM1338 target gene, herein designated TARGET GENE. TCIRG1 BINDING SITE is a target binding site found in the 5` untranslated region

of multiple transcripts of mRNA encoded by TCIRG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCIRG1 BINDING SITE, designated SEQ ID:7780, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40146] Another function of GAM1338 is therefore inhibition of T-cell, immune regulator 1, atpase, h+ transporting, lysosomal v0 protein a isoform 3 (TCIRG1, Accession NP_006010.2), a gene which seems to be directly involved in t cell activation. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCIRG1.

[40147] The function of TCIRG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.T-cell leukemia/lymphoma 6 (TCL6, Accession NP_036600.2) is another GAM1338 target gene, herein designated TARGET GENE. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TCL6, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:12973 and SEQ ID:12973 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40148] Another function of GAM1338 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_036600.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[40149] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065579.2) is another GAM1338 target gene, herein designated TARGET GENE. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TCL6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:6911 and SEQ ID:12973 respectively, to the nucleotide sequence of GAM1338 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:360.

[40150] Another function of GAM1338 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065579.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[40151] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065578.2) is another GAM1338 target gene, herein designated TARGET GENE. TCL6 BINDING SITE1 and TCL6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TCL6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE1 and TCL6 BINDING SITE2, designated SEQ ID:6911 and SEQ ID:12973 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40152] Another function of GAM1338 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065578.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[40153] TERA (Accession NP_067061.1) is another GAM1338 target gene, herein designated TARGET GENE. TERA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TERA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERA BINDING SITE, designated SEQ ID:971, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40154] Another function of GAM1338 is therefore inhibition of TERA (Accession NP_067061.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERA.

[40155] Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_003209.1) is another GAM1338 target gene, herein designated TARGET GENE. TERF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TERF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF1 BINDING SITE, designated

SEQ ID:13870, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40156] Another function of GAM1338 is therefore inhibition of Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_003209.1), a gene which negatively regulates telomere length, involves in regulation of the mitotic spindle. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF1.

[40157] The function of TERF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_059523.1) is another GAM1338 target gene, herein designated TARGET GENE. TERF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TERF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF1 BINDING SITE, designated SEQ ID:13870, to the nucleotide sequence of

GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40158] Another function of GAM1338 is therefore inhibition of Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_059523.1), a gene which negatively regulates telomere length, involves in regulation of the mitotic spindle. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF1.

[40159] The function of TERF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Telomeric repeat binding factor 2 (TERF2, Accession NP_005643.1) is another GAM1338 target gene, herein designated TARGET GENE. TERF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TERF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF2 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40160] Another function of GAM1338 is therefore inhibition of Telomeric repeat binding factor 2 (TERF2, Accession NP_005643.1), a gene which plays a key role in the protective activity of telomeres. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF2.

[40161] The function of TERF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM133.2.Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) is another GAM1338 target gene, herein designated TARGET GENE. TGIF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGIF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGIF2 BINDING SITE, designated SEQ ID:7274, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40162] Another function of GAM1338 is therefore inhibition of Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) . Accordingly, utilities of GAM1338

include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGIF2.

[40163] Tigger transposable element derived 6 (TIGD6, Accession NP_112215.1) is another GAM1338 target gene, herein designated TARGET GENE. TIGD6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TIGD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TIGD6 BINDING SITE, designated SEQ ID:17302, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40164] Another function of GAM1338 is therefore inhibition of Tigger transposable element derived 6 (TIGD6, Accession NP_112215.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIGD6.

[40165] TIM50L (Accession XP_053074.2) is another GAM1338 target gene, herein designated TARGET GENE. TIM50L BINDING SITE1 and TIM50L BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TIM50L, corresponding to target binding sites such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TIM50L BINDING SITE1 and TIM50L BINDING SITE2, designated SEQ ID:7201 and SEQ ID:7571 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40166] Another function of GAM1338 is therefore inhibition of TIM50L (Accession XP_053074.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIM50L.

[40167] Toll-like receptor 5 (TLR5, Accession NP_003259.2) is another GAM1338 target gene, herein designated TARGET GENE. TLR5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TLR5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLR5 BINDING SITE, designated SEQ ID:16358, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40168] Another function of GAM1338 is therefore inhibition of Toll-like receptor 5 (TLR5, Accession NP_003259.2), a

gene which participates in the innate immune response to bacterial flagellins. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLR5.

[40169] The function of TLR5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Transmembrane, cochlear expressed, 1 (TMC1, Accession NP_619636.2) is another GAM1338 target gene, herein designated TARGET GENE. TMC1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TMC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMC1 BINDING SITE, designated SEQ ID:19429, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40170] Another function of GAM1338 is therefore inhibition of Transmembrane, cochlear expressed, 1 (TMC1, Accession NP_619636.2), a gene which is required for normal function of cochlear hair cells and therefore may be associated with Autosomal recessive nonsyndromic neurosensory

deafness and autosomal dominant nonsyndromic sensorineural hearing loss . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Autosomal recessive nonsyndromic neurosensory deafness and autosomal dominant nonsyndromic sensorineural hearing loss ., and of other diseases and clinical conditions associated with TMC1.

[40171] The function of TMC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.TMEM14A (Accession NP_054770.1) is another GAM1338 target gene, herein designated TARGET GENE. TMEM14A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TMEM14A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMEM14A BINDING SITE, designated SEQ ID:7622, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40172] Another function of GAM1338 is therefore inhibition of TMEM14A (Accession NP_054770.1) . Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEM14A.

[40173] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115780.1) is another GAM1338 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE, designated SEQ ID:15133, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40174] Another function of GAM1338 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115780.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[40175] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_076927.1) is another GAM1338 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE, designated SEQ ID:15133, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40176] Another function of GAM1338 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_076927.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[40177] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115777.1) is another GAM1338 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE, designated SEQ ID:15133, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40178] Another function of GAM1338 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115777.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[40179] Tumor necrosis factor, alpha-induced protein 2 (TNFAIP2, Accession NP_006282.2) is another GAM1338 target gene, herein designated TARGET GENE. TNFAIP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFAIP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFAIP2 BINDING SITE, designated SEQ ID:14228, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40180] Another function of GAM1338 is therefore inhibition of Tumor necrosis factor, alpha-induced protein 2 (TNFAIP2, Accession NP_006282.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFAIP2.

[40181] Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_003833.3) is another

GAM1338 target gene, herein designated TARGET GENE. TNFRSF10B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF10B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE, designated SEQ ID:9933, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40182] Another function of GAM1338 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_003833.3), a gene which forms complex that induces apoptosis. and therefore may be associated with Squamous cell carcinoma . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Squamous cell carcinoma ., and of other diseases and clinical conditions associated with TNFRSF10B.

[40183] The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_671716.1)

is another GAM1338 target gene, herein designated TARGET GENE. TNFRSF10B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TNFRSF10B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE, designated SEQ ID:9933, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40184] Another function of GAM1338 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_671716.1), a gene which forms complex that induces apoptosis. and therefore may be associated with Squamous cell carcinoma . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Squamous cell carcinoma ., and of other diseases and clinical conditions associated with TNFRSF10B.

[40185] The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tumor necrosis factor receptor superfamily, member 11a, activator of nfkb (TNFRSF11A, Ac-

cession NP_003830.1) is another GAM1338 target gene, herein designated TARGET GENE. TNFRSF11A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF11A BINDING SITE, designated SEQ ID:11190, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40186] Another function of GAM1338 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 11a, activator of nfkb (TNFRSF11A, Accession NP_003830.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF11A.

[40187] Tumor necrosis factor receptor superfamily, member 9 (TNFRSF9, Accession NP_001552.2) is another GAM1338 target gene, herein designated TARGET GENE. TNFRSF9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of TNFRSF9 BINDING SITE, designated SEQ ID:438, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40188] Another function of GAM1338 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 9 (TNFRSF9, Accession NP_001552.2), a gene which inhibits proliferation of activated T lymphocytes. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF9.

[40189] The function of TNFRSF9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Torsin family 1, member b (torsin b) (TOR1B, Accession NP_055321.1) is another GAM1338 target gene, herein designated TARGET GENE. TOR1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TOR1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOR1B BINDING SITE, designated SEQ ID:2429, to the nu-

cleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40190] Another function of GAM1338 is therefore inhibition of Torsin family 1, member b (torsin b) (TOR1B, Accession NP_055321.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOR1B.

[40191] Tumor protein p53 (li-fraumeni syndrome) (TP53, Accession NP_000537.2) is another GAM1338 target gene, herein designated TARGET GENE. TP53 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TP53, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TP53 BINDING SITE, designated SEQ ID:2118, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40192] Another function of GAM1338 is therefore inhibition of Tumor protein p53 (li-fraumeni syndrome) (TP53, Accession NP_000537.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53.

[40193] Thiopurine s-methyltransferase (TPMT, Accession NP_000358.1) is another GAM1338 target gene, herein designated TARGET GENE. TPMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TPMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPMT BINDING SITE, designated SEQ ID:10218, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40194] Another function of GAM1338 is therefore inhibition of Thiopurine s-methyltransferase (TPMT, Accession NP_000358.1), a gene which catalyzes the s- methylation of thiopurine drugs such as 6- mercaptopurine. and therefore may be associated with Thiopurine s- methyl-transferase polymorphism. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Thiopurine s- methyltransferase polymorphism, and of other diseases and clinical conditions associated with TPMT.

[40195] The function of TPMT and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM130.1.Tnf receptor-associated factor 5 (TRAF5, Accession NP_665702.1) is another GAM1338 target gene, herein designated TARGET GENE. TRAF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRAF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:10175, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40196] Another function of GAM1338 is therefore inhibition of Tnf receptor-associated factor 5 (TRAF5, Accession NP_665702.1), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5.

[40197] The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Tnf receptor-associated factor 5 (TRAF5, Ac-

cession NP_004610.1) is another GAM1338 target gene, herein designated TARGET GENE. TRAF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRAF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:10175, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40198] Another function of GAM1338 is therefore inhibition of Tnf receptor-associated factor 5 (TRAF5, Accession NP_004610.1), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5.

[40199] The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Tripartite motif-containing 16 (TRIM16, Accession NP_006461.2) is another GAM1338 target gene, herein designated TARGET GENE. TRIM16 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by TRIM16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM16 BINDING SITE, designated SEQ ID:13321, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40200] Another function of GAM1338 is therefore inhibition of Tripartite motif-containing 16 (TRIM16, Accession NP_006461.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM16.

[40201] Tripartite motif-containing 5 (TRIM5, Accession NP_149023.1) is another GAM1338 target gene, herein designated TARGET GENE. TRIM5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRIM5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM5 BINDING SITE, designated SEQ ID:9916, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA,

also designated SEQ ID:360.

[40202] Another function of GAM1338 is therefore inhibition of Tripartite motif-containing 5 (TRIM5, Accession NP_149023.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM5.

[40203] Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542437.1) is another GAM1338 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:1587 and SEQ ID:15897 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40204] Another function of GAM1338 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542437.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities

of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[40205] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542437.1) is another GAM1338 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:15897 and SEQ ID:15897 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40206] Another function of GAM1338 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542437.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with TRPV1.

[40207] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_061197.3) is another GAM1338 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:15897 and SEQ ID:1587 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40208] Another function of GAM1338 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_061197.3), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[40209] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1) is another GAM1338 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:1587 and SEQ ID:1587 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40210] Another function of GAM1338 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[40211] The function of TRPV1 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Tspy-like (TSPYL, Accession XP_166325.1) is another GAM1338 target gene, herein designated TARGET GENE. TSPYL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSPYL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TSPYL BINDING SITE, designated SEQ ID:9101, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40212] Another function of GAM1338 is therefore inhibition of Tspy-like (TSPYL, Accession XP_166325.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSPYL.

[40213] TTY7 (Accession NP_114132.1) is another GAM1338 target gene, herein designated TARGET GENE. TTY7 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TTY7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of TTY7 BINDING SITE, designated SEQ ID:16664, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40214] Another function of GAM1338 is therefore inhibition of TTY7 (Accession NP_114132.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTY7.

[40215] TU12B1-TY (Accession NP_057659.1) is another GAM1338 target gene, herein designated TARGET GENE. TU12B1-TY BINDING SITE1 through TU12B1-TY BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by TU12B1-TY, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TU12B1-TY BINDING SITE1 through TU12B1-TY BINDING SITE3, designated SEQ ID:7327, SEQ ID:12270 and SEQ ID:17849 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40216] Another function of GAM1338 is therefore inhibition of TU12B1-TY (Accession NP_057659.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with TU12B1-TY.

[40217] Tubby homolog (mouse) (TUB, Accession NP_813977.1) is another GAM1338 target gene, herein designated TARGET GENE. TUB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TUB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUB BINDING SITE, designated SEQ ID:10826, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40218] Another function of GAM1338 is therefore inhibition of Tubby homolog (mouse) (TUB, Accession NP_813977.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUB.

[40219] Tubby homolog (mouse) (TUB, Accession NP_003311.2) is another GAM1338 target gene, herein designated TARGET GENE. TUB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TUB, corresponding to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUB BINDING SITE, designated SEQ ID:10826, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40220] Another function of GAM1338 is therefore inhibition of Tubby homolog (mouse) (TUB, Accession NP_003311.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUB.

[40221] TUCAN (Accession NP_055774.1) is another GAM1338 target gene, herein designated TARGET GENE. TUCAN BINDING SITE1 and TUCAN BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TUCAN, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUCAN BINDING SITE1 and TUCAN BINDING SITE2, designated SEQ ID:2265 and SEQ ID:10630 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40222] Another function of GAM1338 is therefore inhibition of TUCAN (Accession NP_055774.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUCAN.

[40223] Tuftelin 1 (TUFT1, Accession NP_064512.1) is another GAM1338 target gene, herein designated TARGET GENE. TUFT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TUFT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUFT1 BINDING SITE, designated SEQ ID:19342, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40224] Another function of GAM1338 is therefore inhibition of Tuftelin 1 (TUFT1, Accession NP_064512.1), a gene which appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and capping. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUFT1.

[40225] The function of TUFT1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM136.1.TXL-2 (Accession NP_835231.1) is another GAM1338 target gene, herein designated TARGET GENE. TXL-2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TXL-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TXL-2 BINDING SITE, designated SEQ ID:7572, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40226] Another function of GAM1338 is therefore inhibition of TXL-2 (Accession NP_835231.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TXL-2.

[40227] Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) is another GAM1338 target gene, herein designated TARGET GENE. TXNL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TXNL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TXNL2 BINDING SITE, designated SEQ ID:1413,

to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40228] Another function of GAM1338 is therefore inhibition of Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TXNL2.

[40229] U1SNRNPBP (Accession NP_851034.1) is another GAM1338 target gene, herein designated TARGET GENE. U1SNRNPBP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by U1SNRNPBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of U1SNRNPBP BINDING SITE, designated SEQ ID:18791, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40230] Another function of GAM1338 is therefore inhibition of U1SNRNPBP (Accession NP_851034.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U1SNRNPBP.

[40231] U1SNRNPBP (Accession NP_851030.1) is another GAM1338 target gene, herein designated TARGET GENE. U1SNRNPBP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by U1SNRNPBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of U1SNRNPBP BINDING SITE, designated SEQ ID:18791, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40232] Another function of GAM1338 is therefore inhibition of U1SNRNPBP (Accession NP_851030.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U1SNRNPBP.

[40233] U1SNRNPBP (Accession NP_008951.1) is another GAM1338 target gene, herein designated TARGET GENE. U1SNRNPBP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by U1SNRNPBP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of U1SNRNPBP BINDING SITE, designated SEQ ID:18791, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40234] Another function of GAM1338 is therefore inhibition of U1SNRNPBP (Accession NP_008951.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U1SNRNPBP.

[40235] UBCE7IP5 (Accession NP_055763.1) is another GAM1338 target gene, herein designated TARGET GENE. UBCE7IP5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBCE7IP5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBCE7IP5 BINDING SITE, designated SEQ ID:2287, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40236] Another function of GAM1338 is therefore inhibition of UBCE7IP5 (Accession NP_055763.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

UBCE7IP5.

[40237] Ubiquitin-conjugating enzyme e2l 3 (UBE2L3, Accession NP_003338.1) is another GAM1338 target gene, herein designated TARGET GENE. UBE2L3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBE2L3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBE2L3 BINDING SITE, designated SEQ ID:11811, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40238] Another function of GAM1338 is therefore inhibition of Ubiquitin-conjugating enzyme e2l 3 (UBE2L3, Accession NP_003338.1), a gene which catalyzes the covalent attachment of ubiquitin to other proteins. and therefore may be associated with Parkinson disease. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Parkinson disease, and of other diseases and clinical conditions associated with UBE2L3.

[40239] The function of UBE2L3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM169.1.Udp-glucose dehydrogenase (UGDH, Accession NP_003350.1) is another GAM1338 target gene, herein designated TARGET GENE. UGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGDH BINDING SITE, designated SEQ ID:12092, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40240] Another function of GAM1338 is therefore inhibition of Udp-glucose dehydrogenase (UGDH, Accession NP_003350.1), a gene which is an UDP- glucose dehydrogenase. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGDH.

[40241] The function of UGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS, Accession NP_000364.1) is an-

other GAM1338 target gene, herein designated TARGET GENE. UMPS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UMPS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UMPS BINDING SITE, designated SEQ ID:19428, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40242] Another function of GAM1338 is therefore inhibition of Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS, Accession NP_000364.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UMPS.

[40243] Ubiquitin specific protease 22 (USP22, Accession XP_042698.2) is another GAM1338 target gene, herein designated TARGET GENE. USP22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by USP22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of USP22 BINDING SITE, designated

SEQ ID:20055, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40244] Another function of GAM1338 is therefore inhibition of Ubiquitin specific protease 22 (USP22, Accession XP_042698.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP22.

[40245] VDU1 (Accession NP_055832.2) is another GAM1338 target gene, herein designated TARGET GENE. VDU1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VDU1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VDU1 BINDING SITE, designated SEQ ID:794, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40246] Another function of GAM1338 is therefore inhibition of VDU1 (Accession NP_055832.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VDU1.

[40247] Von hippel-lindau syndrome (VHL, Accession

NP_000542.1) is another GAM1338 target gene, herein designated TARGET GENE. VHL BINDING SITE1 and VHL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by VHL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VHL BINDING SITE1 and VHL BINDING SITE2, designated SEQ ID:19946 and SEQ ID:969 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40248] Another function of GAM1338 is therefore inhibition of Von hippel-lindau syndrome (VHL, Accession NP_000542.1), a gene which may control rna stability through the selective degradation of rna- bound proteins. and therefore is associated with Von hippel- lindau disease. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Von hippel- lindau disease, and of other diseases and clinical conditions associated with VHL.

[40249] The function of VHL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM72.1.Vasoactive intestinal peptide receptor 2 (VIPR2, Accession NP_003373.2) is another GAM1338 target gene, herein designated TARGET GENE. VIPR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VIPR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VIPR2 BINDING SITE, designated SEQ ID:861, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40250] Another function of GAM1338 is therefore inhibition of Vasoactive intestinal peptide receptor 2 (VIPR2, Accession NP_003373.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIPR2.

[40251] Vesicle transport through interaction with t-snares homolog 1a (yeast) (VTI1A, Accession NP_660207.1) is another GAM1338 target gene, herein designated TARGET GENE. VTI1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VTI1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of VTI1A BINDING SITE, designated SEQ ID:1472, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40252] Another function of GAM1338 is therefore inhibition of Vesicle transport through interaction with t-snares homolog 1a (yeast) (VTI1A, Accession NP_660207.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VTI1A.

[40253] Williams beuren syndrome chromosome region 18 (WBSCR18, Accession NP_115693.2) is another GAM1338 target gene, herein designated TARGET GENE. WBSCR18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WBSCR18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR18 BINDING SITE, designated SEQ ID:10631, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40254] Another function of GAM1338 is therefore inhibition of Williams beuren syndrome chromosome region 18

(WBSCR18, Accession NP_115693.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WB-SCR18.

[40255] Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_579889.1) is another GAM1338 target gene, herein designated TARGET GENE. WHSC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WHSC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE, designated SEQ ID:12602, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40256] Another function of GAM1338 is therefore inhibition of Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_579889.1), a gene which binds covalently to and repairs g/t mismatches. and therefore may be associated with Wolf- hirschhorn syndrome. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of Wolf- hirschhorn syndrome, and of other diseases and clinical conditions associated with WHSC1.

[40257] The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1) is another GAM1338 target gene, herein designated TARGET GENE. XRCC2 BINDING SITE1 through XRCC2 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by XRCC2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of XRCC2 BINDING SITE1 through XRCC2 BINDING SITE3, designated SEQ ID:16920, SEQ ID:19967 and SEQ ID:6034 respectively, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40258] Another function of GAM1338 is therefore inhibition of X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1), a gene which involves in the homologous recombination repair (hrr) pathway of double- stranded dna. Accordingly, utilities of GAM1338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with XRCC2.

[40259] The function of XRCC2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.V-yes-1 yamaguchi sarcoma viral oncogene homolog 1 (YES1, Accession NP_005424.1) is another GAM1338 target gene, herein designated TARGET GENE. YES1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by YES1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of YES1 BINDING SITE, designated SEQ ID:18699, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40260] Another function of GAM1338 is therefore inhibition of V-yes-1 yamaguchi sarcoma viral oncogene homolog 1 (YES1, Accession NP_005424.1), a gene which is a putative protein- tyrosine kinase. Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YES1.

[40261] The function of YES1 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.ZAP (Accession NP_064504.2) is another GAM1338 target gene, herein designated TARGET GENE. ZAP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAP BINDING SITE, designated SEQ ID:19083, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40262] Another function of GAM1338 is therefore inhibition of ZAP (Accession NP_064504.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAP.

[40263] ZFP30 (Accession NP_055713.1) is another GAM1338 target gene, herein designated TARGET GENE. ZFP30 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZFP30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP30

BINDING SITE, designated SEQ ID:432, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40264] Another function of GAM1338 is therefore inhibition of ZFP30 (Accession NP_055713.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP30.

[40265] ZFP42 (Accession NP_777560.1) is another GAM1338 target gene, herein designated TARGET GENE. ZFP42 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZFP42, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP42 BINDING SITE, designated SEQ ID:6576, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40266] Another function of GAM1338 is therefore inhibition of ZFP42 (Accession NP_777560.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP42.

[40267] Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_071371.2) is another GAM1338 target gene, herein

designated TARGET GENE. ZFP64 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP64, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP64 BINDING SITE, designated SEQ ID:13869, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40268] Another function of GAM1338 is therefore inhibition of Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_071371.2) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP64.

[40269] Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_060667.1) is another GAM1338 target gene, herein designated TARGET GENE. ZFP64 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP64, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP64 BINDING SITE, designated SEQ ID:13869, to the nucleotide

sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40270] Another function of GAM1338 is therefore inhibition of Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_060667.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP64.

[40271] ZMYND17 (Accession NP_848546.1) is another GAM1338 target gene, herein designated TARGET GENE. ZMYND17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZMYND17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZMYND17 BINDING SITE, designated SEQ ID:11022, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40272] Another function of GAM1338 is therefore inhibition of ZMYND17 (Accession NP_848546.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZMYND17.

[40273] Zinc finger protein 264 (ZNF264, Accession NP_003408.1)

is another GAM1338 target gene, herein designated TARGET GENE. ZNF264 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF264, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF264 BINDING SITE, designated SEQ ID:438, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40274] Another function of GAM1338 is therefore inhibition of Zinc finger protein 264 (ZNF264, Accession NP_003408.1). Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF264.

[40275] Zinc finger protein 273 (ZNF273, Accession XP_088082.1) is another GAM1338 target gene, herein designated TARGET GENE. ZNF273 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF273, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF273 BINDING SITE, designated SEQ ID:19693, to the nucleotide sequence of GAM1338

RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40276] Another function of GAM1338 is therefore inhibition of Zinc finger protein 273 (ZNF273, Accession XP_088082.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF273.

[40277] Zinc finger protein 339 (ZNF339, Accession NP_067043.1) is another GAM1338 target gene, herein designated TARGET GENE. ZNF339 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF339, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF339 BINDING SITE, designated SEQ ID:9097, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40278] Another function of GAM1338 is therefore inhibition of Zinc finger protein 339 (ZNF339, Accession NP_067043.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF339.

[40279] Zinc finger protein 345 (ZNF345, Accession NP_003410.1) is another GAM1338 target gene, herein designated TARGET GENE. ZNF345 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF345, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF345 BINDING SITE, designated SEQ ID:11758, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40280] Another function of GAM1338 is therefore inhibition of Zinc finger protein 345 (ZNF345, Accession NP_003410.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF345.

[40281] Zinc finger protein 398 (ZNF398, Accession NP_065832.1) is another GAM1338 target gene, herein designated TARGET GENE. ZNF398 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ZNF398, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of ZNF398 BINDING SITE, designated SEQ ID:9774, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40282] Another function of GAM1338 is therefore inhibition of Zinc finger protein 398 (ZNF398, Accession NP_065832.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF398.

[40283] ZNF432 (Accession NP_055465.1) is another GAM1338 target gene, herein designated TARGET GENE. ZNF432 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF432, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF432 BINDING SITE, designated SEQ ID:7826, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40284] Another function of GAM1338 is therefore inhibition of ZNF432 (Accession NP_055465.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

ZNF432.

[40285] ZNF440 (Accession NP_689570.1) is another GAM1338 target gene, herein designated TARGET GENE. ZNF440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF440 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40286] Another function of GAM1338 is therefore inhibition of ZNF440 (Accession NP_689570.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF440.

[40287] Zinc finger protein 70 (cos17) (ZNF70, Accession NP_852101.1) is another GAM1338 target gene, herein designated TARGET GENE. ZNF70 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZNF70, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates

the complementarity of the nucleotide sequences of ZNF70 BINDING SITE, designated SEQ ID:18371, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40288] Another function of GAM1338 is therefore inhibition of Zinc finger protein 70 (cos17) (ZNF70, Accession NP_852101.1) . Accordingly, utilities of GAM1338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF70.

[40289] Zinc finger protein 70 (cos17) (ZNF70, Accession NP_068735.1) is another GAM1338 target gene, herein designated TARGET GENE. ZNF70 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZNF70, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF70 BINDING SITE, designated SEQ ID:18371, to the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, also designated SEQ ID:360.

[40290] Another function of GAM1338 is therefore inhibition of Zinc finger protein 70 (cos17) (ZNF70, Accession NP_068735.1) . Accordingly, utilities of GAM1338 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF70.

[40291]

[40292] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 2033 (GAM2033), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[40293] GAM2033 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2033 was detected is described hereinabove with reference to Figs. 8-15.

[40294] GAM2033 gene, herein designated GAM GENE, and GAM2033 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[40295] GAM2033 gene encodes a GAM2033 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2033 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2033 precursor RNA is designated SEQ ID:117, and is provided hereinbelow with reference to the

sequence listing part.

[40296] GAM2033 precursor RNA folds onto itself, forming GAM2033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[40297] GAM2033 precursor RNA folds onto itself, forming GAM2033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[40298] Nucleotide sequence of GAM2033 precursor RNA, designated SEQ-ID: 117, and a schematic representation of a predicted secondary folding of GAM2033 folded precursor RNA are further described with reference to Table 2,

hereby incorporated by reference.

[40299] An enzyme complex designated DICER COMPLEX, `dices` the GAM2033 folded precursor RNA into GAM2033 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM2033 RNA is designated SEQ ID:305, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[40300] GAM2033 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM2033 target RNA, herein designated GAM TARGET RNA. GAM2033 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[40301] GAM2033 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2033 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2033 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2033 RNA may have a different number of target binding sites in untranslated regions of a GAM2033 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[40302] The complementary binding of GAM2033 RNA, herein designated GAM RNA, to target binding sites on GAM2033 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2033 target RNA into GAM2033 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[40303] It is appreciated that GAM2033 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM2033 target genes. The mRNA of each one of this plurality of GAM2033 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2033 RNA, herein designated GAM RNA, and which when bound by GAM2033 RNA causes inhibition of translation of respective one or more GAM2033 target proteins.

[40304] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2033 gene, herein designated GAM GENE, on one or more GAM2033 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[40305] It is appreciated that specific functions and accordingly utilities of GAM2033 correlate with, and may be deduced from, the identity of the target genes which GAM2033 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[40306]

[40307]

[40308] AGS3 (Accession XP_054763.1) is a GAM2033 target gene, herein designated TARGET GENE. AGS3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by AGS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGS3 BINDING SITE, designated SEQ ID:749, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40309] A function of GAM2033 is therefore inhibition of AGS3 (Accession XP_054763.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with AGS3.

[40310] Adenylate kinase 5 (AK5, Accession NP_036225.2) is another GAM2033 target gene, herein designated TARGET GENE. AK5 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by AK5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AK5 BINDING SITE, designated SEQ ID:8265, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40311] Another function of GAM2033 is therefore inhibition of Adenylate kinase 5 (AK5, Accession NP_036225.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AK5.

[40312] Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3, Accession NP_055864.1) is another GAM2033 target gene, herein designated TARGET GENE. ALS2CR3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALS2CR3, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALS2CR3 BINDING SITE, designated SEQ ID:735, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40313] Another function of GAM2033 is therefore inhibition of Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3, Accession NP_055864.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALS2CR3.

[40314] Angiopoietin 1 (ANGPT1, Accession NP_001137.2) is another GAM2033 target gene, herein designated TARGET GENE. ANGPT1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ANGPT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANGPT1 BINDING SITE, designated SEQ ID:19390, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40315] Another function of GAM2033 is therefore inhibition of

Angiopoietin 1 (ANGPT1, Accession NP_001137.2), a gene which binds and activates tie2 receptor by inducing its tyrosine phosphorylation. and therefore may be associated with Tumor. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of Tumor., and of other diseases and clinical conditions associated with ANGPT1.

[40316] The function of ANGPT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.2.Angiopoietin 1 (ANGPT1, Accession NP_647451.1) is another GAM2033 target gene, herein designated TARGET GENE. ANGPT1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ANGPT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANGPT1 BINDING SITE, designated SEQ ID:19390, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40317] Another function of GAM2033 is therefore inhibition of Angiopoietin 1 (ANGPT1, Accession NP_647451.1), a gene which binds and activates tie2 receptor by inducing its ty-

rosine phosphorylation. and therefore may be associated with Tumor. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of Tumor., and of other diseases and clinical conditions associated with ANGPT1.

[40318] The function of ANGPT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM205.2.ANKFY1 (Accession NP_057460.2) is another GAM2033 target gene, herein designated TARGET GENE. ANKFY1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ANKFY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANKFY1 BINDING SITE, designated SEQ ID:1403, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40319] Another function of GAM2033 is therefore inhibition of ANKFY1 (Accession NP_057460.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKFY1.

[40320] Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1) is another GAM2033 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:1506, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40321] Another function of GAM2033 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[40322] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Aquaporin 6, kidney specific (AQP6, Acces-

sion NP_445738.1) is another GAM2033 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:1506, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40323] Another function of GAM2033 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[40324] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.B7-H4 (Accession NP_078902.1) is another GAM2033 target gene, herein designated TARGET GENE.

B7-H4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B7-H4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B7-H4 BINDING SITE, designated SEQ ID:13436, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40325] Another function of GAM2033 is therefore inhibition of B7-H4 (Accession NP_078902.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B7-H4.

[40326] Breast carcinoma amplified sequence 1 (BCAS1, Accession NP_003648.1) is another GAM2033 target gene, herein designated TARGET GENE. BCAS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCAS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCAS1 BINDING SITE, designated SEQ ID:8961, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40327] Another function of GAM2033 is therefore inhibition of Breast carcinoma amplified sequence 1 (BCAS1, Accession NP_003648.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCAS1.

[40328] Basic, immunoglobulin-like variable motif containing (BIVM, Accession NP_060163.2) is another GAM2033 target gene, herein designated TARGET GENE. BIVM BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BIVM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BIVM BINDING SITE, designated SEQ ID:19466, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40329] Another function of GAM2033 is therefore inhibition of Basic, immunoglobulin-like variable motif containing (BIVM, Accession NP_060163.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIVM.

[40330] C13orf17 (Accession NP_060655.1) is another GAM2033 target gene, herein designated TARGET GENE. C13orf17

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C13orf17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C13orf17 BINDING SITE, designated SEQ ID:5972, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40331] Another function of GAM2033 is therefore inhibition of C13orf17 (Accession NP_060655.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C13orf17.

[40332] Chromosome 20 open reading frame 110 (C20orf110, Accession XP_086728.2) is another GAM2033 target gene, herein designated TARGET GENE. C20orf110 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf110, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf110 BINDING SITE, designated SEQ ID:2658, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA,

also designated SEQ ID:305.

[40333] Another function of GAM2033 is therefore inhibition of Chromosome 20 open reading frame 110 (C20orf110, Accession XP_086728.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf110.

[40334] Chromosome 2 open reading frame 7 (C2orf7, Accession NP_115695.1) is another GAM2033 target gene, herein designated TARGET GENE. C2orf7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C2orf7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C2orf7 BINDING SITE, designated SEQ ID:7328, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40335] Another function of GAM2033 is therefore inhibition of Chromosome 2 open reading frame 7 (C2orf7, Accession NP_115695.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C2orf7.

[40336] C6orf69 (Accession NP_775833.1) is another GAM2033

target gene, herein designated TARGET GENE. C6orf69 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf69, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf69 BINDING SITE, designated SEQ ID:2839, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40337] Another function of GAM2033 is therefore inhibition of C6orf69 (Accession NP_775833.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf69.

[40338] C6orf76 (Accession NP_079083.1) is another GAM2033 target gene, herein designated TARGET GENE. C6orf76 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf76, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf76 BINDING SITE, designated SEQ ID:6766, to the nucleotide sequence of GAM2033 RNA, herein designated

GAM RNA, also designated SEQ ID:305.

[40339] Another function of GAM2033 is therefore inhibition of C6orf76 (Accession NP_079083.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf76.

[40340] Reserved (C8orf6, Accession NP_663631.1) is another GAM2033 target gene, herein designated TARGET GENE. C8orf6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C8orf6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C8orf6 BINDING SITE, designated SEQ ID:2293, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40341] Another function of GAM2033 is therefore inhibition of Reserved (C8orf6, Accession NP_663631.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf6.

[40342] Cas-br-m (murine) ecotropic retroviral transforming sequence (CBL, Accession NP_005179.1) is another

GAM2033 target gene, herein designated TARGET GENE. CBL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CBL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CBL BINDING SITE, designated SEQ ID:1024, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40343] Another function of GAM2033 is therefore inhibition of Cas-br-m (murine) ecotropic retroviral transforming sequence (CBL, Accession NP_005179.1), a gene which may modify receptor tyrosine kinase- mediated signal transduction. and therefore may be associated with B- lineage lymphomas. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of B- lineage lymphomas., and of other diseases and clinical conditions associated with CBL.

[40344] The function of CBL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM767.1.Chromobox homolog 8 (pc class homolog, drosophila) (CBX8, Accession NP_065700.1) is another

GAM2033 target gene, herein designated TARGET GENE. CBX8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CBX8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CBX8 BINDING SITE, designated SEQ ID:14537, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40345] Another function of GAM2033 is therefore inhibition of Chromobox homolog 8 (pc class homolog, drosophila) (CBX8, Accession NP_065700.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBX8.

[40346] Cholecystokinin a receptor (CCKAR, Accession NP_000721.1) is another GAM2033 target gene, herein designated TARGET GENE. CCKAR BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CCKAR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCKAR BINDING SITE, designated SEQ ID:7362, to the nucleotide sequence of GAM2033

RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40347] Another function of GAM2033 is therefore inhibition of Cholecystokinin a receptor (CCKAR, Accession NP_000721.1), a gene which Cholecystokinin A receptor, a G protein- coupled receptor; regulates gallbladder contraction and secretion of pancreatic enzymes. and therefore may be associated with Diabetes and obesity. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of Diabetes and obesity., and of other diseases and clinical conditions associated with CCKAR.

[40348] The function of CCKAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.1.Cd8 antigen, beta polypeptide 1 (p37) (CD8B1, Accession NP_742097.1) is another GAM2033 target gene, herein designated TARGET GENE. CD8B1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CD8B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD8B1 BINDING SITE, designated

SEQ ID:16062, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40349] Another function of GAM2033 is therefore inhibition of Cd8 antigen, beta polypeptide 1 (p37) (CD8B1, Accession NP_742097.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD8B1.

[40350] Cd8 antigen, beta polypeptide 1 (p37) (CD8B1, Accession NP_004922.1) is another GAM2033 target gene, herein designated TARGET GENE. CD8B1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CD8B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD8B1 BINDING SITE, designated SEQ ID:16062, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40351] Another function of GAM2033 is therefore inhibition of Cd8 antigen, beta polypeptide 1 (p37) (CD8B1, Accession NP_004922.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with CD8B1.

[40352] Cadherin 3, type 1, p-cadherin (placental) (CDH3, Accession NP_001784.2) is another GAM2033 target gene, herein designated TARGET GENE. CDH3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDH3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH3 BINDING SITE, designated SEQ ID:19023, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40353] Another function of GAM2033 is therefore inhibition of Cadherin 3, type 1, p-cadherin (placental) (CDH3, Accession NP_001784.2), a gene which is a calcium dependent cell adhesion protein. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH3.

[40354] The function of CDH3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM385.2.Cadherin 6, type 2, k-cadherin (fetal kidney) (CDH6, Accession NP_004923.1) is another GAM2033 tar-

get gene, herein designated TARGET GENE. CDH6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CDH6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH6 BINDING SITE, designated SEQ ID:19553, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40355] Another function of GAM2033 is therefore inhibition of Cadherin 6, type 2, k-cadherin (fetal kidney) (CDH6, Accession NP_004923.1), a gene which is a calcium dependent cell adhesion protein. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH6.

[40356] The function of CDH6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.2.CG012 (Accession XP_096710.1) is another GAM2033 target gene, herein designated TARGET GENE. CG012 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CG012, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CG012 BINDING SITE, designated SEQ ID:7096, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40357] Another function of GAM2033 is therefore inhibition of CG012 (Accession XP_096710.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CG012.

[40358] CGI-19 (Accession NP_057032.2) is another GAM2033 target gene, herein designated TARGET GENE. CGI-19 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CGI-19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-19 BINDING SITE, designated SEQ ID:12830, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40359] Another function of GAM2033 is therefore inhibition of CGI-19 (Accession NP_057032.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-19.

[40360] CGI-37 (Accession NP_057185.1) is another GAM2033 target gene, herein designated TARGET GENE. CGI-37 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CGI-37, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-37 BINDING SITE, designated SEQ ID:13579, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40361] Another function of GAM2033 is therefore inhibition of CGI-37 (Accession NP_057185.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-37.

[40362] Claudin 14 (CLDN14, Accession NP_652763.1) is another GAM2033 target gene, herein designated TARGET GENE. CLDN14 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CLDN14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLDN14 BINDING SITE, designated SEQ ID:13780, to the nucleotide sequence of

GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40363] Another function of GAM2033 is therefore inhibition of Claudin 14 (CLDN14, Accession NP_652763.1), a gene which provides structural support for the auditory neuroepithelium. and therefore is associated with Deafness. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of Deafness., and of other diseases and clinical conditions associated with CLDN14.

[40364] The function of CLDN14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Contactin 5 (CNTN5, Accession NP_055176.1) is another GAM2033 target gene, herein designated TARGET GENE. CNTN5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CNTN5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNTN5 BINDING SITE, designated SEQ ID:14059, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40365] Another function of GAM2033 is therefore inhibition of Contactin 5 (CNTN5, Accession NP_055176.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNTN5.

[40366] Contactin 5 (CNTN5, Accession NP_780775.1) is another GAM2033 target gene, herein designated TARGET GENE. CNTN5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CNTN5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNTN5 BINDING SITE, designated SEQ ID:14059, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40367] Another function of GAM2033 is therefore inhibition of Contactin 5 (CNTN5, Accession NP_780775.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNTN5.

[40368] Dihydrolipoamide branched chain transacylase (e2 component of branched chain keto acid dehydrogenase com-

plex; maple syrup urine disease) (DBT, Accession NP_001909.1) is another GAM2033 target gene, herein designated TARGET GENE. DBT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DBT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DBT BINDING SITE, designated SEQ ID:4072, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40369] Another function of GAM2033 is therefore inhibition of Dihydrolipoamide branched chain transacylase (e2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) (DBT, Accession NP_001909.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBT.

[40370] Doublecortin and cam kinase-like 1 (DCAMKL1, Accession NP_004725.1) is another GAM2033 target gene, herein designated TARGET GENE. DCAMKL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DCAMKL1, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCAMKL1 BINDING SITE, designated SEQ ID:17620, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40371] Another function of GAM2033 is therefore inhibition of Doublecortin and cam kinase-like 1 (DCAMKL1, Accession NP_004725.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCAMKL1.

[40372] DKFZp434F1719 (Accession NP_115624.1) is another GAM2033 target gene, herein designated TARGET GENE. DKFZp434F1719 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434F1719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434F1719 BINDING SITE, designated SEQ ID:12168, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40373] Another function of GAM2033 is therefore inhibition of

DKFZp434F1719 (Accession NP_115624.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434F1719.

[40374] DKFZp434H247 (Accession XP_290829.1) is another GAM2033 target gene, herein designated TARGET GENE. DKFZp434H247 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434H247, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434H247 BINDING SITE, designated SEQ ID:5311, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40375] Another function of GAM2033 is therefore inhibition of DKFZp434H247 (Accession XP_290829.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434H247.

[40376] DKFZP566M114 (Accession NP_115504.1) is another GAM2033 target gene, herein designated TARGET GENE. DKFZP566M114 BINDING SITE is a target binding site

found in the 5` untranslated region of mRNA encoded by DKFZP566M114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566M114 BINDING SITE, designated SEQ ID:4512, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40377] Another function of GAM2033 is therefore inhibition of DKFZP566M114 (Accession NP_115504.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566M114.

[40378] DPCR1 (Accession NP_543146.1) is another GAM2033 target gene, herein designated TARGET GENE. DPCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DPCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DPCR1 BINDING SITE, designated SEQ ID:18332, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40379] Another function of GAM2033 is therefore inhibition of DPCR1 (Accession NP_543146.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPCR1.

[40380] Eh-domain containing 3 (EHD3, Accession NP_055415.1) is another GAM2033 target gene, herein designated TARGET GENE. EHD3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EHD3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EHD3 BINDING SITE, designated SEQ ID:11360, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40381] Another function of GAM2033 is therefore inhibition of Eh-domain containing 3 (EHD3, Accession NP_055415.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHD3.

[40382] V-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) (ERBB3, Accession NP_001973.1) is another GAM2033 target gene, herein designated TARGET GENE. ERBB3 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by ERBB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ERBB3 BINDING SITE, designated SEQ ID:2087, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40383] Another function of GAM2033 is therefore inhibition of V-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) (ERBB3, Accession NP_001973.1), a gene which binds and is activated by neuregulins and ntak. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERBB3.

[40384] The function of ERBB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.ERdj5 (Accession NP_061854.1) is another GAM2033 target gene, herein designated TARGET GENE. ERdj5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ERdj5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of ERdj5 BINDING SITE, designated SEQ ID:7721, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40385] Another function of GAM2033 is therefore inhibition of ERdj5 (Accession NP_061854.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERdj5.

[40386] Estrogen-related receptor beta (ESRRB, Accession NP_004443.2) is another GAM2033 target gene, herein designated TARGET GENE. ESRRB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ESRRB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ESRRB BINDING SITE, designated SEQ ID:8932, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40387] Another function of GAM2033 is therefore inhibition of Estrogen-related receptor beta (ESRRB, Accession NP_004443.2), a gene which Estrogen- related receptor beta; member of the nuclear hormone receptor family.

Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESRRB.

[40388] The function of ESRRB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM607.2.F-box and leucine-rich repeat protein 7 (FBXL7, Accession NP_036436.1) is another GAM2033 target gene, herein designated TARGET GENE. FBXL7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FBXL7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXL7 BINDING SITE, designated SEQ ID:3073, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40389] Another function of GAM2033 is therefore inhibition of F-box and leucine-rich repeat protein 7 (FBXL7, Accession NP_036436.1), a gene which may be involved in in phosphorylation- dependent ubiquitination. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FBXL7.

[40390] The function of FBXL7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.FLJ10618 (Accession NP_060625.1) is another GAM2033 target gene, herein designated TARGET GENE. FLJ10618 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10618, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10618 BINDING SITE, designated SEQ ID:12018, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40391] Another function of GAM2033 is therefore inhibition of FLJ10618 (Accession NP_060625.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10618.

[40392] FLJ10916 (Accession NP_060741.1) is another GAM2033 target gene, herein designated TARGET GENE. FLJ10916 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by FLJ10916, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10916 BINDING SITE, designated SEQ ID:976, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40393] Another function of GAM2033 is therefore inhibition of FLJ10916 (Accession NP_060741.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10916.

[40394] FLJ10996 (Accession NP_061917.2) is another GAM2033 target gene, herein designated TARGET GENE. FLJ10996 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10996, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10996 BINDING SITE, designated SEQ ID:12447, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40395] Another function of GAM2033 is therefore inhibition of

FLJ10996 (Accession NP_061917.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10996.

[40396] FLJ11565 (Accession NP_078933.2) is another GAM2033 target gene, herein designated TARGET GENE. FLJ11565 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11565, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11565 BINDING SITE, designated SEQ ID:7659, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40397] Another function of GAM2033 is therefore inhibition of FLJ11565 (Accession NP_078933.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11565.

[40398] FLJ13491 (Accession NP_078899.1) is another GAM2033 target gene, herein designated TARGET GENE. FLJ13491 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13491, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13491 BINDING SITE, designated SEQ ID:8459, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40399] Another function of GAM2033 is therefore inhibition of FLJ13491 (Accession NP_078899.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13491.

[40400] FLJ14167 (Accession XP_042704.1) is another GAM2033 target gene, herein designated TARGET GENE. FLJ14167 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14167 BINDING SITE, designated SEQ ID:3447, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40401] Another function of GAM2033 is therefore inhibition of FLJ14167 (Accession XP_042704.1) . Accordingly, utilities

of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14167.

[40402] FLJ14260 (Accession NP_079303.2) is another GAM2033 target gene, herein designated TARGET GENE. FLJ14260 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ14260, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14260 BINDING SITE, designated SEQ ID:18009, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40403] Another function of GAM2033 is therefore inhibition of FLJ14260 (Accession NP_079303.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14260.

[40404] FLJ14442 (Accession NP_116174.1) is another GAM2033 target gene, herein designated TARGET GENE. FLJ14442 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14442, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14442 BINDING SITE, designated SEQ ID:7173, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40405] Another function of GAM2033 is therefore inhibition of FLJ14442 (Accession NP_116174.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14442.

[40406] FLJ14871 (Accession NP_116243.1) is another GAM2033 target gene, herein designated TARGET GENE. FLJ14871 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14871, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14871 BINDING SITE, designated SEQ ID:13495, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40407] Another function of GAM2033 is therefore inhibition of FLJ14871 (Accession NP_116243.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ14871.

[40408] FLJ20139 (Accession NP_060155.1) is another GAM2033 target gene, herein designated TARGET GENE. FLJ20139 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20139, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20139 BINDING SITE, designated SEQ ID:12404, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40409] Another function of GAM2033 is therefore inhibition of FLJ20139 (Accession NP_060155.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20139.

[40410] FLJ20232 (Accession NP_061881.2) is another GAM2033 target gene, herein designated TARGET GENE. FLJ20232 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20232, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ20232 BINDING SITE, designated SEQ ID:17612, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40411] Another function of GAM2033 is therefore inhibition of FLJ20232 (Accession NP_061881.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20232.

[40412] FLJ20625 (Accession NP_060377.1) is another GAM2033 target gene, herein designated TARGET GENE. FLJ20625 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20625, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20625 BINDING SITE, designated SEQ ID:9074, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40413] Another function of GAM2033 is therefore inhibition of FLJ20625 (Accession NP_060377.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20625.

[40414] FLJ23309 (Accession XP_291315.1) is another GAM2033 target gene, herein designated TARGET GENE. FLJ23309 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23309, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23309 BINDING SITE, designated SEQ ID:19596, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40415] Another function of GAM2033 is therefore inhibition of FLJ23309 (Accession XP_291315.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23309.

[40416] FLJ31951 (Accession NP_653327.1) is another GAM2033 target gene, herein designated TARGET GENE. FLJ31951 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31951, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ31951 BINDING SITE, designated SEQ ID:18405, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40417] Another function of GAM2033 is therefore inhibition of FLJ31951 (Accession NP_653327.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31951.

[40418] GALNACT-2 (Accession NP_061060.3) is another GAM2033 target gene, herein designated TARGET GENE. GALNACT-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GALNACT-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GALNACT-2 BINDING SITE, designated SEQ ID:14291, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40419] Another function of GAM2033 is therefore inhibition of GALNACT-2 (Accession NP_061060.3) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

GALNACT-2.

[40420] Gata binding protein 5 (GATA5, Accession NP_536721.1) is another GAM2033 target gene, herein designated TARGET GENE. GATA5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GATA5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GATA5 BINDING SITE, designated SEQ ID:18782, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40421] Another function of GAM2033 is therefore inhibition of Gata binding protein 5 (GATA5, Accession NP_536721.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GATA5.

[40422] Glia maturation factor, beta (GMFB, Accession NP_004115.1) is another GAM2033 target gene, herein designated TARGET GENE. GMFB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GMFB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GMFB BINDING SITE, designated SEQ ID:7743, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40423] Another function of GAM2033 is therefore inhibition of Glia maturation factor, beta (GMFB, Accession NP_004115.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GMFB.

[40424] Guanine nucleotide binding protein (g protein), beta polypeptide 1 (GNB1, Accession NP_002065.1) is another GAM2033 target gene, herein designated TARGET GENE. GNB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GNB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNB1 BINDING SITE, designated SEQ ID:18436, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40425] Another function of GAM2033 is therefore inhibition of Guanine nucleotide binding protein (g protein), beta

polypeptide 1 (GNB1, Accession NP_002065.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNB1.

[40426] Glutamate receptor, ionotropic, n-methyl d-aspartate 2b (GRIN2B, Accession NP_000825.1) is another GAM2033 target gene, herein designated TARGET GENE. GRIN2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRIN2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRIN2B BINDING SITE, designated SEQ ID:13520, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40427] Another function of GAM2033 is therefore inhibition of Glutamate receptor, ionotropic, n-methyl d-aspartate 2b (GRIN2B, Accession NP_000825.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIN2B.

[40428] General transcription factor iie, polypeptide 1, alpha 56kda (GTF2E1, Accession NP_005504.1) is another

GAM2033 target gene, herein designated TARGET GENE. GTF2E1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GTF2E1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2E1 BINDING SITE, designated SEQ ID:994, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40429] Another function of GAM2033 is therefore inhibition of General transcription factor iie, polypeptide 1, alpha 56kda (GTF2E1, Accession NP_005504.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2E1.

[40430] Host cell factor c1 (vp16-accessory protein) (HCFC1, Accession NP_005325.1) is another GAM2033 target gene, herein designated TARGET GENE. HCFC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HCFC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HCFC1 BINDING

SITE, designated SEQ ID:18043, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40431] Another function of GAM2033 is therefore inhibition of Host cell factor c1 (vp16-accessory protein) (HCFC1, Accession NP_005325.1), a gene which is a host cell factor, has a role in cell proliferation and can form a complex with HSV VP16. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCFC1.

[40432] The function of HCFC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM385.2.Hexokinase 2 (HK2, Accession NP_000180.2) is another GAM2033 target gene, herein designated TARGET GENE. HK2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HK2 BINDING SITE, designated SEQ ID:11683, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ

ID:305.

[40433] Another function of GAM2033 is therefore inhibition of Hexokinase 2 (HK2, Accession NP_000180.2), a gene which plays an important role in intracellular glucose metabolism by catalyzing the conversion of glucose to glucose- 6- phosphate. and therefore may be associated with Noninsulin- dependent diabetes mellitus . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of Noninsulin- dependent diabetes mellitus ., and of other diseases and clinical conditions associated with HK2.

[40434] The function of HK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1664.1.Homeo box c4 (HOXC4, Accession NP_055435.2) is another GAM2033 target gene, herein designated TARGET GENE. HOXC4 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by HOXC4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HOXC4 BINDING SITE, designated SEQ ID:19800, to the

nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40435] Another function of GAM2033 is therefore inhibition of Homeo box c4 (HOXC4, Accession NP_055435.2), a gene which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior- posterior axis. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXC4.

[40436] The function of HOXC4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Homeo box c6 (HOXC6, Accession NP_710160.1) is another GAM2033 target gene, herein designated TARGET GENE. HOXC6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by HOXC6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HOXC6 BINDING SITE, designated SEQ ID:19800, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40437] Another function of GAM2033 is therefore inhibition of Homeo box c6 (HOXC6, Accession NP_710160.1), a gene which is part of a developmental regulatory system. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXC6.

[40438] The function of HOXC6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Harakiri, bcl2 interacting protein (contains only bh3 domain) (HRK, Accession NP_003797.1) is another GAM2033 target gene, herein designated TARGET GENE. HRK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HRK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HRK BINDING SITE, designated SEQ ID:11032, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40439] Another function of GAM2033 is therefore inhibition of Harakiri, bcl2 interacting protein (contains only bh3 domain) (HRK, Accession NP_003797.1) . Accordingly, utili-

ties of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRK.

[40440] Heat shock 70kda protein 9b (mortalin-2) (HSPA9B, Accession NP_004125.3) is another GAM2033 target gene, herein designated TARGET GENE. HSPA9B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSPA9B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPA9B BINDING SITE, designated SEQ ID:9911, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40441] Another function of GAM2033 is therefore inhibition of Heat shock 70kda protein 9b (mortalin-2) (HSPA9B, Accession NP_004125.3) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPA9B.

[40442] Inhibin, beta a (activin a, activin ab alpha polypeptide) (INHBA, Accession NP_002183.1) is another GAM2033 target gene, herein designated TARGET GENE. INHBA BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by INHBA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INHBA BINDING SITE, designated SEQ ID:18996, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40443] Another function of GAM2033 is therefore inhibition of Inhibin, beta a (activin a, activin ab alpha polypeptide) (INHBA, Accession NP_002183.1), a gene which inhibit respectively the secretion of follitropin by the pituitary gland. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INHBA.

[40444] The function of INHBA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1033.2.Potassium voltage-gated channel, shaker-related subfamily, member 7 (KCNA7, Accession NP_114092.2) is another GAM2033 target gene, herein designated TARGET GENE. KCNA7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KCNA7, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNA7 BINDING SITE, designated SEQ ID:8004, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40445] Another function of GAM2033 is therefore inhibition of Potassium voltage-gated channel, shaker-related subfamily, member 7 (KCNA7, Accession NP_114092.2), a gene which allows nerve cells to efficiently repolarize following an action potential. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNA7.

[40446] The function of KCNA7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.KIAA0711 (Accession NP_055682.1) is another GAM2033 target gene, herein designated TARGET GENE. KIAA0711 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0711, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of KIAA0711 BINDING SITE, designated SEQ ID:10051, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40447] Another function of GAM2033 is therefore inhibition of KIAA0711 (Accession NP_055682.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0711.

[40448] KIAA1237 (Accession XP_087386.3) is another GAM2033 target gene, herein designated TARGET GENE. KIAA1237 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1237, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1237 BINDING SITE, designated SEQ ID:17086, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40449] Another function of GAM2033 is therefore inhibition of KIAA1237 (Accession XP_087386.3) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1237.

[40450] KIAA1240 (Accession XP_039676.1) is another GAM2033 target gene, herein designated TARGET GENE. KIAA1240 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1240, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1240 BINDING SITE, designated SEQ ID:3069, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40451] Another function of GAM2033 is therefore inhibition of KIAA1240 (Accession XP_039676.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1240.

[40452] KIAA1399 (Accession XP_046685.4) is another GAM2033 target gene, herein designated TARGET GENE. KIAA1399 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1399, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1399 BINDING SITE, designated SEQ ID:18176, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40453] Another function of GAM2033 is therefore inhibition of KIAA1399 (Accession XP_046685.4) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1399.

[40454] KIAA1518 (Accession NP_056308.2) is another GAM2033 target gene, herein designated TARGET GENE. KIAA1518 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA1518, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1518 BINDING SITE, designated SEQ ID:1300, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40455] Another function of GAM2033 is therefore inhibition of KIAA1518 (Accession NP_056308.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1518.

[40456] KIAA1706 (Accession NP_085139.1) is another GAM2033 target gene, herein designated TARGET GENE. KIAA1706 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1706, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1706 BINDING SITE, designated SEQ ID:17708, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40457] Another function of GAM2033 is therefore inhibition of KIAA1706 (Accession NP_085139.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1706.

[40458] KIAA1728 (Accession XP_043492.2) is another GAM2033 target gene, herein designated TARGET GENE. KIAA1728 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1728, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1728 BINDING SITE, designated SEQ ID:6209, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40459] Another function of GAM2033 is therefore inhibition of KIAA1728 (Accession XP_043492.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1728.

[40460] Laminin, gamma 2 (LAMC2, Accession NP_061486.1) is another GAM2033 target gene, herein designated TARGET GENE. LAMC2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LAMC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMC2 BINDING SITE, designated SEQ ID:15830, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40461] Another function of GAM2033 is therefore inhibition of Laminin, gamma 2 (LAMC2, Accession NP_061486.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with LAMC2.

[40462] LOC116228 (Accession XP_300752.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC116228 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC116228, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC116228 BINDING SITE, designated SEQ ID:878, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40463] Another function of GAM2033 is therefore inhibition of LOC116228 (Accession XP_300752.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116228.

[40464] LOC130026 (Accession NP_612477.3) is another GAM2033 target gene, herein designated TARGET GENE. LOC130026 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC130026, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130026 BINDING SITE, designated SEQ ID:9829, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40465] Another function of GAM2033 is therefore inhibition of LOC130026 (Accession NP_612477.3) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130026.

[40466] LOC143381 (Accession XP_084501.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC143381 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC143381, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143381 BINDING SITE, designated SEQ ID:8460, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40467] Another function of GAM2033 is therefore inhibition of LOC143381 (Accession XP_084501.1) . Accordingly, utili-

ties of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143381.

[40468] LOC146013 (Accession XP_096919.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC146013 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146013, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146013 BINDING SITE, designated SEQ ID:7781, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40469] Another function of GAM2033 is therefore inhibition of LOC146013 (Accession XP_096919.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146013.

[40470] LOC146599 (Accession XP_085517.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC146599 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC146599, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146599 BINDING SITE, designated SEQ ID:15848, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40471] Another function of GAM2033 is therefore inhibition of LOC146599 (Accession XP_085517.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146599.

[40472] LOC150311 (Accession XP_086858.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC150311 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150311, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150311 BINDING SITE, designated SEQ ID:6767, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40473] Another function of GAM2033 is therefore inhibition of LOC150311 (Accession XP_086858.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150311.

[40474] LOC150397 (Accession XP_086907.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC150397 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150397, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150397 BINDING SITE, designated SEQ ID:9075, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40475] Another function of GAM2033 is therefore inhibition of LOC150397 (Accession XP_086907.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150397.

[40476] LOC151636 (Accession NP_612144.1) is another GAM2033 target gene, herein designated TARGET GENE.

LOC151636 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151636, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151636 BINDING SITE, designated SEQ ID:18792, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40477] Another function of GAM2033 is therefore inhibition of LOC151636 (Accession NP_612144.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151636.

[40478] LOC152794 (Accession XP_087525.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC152794 BINDING SITE1 and LOC152794 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC152794, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152794 BINDING SITE1 and LOC152794 BINDING SITE2, desig-

nated SEQ ID:11273 and SEQ ID:13308 respectively, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40479] Another function of GAM2033 is therefore inhibition of LOC152794 (Accession XP_087525.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152794.

[40480] LOC153442 (Accession XP_098373.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC153442 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153442 BINDING SITE, designated SEQ ID:482, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40481] Another function of GAM2033 is therefore inhibition of LOC153442 (Accession XP_098373.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC153442.

[40482] LOC154222 (Accession XP_098497.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC154222 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC154222, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154222 BINDING SITE, designated SEQ ID:16834, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40483] Another function of GAM2033 is therefore inhibition of LOC154222 (Accession XP_098497.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154222.

[40484] LOC220038 (Accession XP_166257.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC220038 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC220038, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220038 BINDING SITE, designated SEQ ID:3435, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40485] Another function of GAM2033 is therefore inhibition of LOC220038 (Accession XP_166257.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220038.

[40486] LOC220739 (Accession XP_167548.3) is another GAM2033 target gene, herein designated TARGET GENE. LOC220739 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC220739, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220739 BINDING SITE, designated SEQ ID:4991, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40487] Another function of GAM2033 is therefore inhibition of LOC220739 (Accession XP_167548.3) . Accordingly, utili-

ties of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220739.

[40488] LOC221889 (Accession XP_166513.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC221889 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221889, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221889 BINDING SITE, designated SEQ ID:12817, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40489] Another function of GAM2033 is therefore inhibition of LOC221889 (Accession XP_166513.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221889.

[40490] LOC254826 (Accession XP_173188.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC254826 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC254826, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254826 BINDING SITE, designated SEQ ID:647, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40491] Another function of GAM2033 is therefore inhibition of LOC254826 (Accession XP_173188.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254826.

[40492] LOC283050 (Accession XP_210872.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC283050 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283050, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283050 BINDING SITE, designated SEQ ID:10331, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40493] Another function of GAM2033 is therefore inhibition of LOC283050 (Accession XP_210872.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283050.

[40494] LOC283386 (Accession XP_208656.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC283386 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283386, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283386 BINDING SITE, designated SEQ ID:6632, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40495] Another function of GAM2033 is therefore inhibition of LOC283386 (Accession XP_208656.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283386.

[40496] LOC283403 (Accession XP_211028.1) is another GAM2033 target gene, herein designated TARGET GENE.

LOC283403 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283403, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283403 BINDING SITE, designated SEQ ID:5737, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40497] Another function of GAM2033 is therefore inhibition of LOC283403 (Accession XP_211028.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283403.

[40498] LOC283452 (Accession XP_208679.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC283452 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283452 BINDING SITE, designated SEQ ID:10804, to the nucleotide sequence of

GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40499] Another function of GAM2033 is therefore inhibition of LOC283452 (Accession XP_208679.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283452.

[40500] LOC283588 (Accession NP_787093.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC283588 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283588, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283588 BINDING SITE, designated SEQ ID:1881, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40501] Another function of GAM2033 is therefore inhibition of LOC283588 (Accession NP_787093.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283588.

[40502] LOC283818 (Accession XP_211218.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC283818 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283818 BINDING SITE, designated SEQ ID:11219, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40503] Another function of GAM2033 is therefore inhibition of LOC283818 (Accession XP_211218.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283818.

[40504] LOC284117 (Accession XP_209024.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC284117 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284117 BINDING SITE, designated SEQ ID:3307, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40505] Another function of GAM2033 is therefore inhibition of LOC284117 (Accession XP_209024.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284117.

[40506] LOC284515 (Accession XP_208210.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC284515 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284515, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284515 BINDING SITE, designated SEQ ID:13346, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40507] Another function of GAM2033 is therefore inhibition of LOC284515 (Accession XP_208210.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284515.

[40508] LOC285123 (Accession XP_211773.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC285123 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285123, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285123 BINDING SITE, designated SEQ ID:18981, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40509] Another function of GAM2033 is therefore inhibition of LOC285123 (Accession XP_211773.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285123.

[40510] LOC285399 (Accession XP_211880.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC285399 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285399, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285399 BINDING SITE, designated SEQ ID:9690, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40511] Another function of GAM2033 is therefore inhibition of LOC285399 (Accession XP_211880.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285399.

[40512] LOC285735 (Accession XP_212002.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC285735 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285735 BINDING SITE, designated SEQ ID:11051, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40513] Another function of GAM2033 is therefore inhibition of

LOC285735 (Accession XP_212002.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285735.

[40514] LOC285805 (Accession XP_212027.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC285805 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285805, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285805 BINDING SITE, designated SEQ ID:16704, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40515] Another function of GAM2033 is therefore inhibition of LOC285805 (Accession XP_212027.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285805.

[40516] LOC285950 (Accession XP_212089.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC285950 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC285950, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285950 BINDING SITE, designated SEQ ID:19398, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40517] Another function of GAM2033 is therefore inhibition of LOC285950 (Accession XP_212089.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285950.

[40518] LOC286184 (Accession XP_212216.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC286184 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286184, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286184 BINDING SITE, designated SEQ ID:12741, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:305.

[40519] Another function of GAM2033 is therefore inhibition of LOC286184 (Accession XP_212216.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286184.

[40520] LOC286197 (Accession XP_209940.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC286197 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286197, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286197 BINDING SITE, designated SEQ ID:17366, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40521] Another function of GAM2033 is therefore inhibition of LOC286197 (Accession XP_209940.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286197.

[40522] LOC286211 (Accession XP_209949.1) is another

GAM2033 target gene, herein designated TARGET GENE. LOC286211 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286211, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286211 BINDING SITE, designated SEQ ID:9029, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40523] Another function of GAM2033 is therefore inhibition of LOC286211 (Accession XP_209949.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286211.

[40524] LOC286438 (Accession XP_208421.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC286438 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286438, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286438 BINDING SITE, desig-

nated SEQ ID:14291, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40525] Another function of GAM2033 is therefore inhibition of LOC286438 (Accession XP_208421.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286438.

[40526] LOC339212 (Accession XP_290271.2) is another GAM2033 target gene, herein designated TARGET GENE. LOC339212 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339212, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339212 BINDING SITE, designated SEQ ID:19779, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40527] Another function of GAM2033 is therefore inhibition of LOC339212 (Accession XP_290271.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC339212.

[40528] LOC339414 (Accession XP_170914.2) is another GAM2033 target gene, herein designated TARGET GENE. LOC339414 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339414, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339414 BINDING SITE, designated SEQ ID:16199, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40529] Another function of GAM2033 is therefore inhibition of LOC339414 (Accession XP_170914.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339414.

[40530] LOC339846 (Accession XP_295084.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC339846 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339846, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339846 BINDING SITE, designated SEQ ID:1411, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40531] Another function of GAM2033 is therefore inhibition of LOC339846 (Accession XP_295084.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339846.

[40532] LOC339865 (Accession XP_295089.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC339865 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339865 BINDING SITE, designated SEQ ID:3018, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40533] Another function of GAM2033 is therefore inhibition of LOC339865 (Accession XP_295089.1) . Accordingly, utili-

ties of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339865.

[40534] LOC339894 (Accession XP_295095.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC339894 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339894 BINDING SITE, designated SEQ ID:3796, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40535] Another function of GAM2033 is therefore inhibition of LOC339894 (Accession XP_295095.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339894.

[40536] LOC339975 (Accession XP_295115.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC339975 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC339975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339975 BINDING SITE, designated SEQ ID:1577, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40537] Another function of GAM2033 is therefore inhibition of LOC339975 (Accession XP_295115.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339975.

[40538] LOC348259 (Accession XP_302702.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC348259 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348259, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348259 BINDING SITE, designated SEQ ID:562, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40539] Another function of GAM2033 is therefore inhibition of LOC348259 (Accession XP_302702.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348259.

[40540] LOC348442 (Accession XP_057659.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC348442 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348442 BINDING SITE, designated SEQ ID:878, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40541] Another function of GAM2033 is therefore inhibition of LOC348442 (Accession XP_057659.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348442.

[40542] LOC349059 (Accession XP_302946.1) is another GAM2033 target gene, herein designated TARGET GENE.

LOC349059 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349059, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349059 BINDING SITE, designated SEQ ID:16834, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40543] Another function of GAM2033 is therefore inhibition of LOC349059 (Accession XP_302946.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349059.

[40544] LOC83468 (Accession NP_112592.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC83468 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC83468, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC83468 BINDING SITE, designated SEQ ID:17323, to the nucleotide sequence of GAM2033 RNA, herein designated

GAM RNA, also designated SEQ ID:305.

[40545] Another function of GAM2033 is therefore inhibition of LOC83468 (Accession NP_112592.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC83468.

[40546] LOC84549 (Accession NP_115898.2) is another GAM2033 target gene, herein designated TARGET GENE. LOC84549 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC84549, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC84549 BINDING SITE, designated SEQ ID:19084, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40547] Another function of GAM2033 is therefore inhibition of LOC84549 (Accession NP_115898.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC84549.

[40548] LOC90110 (Accession XP_029046.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC90110

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC90110, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90110 BINDING SITE, designated SEQ ID:19624, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40549] Another function of GAM2033 is therefore inhibition of LOC90110 (Accession XP_029046.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90110.

[40550] LOC91565 (Accession XP_039231.1) is another GAM2033 target gene, herein designated TARGET GENE. LOC91565 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91565, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91565 BINDING SITE, designated SEQ ID:12984, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40551] Another function of GAM2033 is therefore inhibition of LOC91565 (Accession XP_039231.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91565.

[40552] LOC92235 (Accession XP_043739.2) is another GAM2033 target gene, herein designated TARGET GENE. LOC92235 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92235 BINDING SITE, designated SEQ ID:11714, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40553] Another function of GAM2033 is therefore inhibition of LOC92235 (Accession XP_043739.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92235.

[40554] Loss of heterozygosity, 11, chromosomal region 2, gene a (LOH11CR2A, Accession NP_055437.1) is another GAM2033 target gene, herein designated TARGET GENE.

LOH11CR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOH11CR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOH11CR2A BINDING SITE, designated SEQ ID:9708, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40555] Another function of GAM2033 is therefore inhibition of Loss of heterozygosity, 11, chromosomal region 2, gene a (LOH11CR2A, Accession NP_055437.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOH11CR2A.

[40556] LRP15 (Accession NP_443185.1) is another GAM2033 target gene, herein designated TARGET GENE. LRP15 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LRP15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LRP15 BINDING SITE, designated SEQ ID:18470, to the nucleotide

sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40557] Another function of GAM2033 is therefore inhibition of LRP15 (Accession NP_443185.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP15.

[40558] MGC10765 (Accession NP_077321.1) is another GAM2033 target gene, herein designated TARGET GENE. MGC10765 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10765, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10765 BINDING SITE, designated SEQ ID:4067, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40559] Another function of GAM2033 is therefore inhibition of MGC10765 (Accession NP_077321.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10765.

[40560] MGC13017 (Accession NP_542387.1) is another GAM2033 target gene, herein designated TARGET GENE. MGC13017

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13017 BINDING SITE, designated SEQ ID:878, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40561] Another function of GAM2033 is therefore inhibition of MGC13017 (Accession NP_542387.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13017.

[40562] MGC39662 (Accession NP_689607.1) is another GAM2033 target gene, herein designated TARGET GENE. MGC39662 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC39662, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC39662 BINDING SITE, designated SEQ ID:12535, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40563] Another function of GAM2033 is therefore inhibition of MGC39662 (Accession NP_689607.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC39662.

[40564] MGC46336 (Accession XP_290712.1) is another GAM2033 target gene, herein designated TARGET GENE. MGC46336 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC46336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC46336 BINDING SITE, designated SEQ ID:20034, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40565] Another function of GAM2033 is therefore inhibition of MGC46336 (Accession XP_290712.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC46336.

[40566] MGC46680 (Accession NP_776169.1) is another GAM2033 target gene, herein designated TARGET GENE. MGC46680 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC46680, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC46680 BINDING SITE, designated SEQ ID:3484, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40567] Another function of GAM2033 is therefore inhibition of MGC46680 (Accession NP_776169.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC46680.

[40568] Mov10, moloney leukemia virus 10, homolog (mouse) (MOV10, Accession NP_066014.1) is another GAM2033 target gene, herein designated TARGET GENE. MOV10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MOV10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MOV10 BINDING SITE, designated SEQ ID:13490, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40569] Another function of GAM2033 is therefore inhibition of Mov10, moloney leukemia virus 10, homolog (mouse) (MOV10, Accession NP_066014.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOV10.

[40570] Mitochondrial ribosomal protein s15 (MRPS15, Accession NP_112570.2) is another GAM2033 target gene, herein designated TARGET GENE. MRPS15 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MRPS15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPS15 BINDING SITE, designated SEQ ID:14750, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40571] Another function of GAM2033 is therefore inhibition of Mitochondrial ribosomal protein s15 (MRPS15, Accession NP_112570.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS15.

[40572] N-deacetylase/n-sulfotransferase (heparan glucosaminyl)

2 (NDST2, Accession NP_003626.1) is another GAM2033 target gene, herein designated TARGET GENE. NDST2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDST2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDST2 BINDING SITE, designated SEQ ID:17608, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40573] Another function of GAM2033 is therefore inhibition of N-deacetylase/n-sulfotransferase (heparan glucosaminyl) 2 (NDST2, Accession NP_003626.1), a gene which catalyses the n- sulfation and n- deacetylation of glucosamine of the glycosaminoglycan in heparin sulfate. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDST2.

[40574] The function of NDST2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM282.2.Nima (never in mitosis gene a)-related kinase 3 (NEK3, Accession NP_002489.1) is another

GAM2033 target gene, herein designated TARGET GENE. NEK3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NEK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEK3 BINDING SITE, designated SEQ ID:3534, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40575] Another function of GAM2033 is therefore inhibition of Nima (never in mitosis gene a)-related kinase 3 (NEK3, Accession NP_002489.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEK3.

[40576] Nima (never in mitosis gene a)-related kinase 3 (NEK3, Accession NP_689933.1) is another GAM2033 target gene, herein designated TARGET GENE. NEK3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NEK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

NEK3 BINDING SITE, designated SEQ ID:3534, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40577] Another function of GAM2033 is therefore inhibition of Nima (never in mitosis gene a)-related kinase 3 (NEK3, Accession NP_689933.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEK3.

[40578] Nescient helix loop helix 1 (NHLH1, Accession NP_005589.1) is another GAM2033 target gene, herein designated TARGET GENE. NHLH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NHLH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NHLH1 BINDING SITE, designated SEQ ID:2657, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40579] Another function of GAM2033 is therefore inhibition of Nescient helix loop helix 1 (NHLH1, Accession NP_005589.1), a gene which may have a role in development of the nervous system. Accordingly, utilities of

GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NHLH1.

[40580] The function of NHLH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.1.NYD-SP15 (Accession NP_112173.1) is another GAM2033 target gene, herein designated TARGET GENE. NYD-SP15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NYD-SP15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NYD-SP15 BINDING SITE, designated SEQ ID:12731, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40581] Another function of GAM2033 is therefore inhibition of NYD-SP15 (Accession NP_112173.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NYD-SP15.

[40582] Opiate receptor-like 1 (OPRL1, Accession NP_000904.1) is another GAM2033 target gene, herein designated TARGET

GENE. OPRL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by OPRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OPRL1 BINDING SITE, designated SEQ ID:6428, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40583] Another function of GAM2033 is therefore inhibition of Opiate receptor-like 1 (OPRL1, Accession NP_000904.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OPRL1.

[40584] OS4 (Accession NP_005721.2) is another GAM2033 target gene, herein designated TARGET GENE. OS4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OS4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OS4 BINDING SITE, designated SEQ ID:16829, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40585] Another function of GAM2033 is therefore inhibition of OS4 (Accession NP_005721.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OS4.

[40586] Pyrimidinergic receptor p2y, g-protein coupled, 6 (P2RY6, Accession NP_004145.1) is another GAM2033 target gene, herein designated TARGET GENE. P2RY6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by P2RY6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P2RY6 BINDING SITE, designated SEQ ID:999, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40587] Another function of GAM2033 is therefore inhibition of Pyrimidinergic receptor p2y, g-protein coupled, 6 (P2RY6, Accession NP_004145.1), a gene which mediates cellular responses to nucleotides. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RY6.

[40588] The function of P2RY6 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM72.1.Protocadherin 10 (PCDH10, Accession NP_116586.1) is another GAM2033 target gene, herein designated TARGET GENE. PCDH10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PCDH10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDH10 BINDING SITE, designated SEQ ID:12871, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40589] Another function of GAM2033 is therefore inhibition of Protocadherin 10 (PCDH10, Accession NP_116586.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH10.

[40590] Protocadherin 10 (PCDH10, Accession NP_065866.1) is another GAM2033 target gene, herein designated TARGET GENE. PCDH10 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PCDH10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDH10 BINDING SITE, designated SEQ ID:12871, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40591] Another function of GAM2033 is therefore inhibition of Protocadherin 10 (PCDH10, Accession NP_065866.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH10.

[40592] PJA2 (Accession NP_055634.1) is another GAM2033 target gene, herein designated TARGET GENE. PJA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PJA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PJA2 BINDING SITE, designated SEQ ID:8114, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40593] Another function of GAM2033 is therefore inhibition of PJA2 (Accession NP_055634.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with PJA2.

[40594] Peripheral myelin protein 2 (PMP2, Accession NP_002668.1) is another GAM2033 target gene, herein designated TARGET GENE. PMP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMP2 BINDING SITE, designated SEQ ID:3068, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40595] Another function of GAM2033 is therefore inhibition of Peripheral myelin protein 2 (PMP2, Accession NP_002668.1), a gene which is a lipid transport protein in schwann cells. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMP2.

[40596] The function of PMP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM402.1.Pou domain, class 2, associating factor 1 (POU2AF1, Accession NP_006226.1) is another GAM2033

target gene, herein designated TARGET GENE. POU2AF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POU2AF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POU2AF1 BINDING SITE, designated SEQ ID:17878, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40597] Another function of GAM2033 is therefore inhibition of Pou domain, class 2, associating factor 1 (POU2AF1, Accession NP_006226.1), a gene which is a transcriptional coactivator that specifically associates with either oct1 or oct2 and therefore may be associated with A form of b-cell leukemia. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of A form of b- cell leukemia, and of other diseases and clinical conditions associated with POU2AF1.

[40598] The function of POU2AF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Protein phosphatase 1, regulatory subunit 10 (PPP1R10, Accession NP_002705.2) is another GAM2033

target gene, herein designated TARGET GENE. PPP1R10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPP1R10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R10 BINDING SITE, designated SEQ ID:17303, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40599] Another function of GAM2033 is therefore inhibition of Protein phosphatase 1, regulatory subunit 10 (PPP1R10, Accession NP_002705.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R10.

[40600] Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) is another GAM2033 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE, designated

SEQ ID:18058, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40601] Another function of GAM2033 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[40602] Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_115288.1) is another GAM2033 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE, designated SEQ ID:18058, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40603] Another function of GAM2033 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b

(PPP1R12B, Accession NP_115288.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[40604] Rab13, member ras oncogene family (RAB13, Accession NP_002861.1) is another GAM2033 target gene, herein designated TARGET GENE. RAB13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB13 BINDING SITE, designated SEQ ID:5259, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40605] Another function of GAM2033 is therefore inhibition of Rab13, member ras oncogene family (RAB13, Accession NP_002861.1), a gene which is a member of the RAB family of small GTPases. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB13.

[40606] The function of RAB13 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM94.1.Rab7, member ras oncogene family-like 1 (RAB7L1, Accession NP_003920.1) is another GAM2033 target gene, herein designated TARGET GENE. RAB7L1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB7L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB7L1 BINDING SITE, designated SEQ ID:9099, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40607] Another function of GAM2033 is therefore inhibition of Rab7, member ras oncogene family-like 1 (RAB7L1, Accession NP_003920.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB7L1.

[40608] RBT1 (Accession NP_037500.2) is another GAM2033 target gene, herein designated TARGET GENE. RBT1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RBT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of RBT1 BINDING SITE, designated SEQ ID:11335, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40609] Another function of GAM2033 is therefore inhibition of RBT1 (Accession NP_037500.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBT1.

[40610] Rho-related btb domain containing 2 (RHOBTB2, Accession NP_055993.1) is another GAM2033 target gene, herein designated TARGET GENE. RHOBTB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RHOBTB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHOBTB2 BINDING SITE, designated SEQ ID:4604, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40611] Another function of GAM2033 is therefore inhibition of Rho-related btb domain containing 2 (RHOBTB2, Accession NP_055993.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with RHOBTB2.

[40612] Receptor tyrosine kinase-like orphan receptor 1 (ROR1, Accession NP_005003.1) is another GAM2033 target gene, herein designated TARGET GENE. ROR1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ROR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ROR1 BINDING SITE, designated SEQ ID:5888, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40613] Another function of GAM2033 is therefore inhibition of Receptor tyrosine kinase-like orphan receptor 1 (ROR1, Accession NP_005003.1), a gene which is of unknown function. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ROR1.

[40614] The function of ROR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM767.2.Reticulon 2 (RTN2, Accession NP_005610.1) is another GAM2033 target gene, herein designated TAR-

GET GENE. RTN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RTN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RTN2 BINDING SITE, designated SEQ ID:8997, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40615] Another function of GAM2033 is therefore inhibition of Reticulon 2 (RTN2, Accession NP_005610.1), a gene which is a member of the reticulon (neuroendocrine- specific, NSP) family. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RTN2.

[40616] The function of RTN2 has been established by previous studies. Roebroek et al. (1998) identified 3 novel homologs of RTN1 (OMIM Ref. No. 600865) in DNA sequence databases. RTN2 sequences were found in a 106- kb genomic region around the ERCC1 (OMIM Ref. No. 126380) locus sequenced by Martin- Gallardo et al. (1992); thus, the RTN2 gene is localized to human chromosome 19q13.3. The gene consists of 11 exons spanning approximately 12 kb. Northern blots of several cell lines

showed RTN2 expression as mRNAs of 1.3 and 2.3 kb. RT- PCR analysis demonstrated that these bands are produced by 3 alternatively spliced cDNA variants: RTN2A (545 amino acids), RTN2B (472 amino acids), and RTN2C (205 amino acids). Northern blot analysis of human tissues revealed that the RTN2 gene is expressed in a variety of tissues, with strikingly high expression of the 1.3- kb mRNA in skeletal muscle

[40617]

[40618] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[40619] Roebroek, A. J. M.; Contreras, B.; Pauli, I. G. L.; Van de Ven, W. J. M. : cDNA cloning, genomic organization, and expression of the human RTN2 gene, a member of a gene family encoding reticulons. Genomics 51: 98- 106, 1998. ; and

[40620] Martin- Gallardo, A.; McCombie, W. R.; Gocayne, J. D.; FitzGerald, M. G.; Wallace, S.; Lee, B. M. B.; Lamerdin, J.; Trapp, S.; Kelley, J. M.; Liu, L.- I.; Dubnick, M.; Johnston-Dow, L. A.; Ke.

[40621] Further studies establishing the function and utilities of RTN2 are found in John Hopkins OMIM database record ID

603183, and in cited publications listed in Table 5, which are hereby incorporated by reference.Splicing factor 3b, subunit 1, 155kda (SF3B1, Accession NP_036565.1) is another GAM2033 target gene, herein designated TARGET GENE. SF3B1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SF3B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SF3B1 BINDING SITE, designated SEQ ID:13074, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40622] Another function of GAM2033 is therefore inhibition of Splicing factor 3b, subunit 1, 155kda (SF3B1, Accession NP_036565.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SF3B1.

[40623] Surfactant, pulmonary-associated protein a2 (SFTPA2, Accession NP_008857.1) is another GAM2033 target gene, herein designated TARGET GENE. SFTPA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SFTPA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SFTPA2 BINDING SITE, designated SEQ ID:11609, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40624] Another function of GAM2033 is therefore inhibition of Surfactant, pulmonary-associated protein a2 (SFTPA2, Accession NP_008857.1), a gene which plays a role in innate host defense in the lung. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFTPA2.

[40625] The function of SFTPA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.1.N-sulfoglucosamine sulfohydrolase (sulfamidase) (SGSH, Accession NP_000190.1) is another GAM2033 target gene, herein designated TARGET GENE. SGSH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SGSH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SGSH BINDING SITE, designated SEQ ID:2077, to the nu-

cleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40626] Another function of GAM2033 is therefore inhibition of N-sulfoglucosamine sulfohydrolase (sulfamidase) (SGSH, Accession NP_000190.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SGSH.

[40627] Solute carrier family 26, member 7 (SLC26A7, Accession NP_439897.1) is another GAM2033 target gene, herein designated TARGET GENE. SLC26A7 BINDING SITE1 and SLC26A7 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by SLC26A7, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC26A7 BINDING SITE1 and SLC26A7 BINDING SITE2, designated SEQ ID:1641 and SEQ ID:16968 respectively, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40628] Another function of GAM2033 is therefore inhibition of Solute carrier family 26, member 7 (SLC26A7, Accession NP_439897.1) . Accordingly, utilities of GAM2033 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC26A7.

[40629] Solute carrier family 2 (facilitated glucose transporter), member 6 (SLC2A6, Accession NP_060055.1) is another GAM2033 target gene, herein designated TARGET GENE. SLC2A6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC2A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC2A6 BINDING SITE, designated SEQ ID:10370, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40630] Another function of GAM2033 is therefore inhibition of Solute carrier family 2 (facilitated glucose transporter), member 6 (SLC2A6, Accession NP_060055.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC2A6.

[40631] SMYD2 (Accession NP_064582.1) is another GAM2033 target gene, herein designated TARGET GENE. SMYD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SMYD2, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMYD2 BINDING SITE, designated SEQ ID:8651, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40632] Another function of GAM2033 is therefore inhibition of SMYD2 (Accession NP_064582.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMYD2.

[40633] Surfeit 5 (SURF5, Accession NP_852468.1) is another GAM2033 target gene, herein designated TARGET GENE. SURF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SURF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SURF5 BINDING SITE, designated SEQ ID:16437, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40634] Another function of GAM2033 is therefore inhibition of Surfeit 5 (SURF5, Accession NP_852468.1) . Accordingly,

utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURF5.

[40635] Surfeit 6 (SURF6, Accession NP_006744.2) is another GAM2033 target gene, herein designated TARGET GENE. SURF6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SURF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SURF6 BINDING SITE, designated SEQ ID:16547, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40636] Another function of GAM2033 is therefore inhibition of Surfeit 6 (SURF6, Accession NP_006744.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURF6.

[40637] Tyrosyl-dna phosphodiesterase 1 (TDP1, Accession NP_060789.2) is another GAM2033 target gene, herein designated TARGET GENE. TDP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TDP1, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TDP1 BINDING SITE, designated SEQ ID:12885, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40638] Another function of GAM2033 is therefore inhibition of Tyrosyl-dna phosphodiesterase 1 (TDP1, Accession NP_060789.2) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TDP1.

[40639] Telomerase-associated protein 1 (TEP1, Accession NP_009041.2) is another GAM2033 target gene, herein designated TARGET GENE. TEP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TEP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TEP1 BINDING SITE, designated SEQ ID:10717, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40640] Another function of GAM2033 is therefore inhibition of

Telomerase-associated protein 1 (TEP1, Accession NP_009041.2), a gene which interacts with active telomerase RNA. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEP1.

[40641] The function of TEP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Transforming growth factor, alpha (TGFA, Accession NP_003227.1) is another GAM2033 target gene, herein designated TARGET GENE. TGFA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGFA BINDING SITE, designated SEQ ID:16678, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40642] Another function of GAM2033 is therefore inhibition of Transforming growth factor, alpha (TGFA, Accession NP_003227.1), a gene which is able to bind to the egf receptor and to act synergistically with tgf beta to promote

anchorage- independent cell proliferation in soft agar. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFA.

[40643] The function of TGFA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Transforming growth factor, beta 3 (TGFB3, Accession NP_003230.1) is another GAM2033 target gene, herein designated TARGET GENE. TGFB3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGFB3 BINDING SITE, designated SEQ ID:16004, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40644] Another function of GAM2033 is therefore inhibition of Transforming growth factor, beta 3 (TGFB3, Accession NP_003230.1), a gene which is involved in embryogenesis and cell differentiation. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with TGFB3.

[40645] The function of TGFB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM483.1.Tousled-like kinase 2 (TLK2, Accession NP_006843.1) is another GAM2033 target gene, herein designated TARGET GENE. TLK2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TLK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLK2 BINDING SITE, designated SEQ ID:19779, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40646] Another function of GAM2033 is therefore inhibition of Tousled-like kinase 2 (TLK2, Accession NP_006843.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLK2.

[40647] Tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kda) (TNFSF4, Accession NP_003317.1) is another GAM2033

target gene, herein designated TARGET GENE. TNFSF4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFSF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFSF4 BINDING SITE, designated SEQ ID:1426, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40648] Another function of GAM2033 is therefore inhibition of Tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kda) (TNFSF4, Accession NP_003317.1), a gene which co-stimulates t cell proliferation and cytokine production. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFSF4.

[40649] The function of TNFSF4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM841.1.Tumor protein p53 inducible nuclear protein 1 (TP53INP1, Accession NP_150601.1) is another GAM2033 target gene, herein designated TARGET GENE.

TP53INP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TP53INP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TP53INP1 BINDING SITE, designated SEQ ID:15816, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40650] Another function of GAM2033 is therefore inhibition of Tumor protein p53 inducible nuclear protein 1 (TP53INP1, Accession NP_150601.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53INP1.

[40651] TRA16 (Accession NP_795361.1) is another GAM2033 target gene, herein designated TARGET GENE. TRA16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRA16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRA16 BINDING SITE, designated SEQ ID:1186, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA,

also designated SEQ ID:305.

[40652] Another function of GAM2033 is therefore inhibition of TRA16 (Accession NP_795361.1) . Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRA16.

[40653] Tripartite motif-containing 9 (TRIM9, Accession NP_055978.2) is another GAM2033 target gene, herein designated TARGET GENE. TRIM9 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRIM9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM9 BINDING SITE, designated SEQ ID:1798, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40654] Another function of GAM2033 is therefore inhibition of Tripartite motif-containing 9 (TRIM9, Accession NP_055978.2), a gene which may function as a positive regulator for mannosylphosphate transferase and is required to mediate mannosylphosphate transfer in both the core and outer chain portions of n- linked. oligosaccharides. Accordingly, utilities of GAM2033 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with TRIM9.

[40655] The function of TRIM9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Translin (TSN, Accession NP_004613.1) is another GAM2033 target gene, herein designated TARGET GENE. TSN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TSN BINDING SITE, designated SEQ ID:7612, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40656] Another function of GAM2033 is therefore inhibition of Translin (TSN, Accession NP_004613.1), a gene which is a DNA binding protein and involved in DNA repair, replication, or recombination. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSN.

[40657] The function of TSN and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM72.1.Williams-beuren syndrome chromosome region 1 (WBSCR1, Accession NP_114381.1) is another GAM2033 target gene, herein designated TARGET GENE. WBSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WBSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR1 BINDING SITE, designated SEQ ID:12817, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40658] Another function of GAM2033 is therefore inhibition of Williams-beuren syndrome chromosome region 1 (WBSCR1, Accession NP_114381.1), a gene which stimulates protein translation and therefore may be associated with Williams syndrome. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of Williams syndrome, and of other diseases and clinical conditions associated with WBSCR1.

[40659] The function of WBSCR1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM47.1.Williams-beuren syndrome chromosome region 1 (WBSCR1, Accession NP_071496.1) is another GAM2033 target gene, herein designated TARGET GENE. WBSCR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WBSCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR1 BINDING SITE, designated SEQ ID:12817, to the nucleotide sequence of GAM2033 RNA, herein designated GAM RNA, also designated SEQ ID:305.

[40660] Another function of GAM2033 is therefore inhibition of Williams-beuren syndrome chromosome region 1 (WBSCR1, Accession NP_071496.1), a gene which stimulates protein translation and therefore may be associated with Williams syndrome. Accordingly, utilities of GAM2033 include diagnosis, prevention and treatment of Williams syndrome, and of other diseases and clinical conditions associated with WBSCR1.

[40661] The function of WBSCR1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM47.1.

[40662] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 2071 (GAM2071), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[40663] GAM2071 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2071 was detected is described hereinabove with reference to Figs. 8-15.

[40664] GAM2071 gene, herein designated GAM GENE, and GAM2071 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[40665] GAM2071 gene encodes a GAM2071 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2071 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2071 precursor RNA is designated SEQ ID:102, and is provided hereinbelow with reference to the sequence listing part.

[40666] GAM2071 precursor RNA folds onto itself, forming GAM2071 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[40667] GAM2071 precursor RNA folds onto itself, forming GAM2071 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[40668] Nucleotide sequence of GAM2071 precursor RNA, designated SEQ-ID: 102, and a schematic representation of a predicted secondary folding of GAM2071 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[40669] An enzyme complex designated DICER COMPLEX, `dices` the GAM2071 folded precursor RNA into GAM2071 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: B) nucleotide sequence of GAM2071 RNA is designated SEQ ID:371, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[40670] GAM2071 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM2071 target RNA, herein designated GAM TARGET RNA. GAM2071 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[40671] GAM2071 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2071 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM2071 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2071 RNA may have a different number of target binding sites in untranslated regions of a GAM2071 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[40672] The complementary binding of GAM2071 RNA, herein designated GAM RNA, to target binding sites on GAM2071 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2071 target RNA into GAM2071 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[40673] It is appreciated that GAM2071 target gene, herein desig-

nated TARGET GENE, in fact represents a plurality of GAM2071 target genes. The mRNA of each one of this plurality of GAM2071 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2071 RNA, herein designated GAM RNA, and which when bound by GAM2071 RNA causes inhibition of translation of respective one or more GAM2071 target proteins.

[40674] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2071 gene, herein designated GAM GENE, on one or more GAM2071 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[40675] It is appreciated that specific functions and accordingly utilities of GAM2071 correlate with, and may be deduced from, the identity of the target genes which GAM2071 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[40676]

[40677]

[40678] 15E1.2 (Accession XP_290596.1) is a GAM2071 target gene, herein designated TARGET GENE. 15E1.2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by 15E1.2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of 15E1.2 BINDING SITE, designated SEQ ID:13885, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40679] A function of GAM2071 is therefore inhibition of 15E1.2 (Accession XP_290596.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 15E1.2.

[40680] Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2) is another GAM2071 target gene, herein designated TARGET GENE. A1BG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by A1BG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A1BG BINDING SITE, designated SEQ ID:10791, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40681] Another function of GAM2071 is therefore inhibition of Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2), a gene which a plasma protein of unknown function. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A1BG.

[40682] The function of A1BG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Aminoadipate-semialdehyde synthase (AASS, Accession NP_005754.2) is another GAM2071 target gene, herein designated TARGET GENE. AASS BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by AASS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AASS BINDING SITE, designated SEQ ID:18163, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40683] Another function of GAM2071 is therefore inhibition of Aminoadipate-semialdehyde synthase (AASS, Accession NP_005754.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AASS.

[40684] ABCA13 (Accession NP_689914.2) is another GAM2071 target gene, herein designated TARGET GENE. ABCA13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCA13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCA13 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40685] Another function of GAM2071 is therefore inhibition of

ABCA13 (Accession NP_689914.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCA13.

[40686] Actin binding lim protein 1 (ABLIM1, Accession NP_006710.2) is another GAM2071 target gene, herein designated TARGET GENE. ABLIM1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABLIM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABLIM1 BINDING SITE, designated SEQ ID:13022, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40687] Another function of GAM2071 is therefore inhibition of Actin binding lim protein 1 (ABLIM1, Accession NP_006710.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABLIM1.

[40688] Actin binding lim protein 1 (ABLIM1, Accession NP_002304.2) is another GAM2071 target gene, herein designated TARGET GENE. ABLIM1 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABLIM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABLIM1 BINDING SITE, designated SEQ ID:13022, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40689] Another function of GAM2071 is therefore inhibition of Actin binding lim protein 1 (ABLIM1, Accession NP_002304.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABLIM1.

[40690] Actin binding lim protein 1 (ABLIM1, Accession NP_006711.2) is another GAM2071 target gene, herein designated TARGET GENE. ABLIM1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABLIM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABLIM1 BINDING SITE, designated SEQ ID:13022, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[40691] Another function of GAM2071 is therefore inhibition of Actin binding lim protein 1 (ABLIM1, Accession NP_006711.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABLIM1.

[40692] Acyl-coenzyme a dehydrogenase, short/branched chain (ACADSB, Accession NP_001600.1) is another GAM2071 target gene, herein designated TARGET GENE. ACADSB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACADSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACADSB BINDING SITE, designated SEQ ID:14907, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40693] Another function of GAM2071 is therefore inhibition of Acyl-coenzyme a dehydrogenase, short/branched chain (ACADSB, Accession NP_001600.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACADSB.

[40694] A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4 (ADAMTS4, Accession NP_005090.1) is another GAM2071 target gene, herein designated TARGET GENE. ADAMTS4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAMTS4 BINDING SITE, designated SEQ ID:1318, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40695] Another function of GAM2071 is therefore inhibition of A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4 (ADAMTS4, Accession NP_005090.1), a gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAMTS4.

[40696] The function of ADAMTS4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM189.1.Adenylate cyclase 5 (ADCY5, Accession XP_171048.2) is another GAM2071 target gene, herein designated TARGET GENE. ADCY5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADCY5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY5 BINDING SITE, designated SEQ ID:19656, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40697] Another function of GAM2071 is therefore inhibition of Adenylate cyclase 5 (ADCY5, Accession XP_171048.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY5.

[40698] Adenylate cyclase 6 (ADCY6, Accession NP_056085.1) is another GAM2071 target gene, herein designated TARGET GENE. ADCY6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ADCY6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of ADCY6 BINDING SITE, designated SEQ ID:14908, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40699] Another function of GAM2071 is therefore inhibition of Adenylate cyclase 6 (ADCY6, Accession NP_056085.1), a gene which this a membrane- bound, ca(2+)- inhibitable adenylyl cyclase (by similarity). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY6.

[40700] The function of ADCY6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.2.Agmatine ureohydrolase (agmatinase) (AGMAT, Accession NP_079034.2) is another GAM2071 target gene, herein designated TARGET GENE. AGMAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AGMAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGMAT BINDING SITE, designated SEQ ID:2112, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[40701] Another function of GAM2071 is therefore inhibition of Agmatine ureohydrolase (agmatinase) (AGMAT, Accession NP_079034.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGMAT.

[40702] Aryl hydrocarbon receptor (AHR, Accession NP_001612.1) is another GAM2071 target gene, herein designated TARGET GENE. AHR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AHR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AHR BINDING SITE, designated SEQ ID:9011, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40703] Another function of GAM2071 is therefore inhibition of Aryl hydrocarbon receptor (AHR, Accession NP_001612.1), a gene which plays a role in modulating carcinogenesis through the induction of xenobiotic- metabolizing enzymes and therefore may be associated with Stomach tumors. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Stomach tumors, and of

other diseases and clinical conditions associated with AHR.

[40704] The function of AHR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Absent in melanoma 1 (AIM1, Accession XP_166300.1) is another GAM2071 target gene, herein designated TARGET GENE. AIM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AIM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AIM1 BINDING SITE, designated SEQ ID:1383, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40705] Another function of GAM2071 is therefore inhibition of Absent in melanoma 1 (AIM1, Accession XP_166300.1), a gene which is altered in association with tumor suppression in a model of human melanoma and therefore may be associated with Malignant melanoma. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Malignant melanoma, and of other diseases and clinical

conditions associated with AIM1.

[40706] The function of AIM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Aldehyde dehydrogenase 1 family, member b1 (ALDH1B1, Accession NP_000683.3) is another GAM2071 target gene, herein designated TARGET GENE. ALDH1B1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALDH1B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALDH1B1 BINDING SITE, designated SEQ ID:19434, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40707] Another function of GAM2071 is therefore inhibition of Aldehyde dehydrogenase 1 family, member b1 (ALDH1B1, Accession NP_000683.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH1B1.

[40708] Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1) is another GAM2071 target gene, herein

designated TARGET GENE. ALOX15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALOX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALOX15 BINDING SITE, designated SEQ ID:18901, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40709] Another function of GAM2071 is therefore inhibition of Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1), a gene which converts arachidonic acid to 15s- hydroperoxyeicosatetraenoic acid. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALOX15.

[40710] The function of ALOX15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.AMID (Accession NP_116186.1) is another GAM2071 target gene, herein designated TARGET GENE. AMID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AMID, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMID BINDING SITE, designated SEQ ID:2328, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40711] Another function of GAM2071 is therefore inhibition of AMID (Accession NP_116186.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMID.

[40712] Angiomotin like 1 (AMOTL1, Accession NP_570899.1) is another GAM2071 target gene, herein designated TARGET GENE. AMOTL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AMOTL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMOTL1 BINDING SITE, designated SEQ ID:18210, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40713] Another function of GAM2071 is therefore inhibition of Angiomotin like 1 (AMOTL1, Accession NP_570899.1) .

Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMOTL1.

[40714] Ankyrin repeat domain 6 (ANKRD6, Accession NP_055757.1) is another GAM2071 target gene, herein designated TARGET GENE. ANKRD6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ANKRD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANKRD6 BINDING SITE, designated SEQ ID:11653, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40715] Another function of GAM2071 is therefore inhibition of Ankyrin repeat domain 6 (ANKRD6, Accession NP_055757.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKRD6.

[40716] AP1S3 (Accession XP_291023.1) is another GAM2071 target gene, herein designated TARGET GENE. AP1S3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by

AP1S3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1S3 BINDING SITE, designated SEQ ID:15779, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40717] Another function of GAM2071 is therefore inhibition of AP1S3 (Accession XP_291023.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1S3.

[40718] Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) is another GAM2071 target gene, herein designated TARGET GENE. AP3S2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AP3S2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP3S2 BINDING SITE, designated SEQ ID:6113, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40719] Another function of GAM2071 is therefore inhibition of

Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3S2.

[40720] Apoptotic protease activating factor (APAF1, Accession NP_001151.1) is another GAM2071 target gene, herein designated TARGET GENE. APAF1 BINDING SITE1 and APAF1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APAF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE1 and APAF1 BINDING SITE2, designated SEQ ID:1306 and SEQ ID:803 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40721] Another function of GAM2071 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_001151.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM2071 include di-

agnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[40722] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apoptotic protease activating factor (APAF1, Accession NP_001151.1) is another GAM2071 target gene, herein designated TARGET GENE. APAF1 BINDING SITE1 and APAF1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APAF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE1 and APAF1 BINDING SITE2, designated SEQ ID:803 and SEQ ID:1306 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40723] Another function of GAM2071 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_001151.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated

with Cancer. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[40724] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.APM1 (Accession NP_004788.1) is another GAM2071 target gene, herein designated TARGET GENE. APM1 BINDING SITE1 and APM1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APM1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APM1 BINDING SITE1 and APM1 BINDING SITE2, designated SEQ ID:13551 and SEQ ID:1962 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40725] Another function of GAM2071 is therefore inhibition of APM1 (Accession NP_004788.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1.

[40726] Apolipoprotein b mrna editing enzyme, catalytic polypep-

tide-like 3f (APOBEC3F, Accession NP_660341.2) is another GAM2071 target gene, herein designated TARGET GENE. APOBEC3F BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APOBEC3F, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOBEC3F BINDING SITE, designated SEQ ID:5126, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40727] Another function of GAM2071 is therefore inhibition of Apolipoprotein b mrna editing enzyme, catalytic polypeptide-like 3f (APOBEC3F, Accession NP_660341.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOBEC3F.

[40728] Apolipoprotein l, 2 (APOL2, Accession NP_112092.1) is another GAM2071 target gene, herein designated TARGET GENE. APOL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL2 BINDING SITE, designated SEQ ID:16087, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40729] Another function of GAM2071 is therefore inhibition of Apolipoprotein l, 2 (APOL2, Accession NP_112092.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL2.

[40730] Apolipoprotein l, 2 (APOL2, Accession NP_663612.1) is another GAM2071 target gene, herein designated TARGET GENE. APOL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL2 BINDING SITE, designated SEQ ID:16087, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40731] Another function of GAM2071 is therefore inhibition of Apolipoprotein l, 2 (APOL2, Accession NP_663612.1) . Ac-

cordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL2.

[40732] APPL (Accession NP_036228.1) is another GAM2071 target gene, herein designated TARGET GENE. APPL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APPL BINDING SITE, designated SEQ ID:12386, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40733] Another function of GAM2071 is therefore inhibition of APPL (Accession NP_036228.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APPL.

[40734] Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1) is another GAM2071 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:2103, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40735] Another function of GAM2071 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[40736] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1) is another GAM2071 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:2103, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40737] Another function of GAM2071 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[40738] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Adp-ribosylation factor 4-like (ARF4L, Accession NP_001652.1) is another GAM2071 target gene, herein designated TARGET GENE. ARF4L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARF4L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARF4L BINDING SITE,

designated SEQ ID:16932, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40739] Another function of GAM2071 is therefore inhibition of Adp-ribosylation factor 4-like (ARF4L, Accession NP_001652.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARF4L.

[40740] Ras homolog gene family, member a (ARHA, Accession NP_001655.1) is another GAM2071 target gene, herein designated TARGET GENE. ARHA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHA BINDING SITE, designated SEQ ID:2467, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40741] Another function of GAM2071 is therefore inhibition of Ras homolog gene family, member a (ARHA, Accession NP_001655.1), a gene which regulates remodeling of the actin cytoskeleton during cell morphogenesis and motility.

Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHA.

[40742] The function of ARHA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Ras homolog gene family, member f (in filopodia) (ARHF, Accession NP_061907.1) is another GAM2071 target gene, herein designated TARGET GENE. ARHF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHF BINDING SITE, designated SEQ ID:3172, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40743] Another function of GAM2071 is therefore inhibition of Ras homolog gene family, member f (in filopodia) (ARHF, Accession NP_061907.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHF.

[40744] Rho gtpase activating protein 1 (ARHGAP1, Accession

NP_004299.1) is another GAM2071 target gene, herein designated TARGET GENE. ARHGAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP1 BINDING SITE, designated SEQ ID:8690, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40745] Another function of GAM2071 is therefore inhibition of Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP1.

[40746] ARHGAP11A (Accession NP_055598.1) is another GAM2071 target gene, herein designated TARGET GENE. ARHGAP11A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGAP11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP11A BINDING SITE, desig-

nated SEQ ID:7085, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40747] Another function of GAM2071 is therefore inhibition of ARHGAP11A (Accession NP_055598.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP11A.

[40748] ARPP-19 (Accession NP_006619.1) is another GAM2071 target gene, herein designated TARGET GENE. ARPP-19 BINDING SITE1 and ARPP-19 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ARPP-19, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARPP-19 BINDING SITE1 and ARPP-19 BINDING SITE2, designated SEQ ID:18664 and SEQ ID:5121 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40749] Another function of GAM2071 is therefore inhibition of ARPP-19 (Accession NP_006619.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with ARPP-19.

[40750] Ankyrin repeat and socs box-containing 16 (ASB16, Accession NP_543139.4) is another GAM2071 target gene, herein designated TARGET GENE. ASB16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASB16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB16 BINDING SITE, designated SEQ ID:11661, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40751] Another function of GAM2071 is therefore inhibition of Ankyrin repeat and socs box-containing 16 (ASB16, Accession NP_543139.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB16.

[40752] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) is another GAM2071 target gene, herein designated TARGET GENE. ASB6 BINDING SITE1 and ASB6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA en-

coded by ASB6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE1 and ASB6 BINDING SITE2, designated SEQ ID:20186 and SEQ ID:1654 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40753] Another function of GAM2071 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[40754] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) is another GAM2071 target gene, herein designated TARGET GENE. ASB6 BINDING SITE1 and ASB6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ASB6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE1 and ASB6 BINDING SITE2, designated SEQ ID:20186 and SEQ ID:1654

respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40755] Another function of GAM2071 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[40756] ASE-1 (Accession NP_036231.1) is another GAM2071 target gene, herein designated TARGET GENE. ASE-1 BINDING SITE1 and ASE-1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ASE-1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASE-1 BINDING SITE1 and ASE-1 BINDING SITE2, designated SEQ ID:9101 and SEQ ID:9988 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40757] Another function of GAM2071 is therefore inhibition of ASE-1 (Accession NP_036231.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with ASE-1.

[40758] Atpase, (na+)/k+ transporting, beta 4 polypeptide (ATP1B4, Accession NP_036201.1) is another GAM2071 target gene, herein designated TARGET GENE. ATP1B4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP1B4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP1B4 BINDING SITE, designated SEQ ID:15678, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40759] Another function of GAM2071 is therefore inhibition of Atpase, (na+)/k+ transporting, beta 4 polypeptide (ATP1B4, Accession NP_036201.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B4.

[40760] Atpase, ca++ transporting, type 2c, member 1 (ATP2C1, Accession NP_055197.1) is another GAM2071 target gene, herein designated TARGET GENE. ATP2C1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ATP2C1, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP2C1 BINDING SITE, designated SEQ ID:4782, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40761] Another function of GAM2071 is therefore inhibition of Atpase, ca++ transporting, type 2c, member 1 (ATP2C1, Accession NP_055197.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP2C1.

[40762] Atpase, h+ transporting, lysosomal 38kda, v0 subunit d isoform 2 (ATP6V0D2, Accession NP_689778.1) is another GAM2071 target gene, herein designated TARGET GENE. ATP6V0D2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP6V0D2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP6V0D2 BINDING SITE, designated SEQ ID:7490, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40763] Another function of GAM2071 is therefore inhibition of Atpase, h+ transporting, lysosomal 38kda, v0 subunit d isoform 2 (ATP6V0D2, Accession NP_689778.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V0D2.

[40764] Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) is another GAM2071 target gene, herein designated TARGET GENE. ATP7A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:19505, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40765] Another function of GAM2071 is therefore inhibition of Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A.

[40766] Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) is another GAM2071 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:5485, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40767] Another function of GAM2071 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[40768] Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) is another GAM2071 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:5485, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40769] Another function of GAM2071 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[40770] Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5, Accession NP_004767.1) is another GAM2071 target gene, herein designated TARGET GENE. B4GALT5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B4GALT5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B4GALT5 BINDING SITE, designated SEQ ID:10889, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40771] Another function of GAM2071 is therefore inhibition of Udp-gal:betaglcnac beta 1,4- galactosyltransferase,

polypeptide 5 (B4GALT5, Accession NP_004767.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT5.

[40772] Btb and cnc homology 1, basic leucine zipper transcription factor 1 (BACH1, Accession NP_001177.1) is another GAM2071 target gene, herein designated TARGET GENE. BACH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BACH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACH1 BINDING SITE, designated SEQ ID:2969, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40773] Another function of GAM2071 is therefore inhibition of Btb and cnc homology 1, basic leucine zipper transcription factor 1 (BACH1, Accession NP_001177.1), a gene which acts as repressor or activator, binds to nf- e2 binding sites. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BACH1.

[40774] The function of BACH1 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM100.1.Bcl2-associated athanogene 5 (BAG5, Accession NP_004864.1) is another GAM2071 target gene, herein designated TARGET GENE. BAG5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BAG5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAG5 BINDING SITE, designated SEQ ID:19878, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40775] Another function of GAM2071 is therefore inhibition of Bcl2-associated athanogene 5 (BAG5, Accession NP_004864.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAG5.

[40776] Bai1-associated protein 3 (BAIAP3, Accession NP_003924.2) is another GAM2071 target gene, herein designated TARGET GENE. BAIAP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BAIAP3, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAIAP3 BINDING SITE, designated SEQ ID:14634, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40777] Another function of GAM2071 is therefore inhibition of Bai1-associated protein 3 (BAIAP3, Accession NP_003924.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAIAP3.

[40778] B-cell cll/lymphoma 10 (BCL10, Accession NP_003912.1) is another GAM2071 target gene, herein designated TARGET GENE. BCL10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCL10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCL10 BINDING SITE, designated SEQ ID:17565, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40779] Another function of GAM2071 is therefore inhibition of B-

cell cll/lymphoma 10 (BCL10, Accession NP_003912.1), a gene which is a positive regulator of lymphocyte proliferation, NF- kappaB activator. and therefore may be associated with Malt lymphoma, follicular lymphoma. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Malt lymphoma, follicular lymphoma, and of other diseases and clinical conditions associated with BCL10.

[40780] The function of BCL10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Bradykinin receptor b1 (BDKRB1, Accession NP_000701.2) is another GAM2071 target gene, herein designated TARGET GENE. BDKRB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BDKRB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BDKRB1 BINDING SITE, designated SEQ ID:13940, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40781] Another function of GAM2071 is therefore inhibition of Bradykinin receptor b1 (BDKRB1, Accession NP_000701.2), a gene which mediates intracellular calcium flux. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDKRB1.

[40782] The function of BDKRB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.B double prime 1, subunit of rna polymerase iii transcription initiation factor iiib (BDP1, Accession NP_060899.1) is another GAM2071 target gene, herein designated TARGET GENE. BDP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BDP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BDP1 BINDING SITE, designated SEQ ID:4304, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40783] Another function of GAM2071 is therefore inhibition of B double prime 1, subunit of rna polymerase iii transcription

initiation factor iiib (BDP1, Accession NP_060899.1), a gene which activates RNA polymerase III transcription. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDP1.

[40784] The function of BDP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM146.1.BENE (Accession NP_005425.1) is another GAM2071 target gene, herein designated TARGET GENE. BENE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BENE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BENE BINDING SITE, designated SEQ ID:3688, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40785] Another function of GAM2071 is therefore inhibition of BENE (Accession NP_005425.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BENE.

[40786] Bone morphogenetic protein 1 (BMP1, Accession

NP_006120.1) is another GAM2071 target gene, herein designated TARGET GENE. BMP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BMP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BMP1 BINDING SITE, designated SEQ ID:769, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40787] Another function of GAM2071 is therefore inhibition of Bone morphogenetic protein 1 (BMP1, Accession NP_006120.1), a gene which cleaves procollagens leading to formation of extracellular matrix. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMP1.

[40788] The function of BMP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.BNIP-S (Accession NP_612122.1) is another GAM2071 target gene, herein designated TARGET GENE. BNIP-S BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA

encoded by BNIP-S, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BNIP-S BINDING SITE, designated SEQ ID:17763, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40789] Another function of GAM2071 is therefore inhibition of BNIP-S (Accession NP_612122.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BNIP-S.

[40790] Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession NP_008979.2) is another GAM2071 target gene, herein designated TARGET GENE. BTN3A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTN3A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTN3A1 BINDING SITE, designated SEQ ID:17858, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40791] Another function of GAM2071 is therefore inhibition of

Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession NP_008979.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN3A1.

[40792] BXDC1 (Accession XP_166303.1) is another GAM2071 target gene, herein designated TARGET GENE. BXDC1 BINDING SITE1 and BXDC1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by BXDC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BXDC1 BINDING SITE1 and BXDC1 BINDING SITE2, designated SEQ ID:711 and SEQ ID:7070 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40793] Another function of GAM2071 is therefore inhibition of BXDC1 (Accession XP_166303.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BXDC1.

[40794] BY55 (Accession NP_008984.1) is another GAM2071 target gene, herein designated TARGET GENE. BY55 BINDING SITE is a target binding site found in the 5` untranslated

region of mRNA encoded by BY55, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BY55 BINDING SITE, designated SEQ ID:17712, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40795] Another function of GAM2071 is therefore inhibition of BY55 (Accession NP_008984.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BY55.

[40796] Chromosome 11 open reading frame 17 (C11orf17, Accession NP_065693.2) is another GAM2071 target gene, herein designated TARGET GENE. C11orf17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C11orf17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C11orf17 BINDING SITE, designated SEQ ID:13793, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40797] Another function of GAM2071 is therefore inhibition of

Chromosome 11 open reading frame 17 (C11orf17, Accession NP_065693.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf17.

[40798] Chromosome 11 open reading frame 9 (C11orf9, Accession NP_037411.1) is another GAM2071 target gene, herein designated TARGET GENE. C11orf9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C11orf9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C11orf9 BINDING SITE, designated SEQ ID:5710, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40799] Another function of GAM2071 is therefore inhibition of Chromosome 11 open reading frame 9 (C11orf9, Accession NP_037411.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf9.

[40800] Chromosome 13 open reading frame 1 (C13orf1, Accession NP_065189.1) is another GAM2071 target gene, herein designated TARGET GENE. C13orf1 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by C13orf1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C13orf1 BINDING SITE, designated SEQ ID:2596, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40801] Another function of GAM2071 is therefore inhibition of Chromosome 13 open reading frame 1 (C13orf1, Accession NP_065189.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C13orf1.

[40802] Chromosome 14 open reading frame 1 (C14orf1, Accession NP_009107.1) is another GAM2071 target gene, herein designated TARGET GENE. C14orf1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf1 BINDING SITE, designated SEQ ID:2950, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA,

also designated SEQ ID:371.

[40803] Another function of GAM2071 is therefore inhibition of Chromosome 14 open reading frame 1 (C14orf1, Accession NP_009107.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf1.

[40804] C14orf143 (Accession NP_660274.1) is another GAM2071 target gene, herein designated TARGET GENE. C14orf143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf143 BINDING SITE, designated SEQ ID:11599, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40805] Another function of GAM2071 is therefore inhibition of C14orf143 (Accession NP_660274.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf143.

[40806] C14orf92 (Accession NP_055643.1) is another GAM2071 target gene, herein designated TARGET GENE. C14orf92

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf92, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf92 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40807] Another function of GAM2071 is therefore inhibition of C14orf92 (Accession NP_055643.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf92.

[40808] Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) is another GAM2071 target gene, herein designated TARGET GENE. C1orf24 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C1orf24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:601, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[40809] Another function of GAM2071 is therefore inhibition of Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24.

[40810] C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) is another GAM2071 target gene, herein designated TARGET GENE. C1QTNF6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1QTNF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1QTNF6 BINDING SITE, designated SEQ ID:18746, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40811] Another function of GAM2071 is therefore inhibition of C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QTNF6.

[40812] Chromosome 21 open reading frame 108 (C21orf108, Accession XP_114191.2) is another GAM2071 target gene, herein designated TARGET GENE. C21orf108 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C21orf108, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C21orf108 BINDING SITE, designated SEQ ID:2886, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40813] Another function of GAM2071 is therefore inhibition of Chromosome 21 open reading frame 108 (C21orf108, Accession XP_114191.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf108.

[40814] Chromosome 22 open reading frame 19 (C22orf19, Accession NP_003669.2) is another GAM2071 target gene, herein designated TARGET GENE. C22orf19 BINDING SITE1 and C22orf19 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C22orf19, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C22orf19 BINDING SITE1 and C22orf19 BINDING SITE2, designated SEQ ID:16921 and SEQ ID:14748 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40815] Another function of GAM2071 is therefore inhibition of Chromosome 22 open reading frame 19 (C22orf19, Accession NP_003669.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C22orf19.

[40816] C3F (Accession NP_005759.2) is another GAM2071 target gene, herein designated TARGET GENE. C3F BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C3F, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C3F BINDING SITE, designated SEQ ID:15743, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40817] Another function of GAM2071 is therefore inhibition of C3F (Accession NP_005759.2) . Accordingly, utilities of

GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C3F.

[40818] Chromosome 5 open reading frame 4 (C5orf4, Accession NP_115761.1) is another GAM2071 target gene, herein designated TARGET GENE. C5orf4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C5orf4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C5orf4 BINDING SITE, designated SEQ ID:10925, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40819] Another function of GAM2071 is therefore inhibition of Chromosome 5 open reading frame 4 (C5orf4, Accession NP_115761.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf4.

[40820] Chromosome 5 open reading frame 4 (C5orf4, Accession NP_057432.1) is another GAM2071 target gene, herein designated TARGET GENE. C5orf4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C5orf4, correspond-

ing to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C5orf4 BINDING SITE, designated SEQ ID:10925, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40821] Another function of GAM2071 is therefore inhibition of Chromosome 5 open reading frame 4 (C5orf4, Accession NP_057432.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf4.

[40822] Chromosome 5 open reading frame 7 (C5orf7, Accession NP_057688.1) is another GAM2071 target gene, herein designated TARGET GENE. C5orf7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C5orf7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C5orf7 BINDING SITE, designated SEQ ID:7567, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40823] Another function of GAM2071 is therefore inhibition of

Chromosome 5 open reading frame 7 (C5orf7, Accession NP_057688.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf7.

[40824] C6orf141 (Accession NP_699175.1) is another GAM2071 target gene, herein designated TARGET GENE. C6orf141 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf141, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf141 BINDING SITE, designated SEQ ID:12169, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40825] Another function of GAM2071 is therefore inhibition of C6orf141 (Accession NP_699175.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf141.

[40826] Chromosome 6 open reading frame 33 (C6orf33, Accession NP_588608.1) is another GAM2071 target gene, herein designated TARGET GENE. C6orf33 BINDING SITE is a target binding site found in the 3` untranslated region

of mRNA encoded by C6orf33, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf33 BINDING SITE, designated SEQ ID:7278, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40827] Another function of GAM2071 is therefore inhibition of Chromosome 6 open reading frame 33 (C6orf33, Accession NP_588608.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf33.

[40828] C6orf5 (Accession NP_056339.2) is another GAM2071 target gene, herein designated TARGET GENE. C6orf5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf5 BINDING SITE, designated SEQ ID:10778, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40829] Another function of GAM2071 is therefore inhibition of

C6orf5 (Accession NP_056339.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf5.

[40830] C6orf57 (Accession NP_660310.1) is another GAM2071 target gene, herein designated TARGET GENE. C6orf57 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf57, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf57 BINDING SITE, designated SEQ ID:6442, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40831] Another function of GAM2071 is therefore inhibition of C6orf57 (Accession NP_660310.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf57.

[40832] Chromosome 9 open reading frame 9 (C9orf9, Accession NP_061829.2) is another GAM2071 target gene, herein designated TARGET GENE. C9orf9 BINDING SITE1 and C9orf9 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C9orf9, corre-

sponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C9orf9 BINDING SITE1 and C9orf9 BINDING SITE2, designated SEQ ID:13797 and SEQ ID:19273 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40833] Another function of GAM2071 is therefore inhibition of Chromosome 9 open reading frame 9 (C9orf9, Accession NP_061829.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf9.

[40834] Carbonic anhydrase va, mitochondrial (CA5A, Accession NP_001730.1) is another GAM2071 target gene, herein designated TARGET GENE. CA5A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CA5A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CA5A BINDING SITE, designated SEQ ID:6692, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40835] Another function of GAM2071 is therefore inhibition of Carbonic anhydrase va, mitochondrial (CA5A, Accession NP_001730.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CA5A.

[40836] Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203519.1) is another GAM2071 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40837] Another function of GAM2071 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203519.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly,

utilities of GAM2071 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[40838] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203520.1) is another GAM2071 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40839] Another function of GAM2071 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203520.1), a gene which is an apoptosis-related caspase and an upstream component of Fas re-

ceptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[40840] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_001219.2) is another GAM2071 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40841] Another function of GAM2071 is therefore inhibition of

Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_001219.2), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[40842] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203521.1) is another GAM2071 target gene, herein designated TARGET GENE. CASP8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CASP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP8 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM2071

RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40843] Another function of GAM2071 is therefore inhibition of Caspase 8, apoptosis-related cysteine protease (CASP8, Accession NP_203521.1), a gene which is an apoptosis-related caspase and an upstream component of Fas receptor and tumor necrosis factor (TNF) receptor- induced apoptosis. and therefore may be associated with Huntington- related neurodegenerative diseases. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Huntington- related neurodegenerative diseases, and of other diseases and clinical conditions associated with CASP8.

[40844] The function of CASP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_005084.1) is another GAM2071 target gene, herein designated TARGET GENE. CBFA2T2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CBFA2T2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CBFA2T2 BINDING SITE, designated SEQ ID:3868, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40845] Another function of GAM2071 is therefore inhibition of Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_005084.1), a gene which is a putative transcription factor. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T2.

[40846] The function of CBFA2T2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_787060.1) is another GAM2071 target gene, herein designated TARGET GENE. CBFA2T2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CBFA2T2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of CBFA2T2 BINDING SITE, designated SEQ ID:3868, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40847] Another function of GAM2071 is therefore inhibition of Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_787060.1), a gene which is a putative transcription factor. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T2.

[40848] The function of CBFA2T2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Chemokine (c-c motif) ligand 16 (CCL16, Accession NP_004581.1) is another GAM2071 target gene, herein designated TARGET GENE. CCL16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL16 BINDING SITE, designated SEQ ID:10633, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40849] Another function of GAM2071 is therefore inhibition of Chemokine (c-c motif) ligand 16 (CCL16, Accession NP_004581.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL16.

[40850] Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) is another GAM2071 target gene, herein designated TARGET GENE. CCL22 BINDING SITE1 and CCL22 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CCL22, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL22 BINDING SITE1 and CCL22 BINDING SITE2, designated SEQ ID:16005 and SEQ ID:11649 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40851] Another function of GAM2071 is therefore inhibition of Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with CCL22.

[40852] Cyclin f (CCNF, Accession NP_001752.1) is another GAM2071 target gene, herein designated TARGET GENE. CCNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCNF BINDING SITE, designated SEQ ID:14395, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40853] Another function of GAM2071 is therefore inhibition of Cyclin f (CCNF, Accession NP_001752.1), a gene which likely to be involved in the control of the cell cycle during s phase and g2. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNF.

[40854] The function of CCNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Chemokine (c-c motif) receptor 5 (CCR5, Accession NP_000570.1) is another GAM2071 target gene, herein designated TARGET GENE. CCR5 BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by CCR5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCR5 BINDING SITE, designated SEQ ID:17905, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40855] Another function of GAM2071 is therefore inhibition of Chemokine (c-c motif) receptor 5 (CCR5, Accession NP_000570.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCR5.

[40856] Cd209 antigen (CD209, Accession NP_066978.1) is another GAM2071 target gene, herein designated TARGET GENE. CD209 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD209, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD209 BINDING SITE, designated SEQ ID:8229, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ

ID:371.

[40857] Another function of GAM2071 is therefore inhibition of Cd209 antigen (CD209, Accession NP_066978.1), a gene which may play an important role in the CD4- independent association of HIV with cells. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD209.

[40858] The function of CD209 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Cd24 antigen (small cell lung carcinoma cluster 4 antigen) (CD24, Accession NP_037362.1) is another GAM2071 target gene, herein designated TARGET GENE. CD24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD24 BINDING SITE, designated SEQ ID:18593, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40859] Another function of GAM2071 is therefore inhibition of Cd24 antigen (small cell lung carcinoma cluster 4 antigen)

(CD24, Accession NP_037362.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD24.

[40860] Cdc14 cell division cycle 14 homolog b (s. cerevisiae) (CDC14B, Accession NP_201589.1) is another GAM2071 target gene, herein designated TARGET GENE. CDC14B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDC14B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC14B BINDING SITE, designated SEQ ID:7919, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40861] Another function of GAM2071 is therefore inhibition of Cdc14 cell division cycle 14 homolog b (s. cerevisiae) (CDC14B, Accession NP_201589.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC14B.

[40862] Cell division cycle 2-like 2 (CDC2L2, Accession NP_296370.1) is another GAM2071 target gene, herein

designated TARGET GENE. CDC2L2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CDC2L2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC2L2 BINDING SITE, designated SEQ ID:8250, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40863] Another function of GAM2071 is therefore inhibition of Cell division cycle 2-like 2 (CDC2L2, Accession NP_296370.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC2L2.

[40864] CDCP1 (Accession NP_073753.3) is another GAM2071 target gene, herein designated TARGET GENE. CDCP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDCP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDCP1 BINDING SITE, designated SEQ ID:20095, to the nucleotide sequence of GAM2071

RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40865] Another function of GAM2071 is therefore inhibition of CDCP1 (Accession NP_073753.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDCP1.

[40866] Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) is another GAM2071 target gene, herein designated TARGET GENE. CDH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH1 BINDING SITE, designated SEQ ID:3667, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40867] Another function of GAM2071 is therefore inhibition of Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH1.

[40868] CDK11 (Accession XP_166324.1) is another GAM2071 tar-

get gene, herein designated TARGET GENE. CDK11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDK11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDK11 BINDING SITE, designated SEQ ID:5408, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40869] Another function of GAM2071 is therefore inhibition of CDK11 (Accession XP_166324.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDK11.

[40870] CDKAL1 (Accession NP_060244.1) is another GAM2071 target gene, herein designated TARGET GENE. CDKAL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDKAL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDKAL1 BINDING SITE, designated SEQ ID:12153, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[40871] Another function of GAM2071 is therefore inhibition of CDKAL1 (Accession NP_060244.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKAL1.

[40872] Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) is another GAM2071 target gene, herein designated TARGET GENE. CEACAM8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CEACAM8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CEACAM8 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40873] Another function of GAM2071 is therefore inhibition of Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEACAM8.

[40874] Centromere protein h (CENPH, Accession NP_075060.1) is another GAM2071 target gene, herein designated TARGET GENE. CENPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CENPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENPH BINDING SITE, designated SEQ ID:7835, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40875] Another function of GAM2071 is therefore inhibition of Centromere protein h (CENPH, Accession NP_075060.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENPH.

[40876] CGI-150 (Accession NP_057164.1) is another GAM2071 target gene, herein designated TARGET GENE. CGI-150 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CGI-150, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

CGI-150 BINDING SITE, designated SEQ ID:19951, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40877] Another function of GAM2071 is therefore inhibition of CGI-150 (Accession NP_057164.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-150.

[40878] Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2) is another GAM2071 target gene, herein designated TARGET GENE. CIAS1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CIAS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIAS1 BINDING SITE, designated SEQ ID:7985, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40879] Another function of GAM2071 is therefore inhibition of Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2), a gene which may mediate protein- protein interactions; contains a leucine rich repeat and there-

fore may be associated with Familial cold autoinflammatory syndrome, muckle- wells syndrome. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Familial cold autoinflammatory syndrome, muckle- wells syndrome, and of other diseases and clinical conditions associated with CIAS1.

[40880] The function of CIAS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM90.1.CIP29 (Accession NP_115740.3) is another GAM2071 target gene, herein designated TARGET GENE. CIP29 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CIP29, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIP29 BINDING SITE, designated SEQ ID:11639, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40881] Another function of GAM2071 is therefore inhibition of CIP29 (Accession NP_115740.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIP29.

[40882] C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2) is another GAM2071 target gene, herein designated TARGET GENE. CLECSF12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLECSF12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLECSF12 BINDING SITE, designated SEQ ID:10233, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40883] Another function of GAM2071 is therefore inhibition of C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2), a gene which is a pattern- recognition receptor . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLECSF12.

[40884] The function of CLECSF12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Chloride channel, nucleotide-sensitive, 1a

(CLNS1A, Accession NP_001284.1) is another GAM2071 target gene, herein designated TARGET GENE. CLNS1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLNS1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLNS1A BINDING SITE, designated SEQ ID:8322, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40885] Another function of GAM2071 is therefore inhibition of Chloride channel, nucleotide-sensitive, 1a (CLNS1A, Accession NP_001284.1), a gene which may participate in cellular volume control . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLNS1A.

[40886] The function of CLNS1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Cell matrix adhesion regulator (CMAR, Accession NP_005191.2) is another GAM2071 target gene, herein designated TARGET GENE. CMAR BINDING SITE is a target binding site found in the 5` untranslated region of

mRNA encoded by CMAR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CMAR BINDING SITE, designated SEQ ID:19999, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40887] Another function of GAM2071 is therefore inhibition of Cell matrix adhesion regulator (CMAR, Accession NP_005191.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CMAR.

[40888] Calponin 2 (CNN2, Accession NP_004359.1) is another GAM2071 target gene, herein designated TARGET GENE. CNN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNN2 BINDING SITE, designated SEQ ID:6909, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40889] Another function of GAM2071 is therefore inhibition of

Calponin 2 (CNN2, Accession NP_004359.1), a gene which may be involved in the structural organization and/or anchorage of actin filaments. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNN2.

[40890] The function of CNN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Cyclin m3 (CNNM3, Accession NP_060093.2) is another GAM2071 target gene, herein designated TARGET GENE. CNNM3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNNM3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNNM3 BINDING SITE, designated SEQ ID:3981, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40891] Another function of GAM2071 is therefore inhibition of Cyclin m3 (CNNM3, Accession NP_060093.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with CNNM3.

[40892] 2',3'-cyclic nucleotide 3' phosphodiesterase (CNP, Accession NP_149124.1) is another GAM2071 target gene, herein designated TARGET GENE. CNP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNP BINDING SITE, designated SEQ ID:5014, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40893] Another function of GAM2071 is therefore inhibition of 2',3'-cyclic nucleotide 3' phosphodiesterase (CNP, Accession NP_149124.1), a gene which can link tubulin to membranes and may regulate cytoplasmic microtubule distribution. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNP.

[40894] The function of CNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Collectin sub-family member 12 (COLEC12,

Accession NP_110408.2) is another GAM2071 target gene, herein designated TARGET GENE. COLEC12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COLEC12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COLEC12 BINDING SITE, designated SEQ ID:13793, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40895] Another function of GAM2071 is therefore inhibition of Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC12.

[40896] Cop9 constitutive photomorphogenic homolog subunit 7a (arabidopsis) (COPS7A, Accession NP_057403.1) is another GAM2071 target gene, herein designated TARGET GENE. COPS7A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by COPS7A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COPS7A BINDING SITE, designated SEQ ID:5715, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40897] Another function of GAM2071 is therefore inhibition of Cop9 constitutive photomorphogenic homolog subunit 7a (arabidopsis) (COPS7A, Accession NP_057403.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COPS7A.

[40898] CPR8 (Accession NP_065790.1) is another GAM2071 target gene, herein designated TARGET GENE. CPR8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CPR8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPR8 BINDING SITE, designated SEQ ID:9163, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40899] Another function of GAM2071 is therefore inhibition of CPR8 (Accession NP_065790.1) . Accordingly, utilities of

GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPR8.

[40900] Carbamoyl-phosphate synthetase 1, mitochondrial (CPS1, Accession NP_001866.2) is another GAM2071 target gene, herein designated TARGET GENE. CPS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPS1 BINDING SITE, designated SEQ ID:4147, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40901] Another function of GAM2071 is therefore inhibition of Carbamoyl-phosphate synthetase 1, mitochondrial (CPS1, Accession NP_001866.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPS1.

[40902] Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) is another GAM2071 target gene, herein designated TARGET GENE. CPSF2 BINDING SITE1 and CPSF2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by

CPSF2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPSF2 BINDING SITE1 and CPSF2 BINDING SITE2, designated SEQ ID:6739 and SEQ ID:6347 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40903] Another function of GAM2071 is therefore inhibition of Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPSF2.

[40904] Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000642.2) is another GAM2071 target gene, herein designated TARGET GENE. CR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CR1 BINDING SITE, designated SEQ ID:13868, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40905] Another function of GAM2071 is therefore inhibition of Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000642.2). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CR1.

[40906] Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000564.1) is another GAM2071 target gene, herein designated TARGET GENE. CR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CR1 BINDING SITE, designated SEQ ID:13868, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40907] Another function of GAM2071 is therefore inhibition of Complement component (3b/4b) receptor 1, including knops blood group system (CR1, Accession NP_000564.1)

. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CR1.

[40908] Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) is another GAM2071 target gene, herein designated TARGET GENE. CRLF3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRLF3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRLF3 BINDING SITE, designated SEQ ID:9675, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40909] Another function of GAM2071 is therefore inhibition of Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRLF3.

[40910] Cofactor required for sp1 transcriptional activation, subunit 6, 77kda (CRSP6, Accession NP_004259.3) is another GAM2071 target gene, herein designated TARGET GENE. CRSP6 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by CRSP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRSP6 BINDING SITE, designated SEQ ID:12005, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40911] Another function of GAM2071 is therefore inhibition of Cofactor required for sp1 transcriptional activation, subunit 6, 77kda (CRSP6, Accession NP_004259.3), a gene which is required for Sp1 mediated transcriptional activation with TAF(II)s. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRSP6.

[40912] The function of CRSP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.CSE-C (Accession NP_061851.1) is another GAM2071 target gene, herein designated TARGET GENE. CSE-C BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CSE-C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSE-C BINDING SITE, designated SEQ ID:2336, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40913] Another function of GAM2071 is therefore inhibition of CSE-C (Accession NP_061851.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE-C.

[40914] Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_803185.1) is another GAM2071 target gene, herein designated TARGET GENE. CSE1L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CSE1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSE1L BINDING SITE, designated SEQ ID:3997, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40915] Another function of GAM2071 is therefore inhibition of Cse1 chromosome segregation 1-like (yeast) (CSE1L, Accession NP_803185.1) . Accordingly, utilities of GAM2071

include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE1L.

[40916] Calsenilin, presenilin binding protein, ef hand transcription factor (CSEN, Accession NP_038462.1) is another GAM2071 target gene, herein designated TARGET GENE. CSEN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CSEN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSEN BINDING SITE, designated SEQ ID:14933, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40917] Another function of GAM2071 is therefore inhibition of Calsenilin, presenilin binding protein, ef hand transcription factor (CSEN, Accession NP_038462.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSEN.

[40918] Casein kinase 2, alpha prime polypeptide (CSNK2A2, Accession NP_001887.1) is another GAM2071 target gene, herein designated TARGET GENE. CSNK2A2 BINDING SITE is a target binding site found in the 5` untranslated re-

gion of mRNA encoded by CSNK2A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSNK2A2 BINDING SITE, designated SEQ ID:15382, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40919] Another function of GAM2071 is therefore inhibition of Casein kinase 2, alpha prime polypeptide (CSNK2A2, Accession NP_001887.1), a gene which catalyzes the phosphorylation of serine or threonine residues in proteins. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK2A2.

[40920] The function of CSNK2A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.CST (Accession NP_004852.1) is another GAM2071 target gene, herein designated TARGET GENE. CST BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of CST BINDING SITE, designated SEQ ID:3944, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40921] Another function of GAM2071 is therefore inhibition of CST (Accession NP_004852.1), a gene which nucleotide-sugar transporter. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CST.

[40922] The function of CST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM221.1.CTEN (Accession NP_116254.3) is another GAM2071 target gene, herein designated TARGET GENE. CTEN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTEN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTEN BINDING SITE, designated SEQ ID:14087, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40923] Another function of GAM2071 is therefore inhibition of

CTEN (Accession NP_116254.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTEN.

[40924] Cathepsin s (CTSS, Accession NP_004070.3) is another GAM2071 target gene, herein designated TARGET GENE. CTSS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTSS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSS BINDING SITE, designated SEQ ID:7946, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40925] Another function of GAM2071 is therefore inhibition of Cathepsin s (CTSS, Accession NP_004070.3), a gene which is a lysosomal cysteine (thiol) protease that cleaves elastin. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSS.

[40926] The function of CTSS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Chemokine (c-x-c motif) ligand 16 (CXCL16,

Accession NP_071342.1) is another GAM2071 target gene, herein designated TARGET GENE. CXCL16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CXCL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CXCL16 BINDING SITE, designated SEQ ID:11701, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40927] Another function of GAM2071 is therefore inhibition of Chemokine (c-x-c motif) ligand 16 (CXCL16, Accession NP_071342.1), a gene which induces calcium mobilization. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCL16.

[40928] The function of CXCL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.CXYorf1 (Accession XP_088704.2) is another GAM2071 target gene, herein designated TARGET GENE. CXYorf1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CXYorf1,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CXYorf1 BINDING SITE, designated SEQ ID:6801, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40929] Another function of GAM2071 is therefore inhibition of CXYorf1 (Accession XP_088704.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXYorf1.

[40930] CYCS (Accession NP_061820.1) is another GAM2071 target gene, herein designated TARGET GENE. CYCS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYCS BINDING SITE, designated SEQ ID:14950, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40931] Another function of GAM2071 is therefore inhibition of CYCS (Accession NP_061820.1) . Accordingly, utilities of

GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYCS.

[40932] Cytochrome p450, subfamily i (aromatic compound-inducible), polypeptide 2 (CYP1A2, Accession NP_000752.1) is another GAM2071 target gene, herein designated TARGET GENE. CYP1A2 BINDING SITE1 through CYP1A2 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by CYP1A2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP1A2 BINDING SITE1 through CYP1A2 BINDING SITE3, designated SEQ ID:8688, SEQ ID:6816 and SEQ ID:13973 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40933] Another function of GAM2071 is therefore inhibition of Cytochrome p450, subfamily i (aromatic compound-inducible), polypeptide 2 (CYP1A2, Accession NP_000752.1), a gene which intervenes in an NADPH- dependent electron transport pathway. and therefore may be associated with Porphyria cutanea tarda. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Porphyria cutanea tarda, and of other diseases

and clinical conditions associated with CYP1A2.

[40934] The function of CYP1A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1) is another GAM2071 target gene, herein designated TARGET GENE. CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CYP2B6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2, designated SEQ ID:9252 and SEQ ID:3011 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40935] Another function of GAM2071 is therefore inhibition of Cytochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1), a gene which oxidizes a variety of structurally unrelated compounds, including steroids, fatty acids, and xenobiotics. Accordingly, utilities of

GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP2B6.

[40936] The function of CYP2B6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily ivf, polypeptide 3 (leukotriene b4 omega hydroxylase) (CYP4F3, Accession NP_000887.1) is another GAM2071 target gene, herein designated TARGET GENE. CYP4F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP4F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP4F3 BINDING SITE, designated SEQ ID:1417, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40937] Another function of GAM2071 is therefore inhibition of Cytochrome p450, subfamily ivf, polypeptide 3 (leukotriene b4 omega hydroxylase) (CYP4F3, Accession NP_000887.1), a gene which converts leukotriene B4 into the less active 20- hydroxy- leukotriene B4. Accordingly, utilities of GAM2071 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with CYP4F3.

[40938] The function of CYP4F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.1.CYP51A1 (Accession NP_000777.1) is another GAM2071 target gene, herein designated TARGET GENE. CYP51A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP51A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP51A1 BINDING SITE, designated SEQ ID:10631, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40939] Another function of GAM2071 is therefore inhibition of CYP51A1 (Accession NP_000777.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP51A1.

[40940] Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession

NP_004382.1) is another GAM2071 target gene, herein designated TARGET GENE. CYP8B1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP8B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP8B1 BINDING SITE, designated SEQ ID:5584, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40941] Another function of GAM2071 is therefore inhibition of Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1), a gene which functions in bile acid biosynthesis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP8B1.

[40942] The function of CYP8B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Debranching enzyme homolog 1 (s. cerevisiae) (DBR1, Accession NP_057300.1) is another GAM2071 target gene, herein designated TARGET GENE.

DBR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DBR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DBR1 BINDING SITE, designated SEQ ID:1031, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40943] Another function of GAM2071 is therefore inhibition of Debranching enzyme homolog 1 (s. cerevisiae) (DBR1, Accession NP_057300.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBR1.

[40944] Doublecortin and cam kinase-like 1 (DCAMKL1, Accession NP_004725.1) is another GAM2071 target gene, herein designated TARGET GENE. DCAMKL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DCAMKL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCAMKL1 BINDING SITE, designated SEQ ID:4605, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA,

also designated SEQ ID:371.

[40945] Another function of GAM2071 is therefore inhibition of Doublecortin and cam kinase-like 1 (DCAMKL1, Accession NP_004725.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCAMKL1.

[40946] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835364.1) is another GAM2071 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:6035, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40947] Another function of GAM2071 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835364.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[40948] Doublecortex; lissencephaly, x-linked (doublecortin)

(DCX, Accession NP_835366.1) is another GAM2071 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:6035, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40949] Another function of GAM2071 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[40950] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) is another GAM2071 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of DCX BINDING SITE, designated SEQ ID:6035, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40951] Another function of GAM2071 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[40952] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) is another GAM2071 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:6035, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40953] Another function of GAM2071 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with DCX.

[40954] Dead/h (asp-glu-ala-asp/his) box polypeptide 31 (DDX31, Accession NP_619526.1) is another GAM2071 target gene, herein designated TARGET GENE. DDX31 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DDX31, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX31 BINDING SITE, designated SEQ ID:17894, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40955] Another function of GAM2071 is therefore inhibition of Dead/h (asp-glu-ala-asp/his) box polypeptide 31 (DDX31, Accession NP_619526.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX31.

[40956] Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1) is another GAM2071 target gene, herein designated TARGET GENE. DFFB BINDING SITE1 and DFFB BINDING SITE2 are target binding sites found in untranslated regions of

mRNA encoded by DFFB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DFFB BINDING SITE1 and DFFB BINDING SITE2, designated SEQ ID:7574 and SEQ ID:7848 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40957] Another function of GAM2071 is therefore inhibition of Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1), a gene which induces DNA fragmentation and chromatin condensation during apoptosis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DFFB.

[40958] The function of DFFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1) is another GAM2071 target gene, herein designated TARGET GENE. DIAPH2 BINDING SITE is a target binding site found in the 3` un-

translated region of multiple transcripts of mRNA encoded by DIAPH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DIAPH2 BINDING SITE, designated SEQ ID:12586, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40959] Another function of GAM2071 is therefore inhibition of Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1), a gene which may affect in oogenesis and therefore may be associated with Premature ovarian failure . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Premature ovarian failure ., and of other diseases and clinical conditions associated with DIAPH2.

[40960] The function of DIAPH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1) is another GAM2071 target gene, herein designated TARGET GENE. DISC1 BINDING SITE1 through DISC1 BINDING SITE4 are target binding sites

found in untranslated regions of mRNA encoded by DISC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DISC1 BINDING SITE1 through DISC1 BINDING SITE4, designated SEQ ID:5967, SEQ ID:6590, SEQ ID:13620 and SEQ ID:10777 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40961] Another function of GAM2071 is therefore inhibition of Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1), a gene which has globular N- terminal domain(s) and a helical C- terminal domain. and therefore may be associated with Schizophrenia . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Schizophrenia ., and of other diseases and clinical conditions associated with DISC1.

[40962] The function of DISC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1) is another GAM2071 target gene, herein designated TARGET GENE. DISC1 BINDING SITE1

through DISC1 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by DISC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DISC1 BINDING SITE1 through DISC1 BINDING SITE4, designated SEQ ID:6590, SEQ ID:11474, SEQ ID:7947 and SEQ ID:18031 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40963] Another function of GAM2071 is therefore inhibition of Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1), a gene which has globular N- terminal domain(s) and a helical C- terminal domain. and therefore may be associated with Schizophrenia . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Schizophrenia ., and of other diseases and clinical conditions associated with DISC1.

[40964] The function of DISC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.DKFZp434O0320 (Accession XP_097012.2) is another GAM2071 target gene, herein designated TAR-

GET GENE. DKFZp434O0320 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434O0320, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434O0320 BINDING SITE, designated SEQ ID:3669, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40965] Another function of GAM2071 is therefore inhibition of DKFZp434O0320 (Accession XP_097012.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434O0320.

[40966] DKFZp547P234 (Accession NP_694590.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp547P234 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547P234, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547P234 BINDING SITE, designated SEQ ID:3007, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40967] Another function of GAM2071 is therefore inhibition of DKFZp547P234 (Accession NP_694590.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547P234.

[40968] DKFZP564D166 (Accession NP_108648.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZP564D166 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DKFZP564D166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564D166 BINDING SITE, designated SEQ ID:13202, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40969] Another function of GAM2071 is therefore inhibition of DKFZP564D166 (Accession NP_108648.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D166.

[40970] DKFZP564G092 (Accession NP_056416.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZP564G092 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP564G092, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564G092 BINDING SITE, designated SEQ ID:519, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40971] Another function of GAM2071 is therefore inhibition of DKFZP564G092 (Accession NP_056416.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564G092.

[40972] DKFZP564I122 (Accession XP_032397.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZP564I122 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564I122, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of DKFZP564I122 BINDING SITE, designated SEQ ID:19815, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40973] Another function of GAM2071 is therefore inhibition of DKFZP564I122 (Accession XP_032397.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564I122.

[40974] DKFZP564J0863 (Accession NP_056274.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZP564J0863 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564J0863, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564J0863 BINDING SITE, designated SEQ ID:18946, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40975] Another function of GAM2071 is therefore inhibition of DKFZP564J0863 (Accession NP_056274.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZP564J0863.

[40976] DKFZP564K0322 (Accession NP_114429.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZP564K0322 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564K0322, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564K0322 BINDING SITE, designated SEQ ID:1414, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40977] Another function of GAM2071 is therefore inhibition of DKFZP564K0322 (Accession NP_114429.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564K0322.

[40978] DKFZp564K142 (Accession NP_115497.2) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp564K142 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp564K142, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp564K142 BINDING SITE, designated SEQ ID:811, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40979] Another function of GAM2071 is therefore inhibition of DKFZp564K142 (Accession NP_115497.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp564K142.

[40980] DKFZP566K1924 (Accession NP_056278.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZP566K1924 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP566K1924, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566K1924 BINDING SITE, designated SEQ ID:9020, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40981] Another function of GAM2071 is therefore inhibition of

DKFZP566K1924 (Accession NP_056278.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566K1924.

[40982] DKFZP566M114 (Accession NP_115504.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZP566M114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP566M114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566M114 BINDING SITE, designated SEQ ID:1708, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40983] Another function of GAM2071 is therefore inhibition of DKFZP566M114 (Accession NP_115504.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566M114.

[40984] DKFZP586B1621 (Accession NP_056348.2) is another GAM2071 target gene, herein designated TARGET GENE. DKFZP586B1621 BINDING SITE1 and DKFZP586B1621

BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DKFZP586B1621, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586B1621 BINDING SITE1 and DKFZP586B1621 BINDING SITE2, designated SEQ ID:20110 and SEQ ID:4762 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40985] Another function of GAM2071 is therefore inhibition of DKFZP586B1621 (Accession NP_056348.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586B1621.

[40986] DKFZp586C0721 (Accession XP_098416.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp586C0721 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp586C0721, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp586C0721 BINDING SITE,

designated SEQ ID:14672, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40987] Another function of GAM2071 is therefore inhibition of DKFZp586C0721 (Accession XP_098416.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp586C0721.

[40988] DKFZP586D0919 (Accession NP_056248.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZP586D0919 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586D0919, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586D0919 BINDING SITE, designated SEQ ID:5664, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40989] Another function of GAM2071 is therefore inhibition of DKFZP586D0919 (Accession NP_056248.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZP586D0919.

[40990] DKFZp667B1218 (Accession NP_808881.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp667B1218 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp667B1218, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667B1218 BINDING SITE, designated SEQ ID:4387, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40991] Another function of GAM2071 is therefore inhibition of DKFZp667B1218 (Accession NP_808881.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp667B1218.

[40992] DKFZp667E0512 (Accession XP_117353.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp667E0512 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp667E0512, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667E0512 BINDING SITE, designated SEQ ID:9198, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40993] Another function of GAM2071 is therefore inhibition of DKFZp667E0512 (Accession XP_117353.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp667E0512.

[40994] DKFZp761B107 (Accession NP_775734.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp761B107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761B107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B107 BINDING SITE, designated SEQ ID:5298, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40995] Another function of GAM2071 is therefore inhibition of DKFZp761B107 (Accession NP_775734.1) . Accordingly,

utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B107.

[40996] DKFZp761B128 (Accession NP_689650.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp761B128 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761B128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B128 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40997] Another function of GAM2071 is therefore inhibition of DKFZp761B128 (Accession NP_689650.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B128.

[40998] DKFZp761H039 (Accession NP_061181.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp761H039 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

DKFZp761H039, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761H039 BINDING SITE, designated SEQ ID:12709, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[40999] Another function of GAM2071 is therefore inhibition of DKFZp761H039 (Accession NP_061181.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761H039.

[41000] DKFZp761J139 (Accession NP_115656.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp761J139 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761J139, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761J139 BINDING SITE, designated SEQ ID:969, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41001] Another function of GAM2071 is therefore inhibition of DKFZp761J139 (Accession NP_115656.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761J139.

[41002] DKFZp761O0113 (Accession NP_060879.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp761O0113 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761O0113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761O0113 BINDING SITE, designated SEQ ID:11194, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41003] Another function of GAM2071 is therefore inhibition of DKFZp761O0113 (Accession NP_060879.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761O0113.

[41004] DKFZp761P1121 (Accession NP_690870.1) is another GAM2071 target gene, herein designated TARGET GENE.

DKFZp761P1121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761P1121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761P1121 BINDING SITE, designated SEQ ID:1413, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41005] Another function of GAM2071 is therefore inhibition of DKFZp761P1121 (Accession NP_690870.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761P1121.

[41006] DKFZp762C2414 (Accession NP_848637.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp762C2414 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762C2414, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762C2414 BINDING SITE, designated SEQ ID:11830, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41007] Another function of GAM2071 is therefore inhibition of DKFZp762C2414 (Accession NP_848637.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762C2414.

[41008] DKFZp762H185 (Accession XP_172976.2) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp762H185 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762H185, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762H185 BINDING SITE, designated SEQ ID:2137, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41009] Another function of GAM2071 is therefore inhibition of DKFZp762H185 (Accession XP_172976.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762H185.

[41010] DKFZp762I137 (Accession NP_689624.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp762I137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762I137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762I137 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41011] Another function of GAM2071 is therefore inhibition of DKFZp762I137 (Accession NP_689624.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762I137.

[41012] DKFZp762I194 (Accession NP_689597.1) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp762I194 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762I194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of DKFZp762I194 BINDING SITE, designated SEQ ID:19272, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41013] Another function of GAM2071 is therefore inhibition of DKFZp762I194 (Accession NP_689597.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762I194.

[41014] DKFZp762L0311 (Accession NP_061189.2) is another GAM2071 target gene, herein designated TARGET GENE. DKFZp762L0311 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762L0311, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762L0311 BINDING SITE, designated SEQ ID:13546, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41015] Another function of GAM2071 is therefore inhibition of DKFZp762L0311 (Accession NP_061189.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZp762L0311.

[41016] Dystrophia myotonica-containing wd repeat motif (DMWD, Accession XP_027569.1) is another GAM2071 target gene, herein designated TARGET GENE. DMWD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DMWD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DMWD BINDING SITE, designated SEQ ID:10543, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41017] Another function of GAM2071 is therefore inhibition of Dystrophia myotonica-containing wd repeat motif (DMWD, Accession XP_027569.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMWD.

[41018] DRIM (Accession NP_055318.1) is another GAM2071 target gene, herein designated TARGET GENE. DRIM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DRIM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DRIM BINDING SITE, designated SEQ ID:2324, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41019] Another function of GAM2071 is therefore inhibition of DRIM (Accession NP_055318.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRIM.

[41020] Desmocollin 3 (DSC3, Accession NP_001932.1) is another GAM2071 target gene, herein designated TARGET GENE. DSC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE, designated SEQ ID:2085, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41021] Another function of GAM2071 is therefore inhibition of Desmocollin 3 (DSC3, Accession NP_001932.1), a gene which is a component of intercellular desmosome junc-

tions. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC3.

[41022] The function of DSC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Desmocollin 3 (DSC3, Accession NP_077741.1) is another GAM2071 target gene, herein designated TARGET GENE. DSC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE, designated SEQ ID:2085, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41023] Another function of GAM2071 is therefore inhibition of Desmocollin 3 (DSC3, Accession NP_077741.1), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC3.

[41024] The function of DSC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Down syndrome critical region gene 3 (DSCR3, Accession NP_006043.1) is another GAM2071 target gene, herein designated TARGET GENE. DSCR3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DSCR3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSCR3 BINDING SITE, designated SEQ ID:13453, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41025] Another function of GAM2071 is therefore inhibition of Down syndrome critical region gene 3 (DSCR3, Accession NP_006043.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSCR3.

[41026] Down syndrome critical region gene 6 (DSCR6, Accession NP_061835.1) is another GAM2071 target gene, herein designated TARGET GENE. DSCR6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by DSCR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSCR6 BINDING SITE, designated SEQ ID:17339, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41027] Another function of GAM2071 is therefore inhibition of Down syndrome critical region gene 6 (DSCR6, Accession NP_061835.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSCR6.

[41028] DUPLIN (Accession XP_208760.3) is another GAM2071 target gene, herein designated TARGET GENE. DUPLIN BINDING SITE1 and DUPLIN BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DUPLIN, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUPLIN BINDING SITE1 and DUPLIN BINDING SITE2, designated SEQ ID:2517 and SEQ ID:13723 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ

ID:371.

[41029] Another function of GAM2071 is therefore inhibition of DUPLIN (Accession XP_208760.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUPLIN.

[41030] DUSP18 (Accession NP_689724.2) is another GAM2071 target gene, herein designated TARGET GENE. DUSP18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DUSP18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP18 BINDING SITE, designated SEQ ID:19123, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41031] Another function of GAM2071 is therefore inhibition of DUSP18 (Accession NP_689724.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP18.

[41032] Dual specificity phosphatase 19 (DUSP19, Accession NP_543152.1) is another GAM2071 target gene, herein designated TARGET GENE. DUSP19 BINDING SITE1 and

DUSP19 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DUSP19, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP19 BINDING SITE1 and DUSP19 BINDING SITE2, designated SEQ ID:710 and SEQ ID:969 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41033] Another function of GAM2071 is therefore inhibition of Dual specificity phosphatase 19 (DUSP19, Accession NP_543152.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP19.

[41034] Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NP_567824.1) is another GAM2071 target gene, herein designated TARGET GENE. DYRK1A BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by DYRK1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DYRK1A BINDING SITE, desig-

nated SEQ ID:14469, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41035] Another function of GAM2071 is therefore inhibition of Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NP_567824.1), a gene which regulates cell proliferation and may be involved in brain development . and therefore may be associated with Down syndrome. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Down syndrome, and of other diseases and clinical conditions associated with DYRK1A.

[41036] The function of DYRK1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Endothelial differentiation, sphingolipid g-protein-coupled receptor, 8 (EDG8, Accession NP_110387.1) is another GAM2071 target gene, herein designated TARGET GENE. EDG8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EDG8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of EDG8 BINDING SITE, designated SEQ ID:11935, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41037] Another function of GAM2071 is therefore inhibition of Endothelial differentiation, sphingolipid g-protein-coupled receptor, 8 (EDG8, Accession NP_110387.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDG8.

[41038] EEF2K (Accession NP_037434.1) is another GAM2071 target gene, herein designated TARGET GENE. EEF2K BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EEF2K, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EEF2K BINDING SITE, designated SEQ ID:11618, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41039] Another function of GAM2071 is therefore inhibition of EEF2K (Accession NP_037434.1), a gene which phosphorylates serine or threonine on the eukaryotic elongation

factor- 2 and therefore may be associated with Systemic lupus erythematosus and cancer. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Systemic lupus erythematosus and cancer, and of other diseases and clinical conditions associated with EEF2K.

[41040] The function of EEF2K and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Eh-domain containing 2 (EHD2, Accession NP_055416.2) is another GAM2071 target gene, herein designated TARGET GENE. EHD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EHD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EHD2 BINDING SITE, designated SEQ ID:6934, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41041] Another function of GAM2071 is therefore inhibition of Eh-domain containing 2 (EHD2, Accession NP_055416.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with EHD2.

[41042] Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kda (EIF2S3, Accession NP_001406.1) is another GAM2071 target gene, herein designated TARGET GENE. EIF2S3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF2S3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF2S3 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41043] Another function of GAM2071 is therefore inhibition of Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kda (EIF2S3, Accession NP_001406.1), a gene which functions in the early steps of protein synthesis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2S3.

[41044] The function of EIF2S3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Eukaryotic translation initiation factor 5a2

(EIF5A2, Accession NP_065123.1) is another GAM2071 target gene, herein designated TARGET GENE. EIF5A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF5A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF5A2 BINDING SITE, designated SEQ ID:1333, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41045] Another function of GAM2071 is therefore inhibition of Eukaryotic translation initiation factor 5a2 (EIF5A2, Accession NP_065123.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF5A2.

[41046] ELP3 (Accession NP_060561.3) is another GAM2071 target gene, herein designated TARGET GENE. ELP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ELP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ELP3 BINDING SITE, designated SEQ ID:6182, to the nucleotide sequence

of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41047] Another function of GAM2071 is therefore inhibition of ELP3 (Accession NP_060561.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELP3.

[41048] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690883.1) is another GAM2071 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41049] Another function of GAM2071 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690883.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with EMR2.

[41050] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_038475.2) is another GAM2071 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41051] Another function of GAM2071 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_038475.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[41052] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690882.1) is another GAM2071 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in

the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41053] Another function of GAM2071 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690882.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[41054] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690884.1) is another GAM2071 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE,

designated SEQ ID:433, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41055] Another function of GAM2071 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690884.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[41056] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690881.1) is another GAM2071 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41057] Another function of GAM2071 is therefore inhibition of Egf-like module containing, mucin-like, hormone recep-

tor-like sequence 2 (EMR2, Accession NP_690881.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[41058] Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690885.1) is another GAM2071 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41059] Another function of GAM2071 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690885.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[41060] Egf-like module containing, mucin-like, hormone recep-

tor-like sequence 2 (EMR2, Accession NP_690880.1) is another GAM2071 target gene, herein designated TARGET GENE. EMR2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EMR2 BINDING SITE, designated SEQ ID:433, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41061] Another function of GAM2071 is therefore inhibition of Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (EMR2, Accession NP_690880.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMR2.

[41062] Endonuclease g-like 1 (ENDOGL1, Accession NP_005098.1) is another GAM2071 target gene, herein designated TARGET GENE. ENDOGL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ENDOGL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ENDOGL1 BINDING SITE, designated SEQ ID:4223, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41063] Another function of GAM2071 is therefore inhibition of Endonuclease g-like 1 (ENDOGL1, Accession NP_005098.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENDOGL1.

[41064] Ephb6 (EPHB6, Accession NP_004436.1) is another GAM2071 target gene, herein designated TARGET GENE. EPHB6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by EPHB6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EPHB6 BINDING SITE, designated SEQ ID:19635, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41065] Another function of GAM2071 is therefore inhibition of Ephb6 (EPHB6, Accession NP_004436.1), a gene which Putative Eph- related receptor tyrosine kinase B6. Accord-

ingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPHB6.

[41066] The function of EPHB6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Epsin 2 (EPN2, Accession NP_683723.1) is another GAM2071 target gene, herein designated TARGET GENE. EPN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EPN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EPN2 BINDING SITE, designated SEQ ID:4430, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41067] Another function of GAM2071 is therefore inhibition of Epsin 2 (EPN2, Accession NP_683723.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPN2.

[41068] Epsin 2 (EPN2, Accession NP_055779.1) is another

GAM2071 target gene, herein designated TARGET GENE. EPN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EPN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EPN2 BINDING SITE, designated SEQ ID:4430, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41069] Another function of GAM2071 is therefore inhibition of Epsin 2 (EPN2, Accession NP_055779.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPN2.

[41070] Epiregulin (EREG, Accession NP_001423.1) is another GAM2071 target gene, herein designated TARGET GENE. EREG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EREG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EREG BINDING SITE, designated SEQ ID:430, to the nu-

cleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41071] Another function of GAM2071 is therefore inhibition of Epiregulin (EREG, Accession NP_001423.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EREG.

[41072] Ellis van creveld syndrome (EVC, Accession NP_055371.1) is another GAM2071 target gene, herein designated TARGET GENE. EVC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EVC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:4148, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41073] Another function of GAM2071 is therefore inhibition of Ellis van creveld syndrome (EVC, Accession NP_055371.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC.

[41074] Ellis van creveld syndrome (EVC, Accession NP_714928.1) is another GAM2071 target gene, herein designated TARGET GENE. EVC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EVC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:4148, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41075] Another function of GAM2071 is therefore inhibition of Ellis van creveld syndrome (EVC, Accession NP_714928.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC.

[41076] Ecotropic viral integration site 5 (EVI5, Accession NP_005656.2) is another GAM2071 target gene, herein designated TARGET GENE. EVI5 BINDING SITE1 and EVI5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by EVI5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of EVI5 BINDING SITE1 and EVI5 BINDING SITE2, designated SEQ ID:16074 and SEQ ID:18007 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41077] Another function of GAM2071 is therefore inhibition of Ecotropic viral integration site 5 (EVI5, Accession NP_005656.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVI5.

[41078] F11R (Accession NP_058642.1) is another GAM2071 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:16292, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41079] Another function of GAM2071 is therefore inhibition of F11R (Accession NP_058642.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with F11R.

[41080] F11R (Accession NP_653085.1) is another GAM2071 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:16292, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41081] Another function of GAM2071 is therefore inhibition of F11R (Accession NP_653085.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[41082] F11R (Accession NP_653087.1) is another GAM2071 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:16292,

to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41083] Another function of GAM2071 is therefore inhibition of F11R (Accession NP_653087.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[41084] F11R (Accession NP_653086.1) is another GAM2071 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:16292, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41085] Another function of GAM2071 is therefore inhibition of F11R (Accession NP_653086.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[41086] Coagulation factor ii (thrombin) receptor-like 2 (F2RL2, Accession NP_004092.1) is another GAM2071 target gene, herein designated TARGET GENE. F2RL2 BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by F2RL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F2RL2 BINDING SITE, designated SEQ ID:5026, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41087] Another function of GAM2071 is therefore inhibition of Coagulation factor ii (thrombin) receptor-like 2 (F2RL2, Accession NP_004092.1), a gene which receptor for activated thrombin coupled to g proteins that stimulate phosphoinositide hydrolysis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2RL2.

[41088] The function of F2RL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Coagulation factor ii (thrombin) receptor-like 3 (F2RL3, Accession NP_003941.1) is another GAM2071 target gene, herein designated TARGET GENE. F2RL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F2RL3, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F2RL3 BINDING SITE, designated SEQ ID:13324, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41089] Another function of GAM2071 is therefore inhibition of Coagulation factor ii (thrombin) receptor-like 3 (F2RL3, Accession NP_003941.1), a gene which Protease- activated receptor 4; G protein- coupled receptor that increases phosphoinositide hydrolysis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2RL3.

[41090] The function of F2RL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1) is another GAM2071 target gene, herein designated TARGET GENE. F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of F3 BINDING SITE, designated SEQ ID:15547, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41091] Another function of GAM2071 is therefore inhibition of Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1), a gene which functions in normal hemostasis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F3.

[41092] The function of F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Family with sequence similarity 13, member a1 (FAM13A1, Accession NP_055698.1) is another GAM2071 target gene, herein designated TARGET GENE. FAM13A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FAM13A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FAM13A1 BINDING SITE, designated SEQ ID:17686, to the nucleotide sequence of GAM2071

RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41093] Another function of GAM2071 is therefore inhibition of Family with sequence similarity 13, member a1 (FAM13A1, Accession NP_055698.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAM13A1.

[41094] Fanconi anemia, complementation group e (FANCE, Accession NP_068741.1) is another GAM2071 target gene, herein designated TARGET GENE. FANCE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCE BINDING SITE, designated SEQ ID:16751, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41095] Another function of GAM2071 is therefore inhibition of Fanconi anemia, complementation group e (FANCE, Accession NP_068741.1), a gene which is a possible regulator of lymphocyte and platelet function. and therefore is associated with Fanconi anemia, complementation group

e. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Fanconi anemia, complementation group e., and of other diseases and clinical conditions associated with FANCE.

[41096] The function of FANCE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Fanconi anemia, complementation group f (FANCF, Accession NP_073562.1) is another GAM2071 target gene, herein designated TARGET GENE. FANCF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCF BINDING SITE, designated SEQ ID:14445, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41097] Another function of GAM2071 is therefore inhibition of Fanconi anemia, complementation group f (FANCF, Accession NP_073562.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCF.

[41098] FAT3 (Accession XP_061871.5) is another GAM2071 target gene, herein designated TARGET GENE. FAT3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FAT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FAT3 BINDING SITE, designated SEQ ID:7945, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41099] Another function of GAM2071 is therefore inhibition of FAT3 (Accession XP_061871.5) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAT3.

[41100] Fibulin 1 (FBLN1, Accession NP_006476.1) is another GAM2071 target gene, herein designated TARGET GENE. FBLN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBLN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBLN1 BINDING SITE, designated SEQ ID:2764, to the nucleotide sequence of GAM2071

RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41101] Another function of GAM2071 is therefore inhibition of Fibulin 1 (FBLN1, Accession NP_006476.1), a gene which secreted glycoprotein; has EGF- like repeats, similar to anaphylatoxins C3a, C4a, and C5a. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBLN1.

[41102] The function of FBLN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM179.1.FBXW8 (Accession NP_036306.1) is another GAM2071 target gene, herein designated TARGET GENE. FBXW8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXW8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXW8 BINDING SITE, designated SEQ ID:20011, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41103] Another function of GAM2071 is therefore inhibition of

FBXW8 (Accession NP_036306.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW8.

[41104] FBXW8 (Accession NP_699179.2) is another GAM2071 target gene, herein designated TARGET GENE. FBXW8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXW8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXW8 BINDING SITE, designated SEQ ID:20011, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41105] Another function of GAM2071 is therefore inhibition of FBXW8 (Accession NP_699179.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW8.

[41106] Fc fragment of iga, receptor for (FCAR, Accession NP_579812.1) is another GAM2071 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA en-

coded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:18209, SEQ ID:18209 and SEQ ID:10505 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41107] Another function of GAM2071 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579812.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[41108] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Accession NP_579808.1) is another GAM2071 target gene, herein designated TARGET GENE. FCAR BINDING SITE1

through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:18209, SEQ ID:18209 and SEQ ID:441 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41109] Another function of GAM2071 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579808.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[41110] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Ac-

cession NP_579806.1) is another GAM2071 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:18209, SEQ ID:441 and SEQ ID:18209 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41111] Another function of GAM2071 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579806.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[41112] The function of FCAR and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM136.1.Fc fragment of iga, receptor for (FCAR, Accession NP_579807.1) is another GAM2071 target gene, herein designated TARGET GENE. FCAR BINDING SITE1 through FCAR BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FCAR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE1 through FCAR BINDING SITE3, designated SEQ ID:18209, SEQ ID:10188 and SEQ ID:1759 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41113] Another function of GAM2071 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579807.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[41114] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) is another GAM2071 target gene, herein designated TARGET GENE. FER1L4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FER1L4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FER1L4 BINDING SITE, designated SEQ ID:1759, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41115] Another function of GAM2071 is therefore inhibition of Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER1L4.

[41116] Fasciculation and elongation protein zeta 1 (zygin i) (FEZ1, Accession NP_072043.1) is another GAM2071 target gene, herein designated TARGET GENE. FEZ1 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by FEZ1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FEZ1 BINDING SITE, designated SEQ ID:659, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41117] Another function of GAM2071 is therefore inhibition of Fasciculation and elongation protein zeta 1 (zygin i) (FEZ1, Accession NP_072043.1), a gene which Zygin 1; may have a role in axonal outgrowth; has similarity to C. elegans UNC- 76. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEZ1.

[41118] The function of FEZ1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Fibroblast growth factor 5 (FGF5, Accession NP_149134.1) is another GAM2071 target gene, herein designated TARGET GENE. FGF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGF5, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE, designated SEQ ID:3375, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41119] Another function of GAM2071 is therefore inhibition of Fibroblast growth factor 5 (FGF5, Accession NP_149134.1), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5.

[41120] The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.1.Fibroblast growth factor 5 (FGF5, Accession NP_004455.1) is another GAM2071 target gene, herein designated TARGET GENE. FGF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE, designated SEQ ID:3375, to the nucleotide

sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41121] Another function of GAM2071 is therefore inhibition of Fibroblast growth factor 5 (FGF5, Accession NP_004455.1), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5.

[41122] The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.1.Four and a half lim domains 2 (FHL2, Accession NP_001441.2) is another GAM2071 target gene, herein designated TARGET GENE. FHL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FHL2 BINDING SITE, designated SEQ ID:19820, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41123] Another function of GAM2071 is therefore inhibition of

Four and a half lim domains 2 (FHL2, Accession NP_001441.2), a gene which Contains four LIM domains and an additional zinc finger. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHL2.

[41124] The function of FHL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Fk506 binding protein 9, 63 kda (FKBP9, Accession NP_009201.1) is another GAM2071 target gene, herein designated TARGET GENE. FKBP9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FKBP9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FKBP9 BINDING SITE, designated SEQ ID:2718, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41125] Another function of GAM2071 is therefore inhibition of Fk506 binding protein 9, 63 kda (FKBP9, Accession NP_009201.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with FKBP9.

[41126] FLJ00060 (Accession XP_028154.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ00060 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ00060, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ00060 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41127] Another function of GAM2071 is therefore inhibition of FLJ00060 (Accession XP_028154.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00060.

[41128] FLJ10101 (Accession NP_078994.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ10101 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ10101 BINDING SITE, designated SEQ ID:10153, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41129] Another function of GAM2071 is therefore inhibition of FLJ10101 (Accession NP_078994.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10101.

[41130] FLJ10232 (Accession NP_060503.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ10232 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10232, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10232 BINDING SITE, designated SEQ ID:14903, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41131] Another function of GAM2071 is therefore inhibition of FLJ10232 (Accession NP_060503.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10232.

[41132] FLJ10298 (Accession NP_060520.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ10298 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10298, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10298 BINDING SITE, designated SEQ ID:468, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41133] Another function of GAM2071 is therefore inhibition of FLJ10298 (Accession NP_060520.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10298.

[41134] FLJ10346 (Accession NP_060535.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ10346 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10346 BINDING SITE, designated SEQ ID:7836, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41135] Another function of GAM2071 is therefore inhibition of FLJ10346 (Accession NP_060535.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10346.

[41136] FLJ10535 (Accession NP_060599.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ10535 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10535, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10535 BINDING SITE, designated SEQ ID:10633, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41137] Another function of GAM2071 is therefore inhibition of FLJ10535 (Accession NP_060599.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10535.

[41138] FLJ10640 (Accession NP_061896.1) is another GAM2071

target gene, herein designated TARGET GENE. FLJ10640 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10640, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10640 BINDING SITE, designated SEQ ID:16789, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41139] Another function of GAM2071 is therefore inhibition of FLJ10640 (Accession NP_061896.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10640.

[41140] FLJ10713 (Accession NP_060659.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ10713 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10713, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10713 BINDING SITE, designated SEQ ID:12092, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41141] Another function of GAM2071 is therefore inhibition of FLJ10713 (Accession NP_060659.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10713.

[41142] FLJ10737 (Accession NP_060668.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ10737 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10737, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10737 BINDING SITE, designated SEQ ID:2224, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41143] Another function of GAM2071 is therefore inhibition of FLJ10737 (Accession NP_060668.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10737.

[41144] FLJ10846 (Accession NP_060711.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ10846

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10846, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10846 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41145] Another function of GAM2071 is therefore inhibition of FLJ10846 (Accession NP_060711.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10846.

[41146] FLJ10847 (Accession NP_060712.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ10847 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10847, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10847 BINDING SITE, designated SEQ ID:18108, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41147] Another function of GAM2071 is therefore inhibition of FLJ10847 (Accession NP_060712.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10847.

[41148] FLJ10998 (Accession NP_060764.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ10998 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10998, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10998 BINDING SITE, designated SEQ ID:20020, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41149] Another function of GAM2071 is therefore inhibition of FLJ10998 (Accession NP_060764.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10998.

[41150] FLJ11274 (Accession NP_060845.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ11274 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by FLJ11274, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11274 BINDING SITE, designated SEQ ID:7307, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41151] Another function of GAM2071 is therefore inhibition of FLJ11274 (Accession NP_060845.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11274.

[41152] FLJ11323 (Accession NP_060860.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ11323 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ11323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11323 BINDING SITE, designated SEQ ID:13280, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41153] Another function of GAM2071 is therefore inhibition of FLJ11323 (Accession NP_060860.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11323.

[41154] FLJ11467 (Accession NP_079239.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ11467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11467 BINDING SITE, designated SEQ ID:9552, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41155] Another function of GAM2071 is therefore inhibition of FLJ11467 (Accession NP_079239.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11467.

[41156] FLJ11710 (Accession NP_079122.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ11710 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ11710, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11710 BINDING SITE, designated SEQ ID:6034, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41157] Another function of GAM2071 is therefore inhibition of FLJ11710 (Accession NP_079122.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11710.

[41158] FLJ11800 (Accession NP_079250.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ11800 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11800, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11800 BINDING SITE, designated SEQ ID:17222, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41159] Another function of GAM2071 is therefore inhibition of

FLJ11800 (Accession NP_079250.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11800.

[41160] FLJ12363 (Accession NP_115543.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ12363 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12363, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12363 BINDING SITE, designated SEQ ID:14486, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41161] Another function of GAM2071 is therefore inhibition of FLJ12363 (Accession NP_115543.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12363.

[41162] FLJ12572 (Accession NP_075056.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ12572 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ12572, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12572 BINDING SITE, designated SEQ ID:14282, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41163] Another function of GAM2071 is therefore inhibition of FLJ12572 (Accession NP_075056.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12572.

[41164] FLJ12586 (Accession NP_078896.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ12586 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ12586, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12586 BINDING SITE, designated SEQ ID:13509, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41165] Another function of GAM2071 is therefore inhibition of FLJ12586 (Accession NP_078896.2) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12586.

[41166] FLJ12747 (Accession XP_290972.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ12747 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12747, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12747 BINDING SITE, designated SEQ ID:8373, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41167] Another function of GAM2071 is therefore inhibition of FLJ12747 (Accession XP_290972.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12747.

[41168] FLJ12888 (Accession NP_079221.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ12888 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12888, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12888 BINDING SITE, designated SEQ ID:1302, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41169] Another function of GAM2071 is therefore inhibition of FLJ12888 (Accession NP_079221.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12888.

[41170] FLJ12891 (Accession NP_079226.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ12891 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12891, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12891 BINDING SITE, designated SEQ ID:13646, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41171] Another function of GAM2071 is therefore inhibition of FLJ12891 (Accession NP_079226.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12891.

[41172] FLJ12903 (Accession NP_073590.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ12903 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12903, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12903 BINDING SITE, designated SEQ ID:4783, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41173] Another function of GAM2071 is therefore inhibition of FLJ12903 (Accession NP_073590.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12903.

[41174] FLJ12960 (Accession NP_078914.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ12960 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12960, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ12960 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41175] Another function of GAM2071 is therefore inhibition of FLJ12960 (Accession NP_078914.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12960.

[41176] FLJ12975 (Accession NP_079085.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ12975 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12975 BINDING SITE, designated SEQ ID:836, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41177] Another function of GAM2071 is therefore inhibition of FLJ12975 (Accession NP_079085.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ12975.

[41178] FLJ13072 (Accession XP_117117.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ13072 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13072, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13072 BINDING SITE, designated SEQ ID:6870, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41179] Another function of GAM2071 is therefore inhibition of FLJ13072 (Accession XP_117117.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13072.

[41180] FLJ13081 (Accession NP_079110.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ13081 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13081, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ13081 BINDING SITE, designated SEQ ID:3389, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41181] Another function of GAM2071 is therefore inhibition of FLJ13081 (Accession NP_079110.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13081.

[41182] FLJ13188 (Accession NP_071346.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ13188 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13188, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13188 BINDING SITE, designated SEQ ID:12816, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41183] Another function of GAM2071 is therefore inhibition of FLJ13188 (Accession NP_071346.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13188.

[41184] FLJ13197 (Accession NP_078890.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ13197 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13197, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13197 BINDING SITE, designated SEQ ID:7946, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41185] Another function of GAM2071 is therefore inhibition of FLJ13197 (Accession NP_078890.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13197.

[41186] FLJ13456 (Accession XP_038291.5) is another GAM2071 target gene, herein designated TARGET GENE. FLJ13456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13456 BINDING SITE, designated SEQ ID:5409, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41187] Another function of GAM2071 is therefore inhibition of FLJ13456 (Accession XP_038291.5) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13456.

[41188] FLJ13590 (Accession NP_079116.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ13590 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13590, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13590 BINDING SITE, designated SEQ ID:6935, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41189] Another function of GAM2071 is therefore inhibition of FLJ13590 (Accession NP_079116.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13590.

[41190] FLJ13639 (Accession NP_078981.1) is another GAM2071

target gene, herein designated TARGET GENE. FLJ13639 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13639, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13639 BINDING SITE, designated SEQ ID:1788, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41191] Another function of GAM2071 is therefore inhibition of FLJ13639 (Accession NP_078981.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13639.

[41192] FLJ13984 (Accession NP_079046.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ13984 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13984, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13984 BINDING SITE, designated SEQ ID:16972, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41193] Another function of GAM2071 is therefore inhibition of FLJ13984 (Accession NP_079046.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13984.

[41194] FLJ14351 (Accession NP_079008.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ14351 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14351, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14351 BINDING SITE, designated SEQ ID:8244, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41195] Another function of GAM2071 is therefore inhibition of FLJ14351 (Accession NP_079008.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14351.

[41196] FLJ14641 (Accession NP_116206.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ14641

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14641, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14641 BINDING SITE, designated SEQ ID:18641, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41197] Another function of GAM2071 is therefore inhibition of FLJ14641 (Accession NP_116206.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14641.

[41198] FLJ14803 (Accession NP_116231.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ14803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14803 BINDING SITE, designated SEQ ID:3409, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41199] Another function of GAM2071 is therefore inhibition of FLJ14803 (Accession NP_116231.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14803.

[41200] FLJ20045 (Accession NP_060108.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ20045 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20045 BINDING SITE, designated SEQ ID:19070, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41201] Another function of GAM2071 is therefore inhibition of FLJ20045 (Accession NP_060108.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20045.

[41202] FLJ20095 (Accession NP_060136.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ20095 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ20095, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20095 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41203] Another function of GAM2071 is therefore inhibition of FLJ20095 (Accession NP_060136.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20095.

[41204] FLJ20344 (Accession NP_060246.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ20344 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20344, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20344 BINDING SITE, designated SEQ ID:8639, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41205] Another function of GAM2071 is therefore inhibition of

FLJ20344 (Accession NP_060246.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20344.

[41206] FLJ20507 (Accession NP_060319.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ20507 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20507 BINDING SITE, designated SEQ ID:12154, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41207] Another function of GAM2071 is therefore inhibition of FLJ20507 (Accession NP_060319.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20507.

[41208] FLJ20511 (Accession NP_060323.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ20511 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20511, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20511 BINDING SITE, designated SEQ ID:969, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41209] Another function of GAM2071 is therefore inhibition of FLJ20511 (Accession NP_060323.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20511.

[41210] FLJ20671 (Accession NP_060394.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ20671 BINDING SITE1 and FLJ20671 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ20671, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20671 BINDING SITE1 and FLJ20671 BINDING SITE2, designated SEQ ID:13745 and SEQ ID:10861 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41211] Another function of GAM2071 is therefore inhibition of FLJ20671 (Accession NP_060394.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20671.

[41212] FLJ20700 (Accession NP_060402.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ20700 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20700, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20700 BINDING SITE, designated SEQ ID:20156, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41213] Another function of GAM2071 is therefore inhibition of FLJ20700 (Accession NP_060402.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20700.

[41214] FLJ20813 (Accession NP_060431.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ20813 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ20813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20813 BINDING SITE, designated SEQ ID:18464, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41215] Another function of GAM2071 is therefore inhibition of FLJ20813 (Accession NP_060431.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20813.

[41216] FLJ21603 (Accession NP_079038.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ21603 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21603 BINDING SITE, designated SEQ ID:11662, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41217] Another function of GAM2071 is therefore inhibition of

FLJ21603 (Accession NP_079038.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21603.

[41218] FLJ21673 (Accession NP_112160.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ21673 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ21673, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21673 BINDING SITE, designated SEQ ID:1926, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41219] Another function of GAM2071 is therefore inhibition of FLJ21673 (Accession NP_112160.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21673.

[41220] FLJ21777 (Accession NP_115585.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ21777 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21777, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21777 BINDING SITE, designated SEQ ID:13303, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41221] Another function of GAM2071 is therefore inhibition of FLJ21777 (Accession NP_115585.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21777.

[41222] FLJ22167 (Accession NP_078809.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ22167 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22167 BINDING SITE, designated SEQ ID:2733, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41223] Another function of GAM2071 is therefore inhibition of FLJ22167 (Accession NP_078809.2) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22167.

[41224] FLJ22329 (Accession NP_078932.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ22329 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22329 BINDING SITE, designated SEQ ID:10803, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41225] Another function of GAM2071 is therefore inhibition of FLJ22329 (Accession NP_078932.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22329.

[41226] FLJ22531 (Accession NP_078926.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ22531 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22531, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22531 BINDING SITE, designated SEQ ID:3548, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41227] Another function of GAM2071 is therefore inhibition of FLJ22531 (Accession NP_078926.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22531.

[41228] FLJ22965 (Accession NP_071384.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ22965 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22965, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22965 BINDING SITE, designated SEQ ID:9754, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41229] Another function of GAM2071 is therefore inhibition of FLJ22965 (Accession NP_071384.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ22965.

[41230] FLJ23022 (Accession NP_079327.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ23022 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23022, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23022 BINDING SITE, designated SEQ ID:541, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41231] Another function of GAM2071 is therefore inhibition of FLJ23022 (Accession NP_079327.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23022.

[41232] FLJ23040 (Accession NP_079450.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ23040 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23040, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ23040 BINDING SITE, designated SEQ ID:12648, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41233] Another function of GAM2071 is therefore inhibition of FLJ23040 (Accession NP_079450.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23040.

[41234] FLJ23053 (Accession NP_075058.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ23053 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23053, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23053 BINDING SITE, designated SEQ ID:16973, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41235] Another function of GAM2071 is therefore inhibition of FLJ23053 (Accession NP_075058.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ23053.

[41236] FLJ23186 (Accession NP_078892.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ23186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23186 BINDING SITE, designated SEQ ID:10010, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41237] Another function of GAM2071 is therefore inhibition of FLJ23186 (Accession NP_078892.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23186.

[41238] FLJ23263 (Accession NP_079391.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ23263 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ23263, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ23263 BINDING SITE, designated SEQ ID:13801, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41239] Another function of GAM2071 is therefore inhibition of FLJ23263 (Accession NP_079391.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23263.

[41240] FLJ23356 (Accession NP_115613.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ23356 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23356 BINDING SITE, designated SEQ ID:14440, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41241] Another function of GAM2071 is therefore inhibition of FLJ23356 (Accession NP_115613.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23356.

[41242] FLJ23392 (Accession NP_079060.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ23392 BINDING SITE1 through FLJ23392 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ23392, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23392 BINDING SITE1 through FLJ23392 BINDING SITE3, designated SEQ ID:11425, SEQ ID:4022 and SEQ ID:431 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41243] Another function of GAM2071 is therefore inhibition of FLJ23392 (Accession NP_079060.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23392.

[41244] FLJ23416 (Accession NP_115614.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ23416 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23416, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ23416 BINDING SITE, designated SEQ ID:4771, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41245] Another function of GAM2071 is therefore inhibition of FLJ23416 (Accession NP_115614.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23416.

[41246] FLJ23556 (Accession NP_079156.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ23556 BINDING SITE1 and FLJ23556 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ23556, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23556 BINDING SITE1 and FLJ23556 BINDING SITE2, designated SEQ ID:6906 and SEQ ID:436 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41247] Another function of GAM2071 is therefore inhibition of FLJ23556 (Accession NP_079156.1) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23556.

[41248] FLJ23834 (Accession NP_689963.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ23834 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23834 BINDING SITE, designated SEQ ID:14133, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41249] Another function of GAM2071 is therefore inhibition of FLJ23834 (Accession NP_689963.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23834.

[41250] FLJ25416 (Accession NP_659455.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ25416 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ25416, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25416 BINDING SITE, designated SEQ ID:8998, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41251] Another function of GAM2071 is therefore inhibition of FLJ25416 (Accession NP_659455.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25416.

[41252] FLJ25795 (Accession NP_689633.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ25795 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25795, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25795 BINDING SITE, designated SEQ ID:18075, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41253] Another function of GAM2071 is therefore inhibition of FLJ25795 (Accession NP_689633.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ25795.

[41254] FLJ31139 (Accession NP_775928.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ31139 BINDING SITE1 and FLJ31139 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ31139, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31139 BINDING SITE1 and FLJ31139 BINDING SITE2, designated SEQ ID:7279 and SEQ ID:1817 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41255] Another function of GAM2071 is therefore inhibition of FLJ31139 (Accession NP_775928.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31139.

[41256] FLJ31153 (Accession NP_653201.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ31153 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31153, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31153 BINDING SITE, designated SEQ ID:13799, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41257] Another function of GAM2071 is therefore inhibition of FLJ31153 (Accession NP_653201.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31153.

[41258] FLJ31401 (Accession NP_689877.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ31401 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31401, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31401 BINDING SITE, designated SEQ ID:11498, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41259] Another function of GAM2071 is therefore inhibition of FLJ31401 (Accession NP_689877.1) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31401.

[41260] FLJ31958 (Accession NP_694575.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ31958 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31958, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31958 BINDING SITE, designated SEQ ID:12975, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41261] Another function of GAM2071 is therefore inhibition of FLJ31958 (Accession NP_694575.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31958.

[41262] FLJ31978 (Accession NP_653270.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ31978 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31978, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31978 BINDING SITE, designated SEQ ID:10814, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41263] Another function of GAM2071 is therefore inhibition of FLJ31978 (Accession NP_653270.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31978.

[41264] FLJ32130 (Accession NP_689671.2) is another GAM2071 target gene, herein designated TARGET GENE. FLJ32130 BINDING SITE1 and FLJ32130 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ32130, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32130 BINDING SITE1 and FLJ32130 BINDING SITE2, designated SEQ ID:17307 and SEQ ID:9100 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41265] Another function of GAM2071 is therefore inhibition of

FLJ32130 (Accession NP_689671.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32130.

[41266] FLJ32499 (Accession NP_653208.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ32499 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32499, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32499 BINDING SITE, designated SEQ ID:2883, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41267] Another function of GAM2071 is therefore inhibition of FLJ32499 (Accession NP_653208.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32499.

[41268] FLJ32803 (Accession NP_694584.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ32803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32803, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32803 BINDING SITE, designated SEQ ID:7824, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41269] Another function of GAM2071 is therefore inhibition of FLJ32803 (Accession NP_694584.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32803.

[41270] FLJ32865 (Accession NP_653214.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ32865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32865 BINDING SITE, designated SEQ ID:19864, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41271] Another function of GAM2071 is therefore inhibition of FLJ32865 (Accession NP_653214.1) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865.

[41272] FLJ32894 (Accession NP_653268.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ32894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32894 BINDING SITE, designated SEQ ID:3716, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41273] Another function of GAM2071 is therefore inhibition of FLJ32894 (Accession NP_653268.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32894.

[41274] FLJ32932 (Accession NP_690873.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ32932 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32932, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32932 BINDING SITE, designated SEQ ID:4748, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41275] Another function of GAM2071 is therefore inhibition of FLJ32932 (Accession NP_690873.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32932.

[41276] FLJ33505 (Accession NP_689530.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ33505 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33505, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33505 BINDING SITE, designated SEQ ID:2450, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41277] Another function of GAM2071 is therefore inhibition of FLJ33505 (Accession NP_689530.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ33505.

[41278] FLJ34917 (Accession NP_694995.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ34917 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ34917, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34917 BINDING SITE, designated SEQ ID:13154, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41279] Another function of GAM2071 is therefore inhibition of FLJ34917 (Accession NP_694995.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34917.

[41280] FLJ34922 (Accession NP_689483.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ34922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ34922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ34922 BINDING SITE, designated SEQ ID:14214, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41281] Another function of GAM2071 is therefore inhibition of FLJ34922 (Accession NP_689483.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34922.

[41282] FLJ35105 (Accession NP_689890.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ35105 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ35105, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35105 BINDING SITE, designated SEQ ID:6840, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41283] Another function of GAM2071 is therefore inhibition of FLJ35105 (Accession NP_689890.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ35105.

[41284] FLJ35283 (Accession NP_689915.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ35283 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35283, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35283 BINDING SITE, designated SEQ ID:7525, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41285] Another function of GAM2071 is therefore inhibition of FLJ35283 (Accession NP_689915.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35283.

[41286] FLJ35487 (Accession NP_776181.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ35487 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35487, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ35487 BINDING SITE, designated SEQ ID:7675, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41287] Another function of GAM2071 is therefore inhibition of FLJ35487 (Accession NP_776181.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35487.

[41288] FLJ35681 (Accession NP_787096.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ35681 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35681, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35681 BINDING SITE, designated SEQ ID:3105, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41289] Another function of GAM2071 is therefore inhibition of FLJ35681 (Accession NP_787096.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35681.

[41290] FLJ35848 (Accession XP_290755.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ35848 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35848, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35848 BINDING SITE, designated SEQ ID:12720, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41291] Another function of GAM2071 is therefore inhibition of FLJ35848 (Accession XP_290755.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35848.

[41292] FLJ36032 (Accession XP_290874.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ36032 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ36032, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36032 BINDING SITE, designated SEQ ID:17613, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41293] Another function of GAM2071 is therefore inhibition of FLJ36032 (Accession XP_290874.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36032.

[41294] FLJ36445 (Accession NP_694965.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ36445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36445 BINDING SITE, designated SEQ ID:10632, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41295] Another function of GAM2071 is therefore inhibition of FLJ36445 (Accession NP_694965.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36445.

[41296] FLJ37078 (Accession NP_694588.1) is another GAM2071

target gene, herein designated TARGET GENE. FLJ37078 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ37078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37078 BINDING SITE, designated SEQ ID:3106, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41297] Another function of GAM2071 is therefore inhibition of FLJ37078 (Accession NP_694588.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37078.

[41298] FLJ37433 (Accession NP_848612.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ37433 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37433, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37433 BINDING SITE, designated SEQ ID:18178, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41299] Another function of GAM2071 is therefore inhibition of FLJ37433 (Accession NP_848612.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37433.

[41300] FLJ37543 (Accession NP_775938.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ37543 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37543, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37543 BINDING SITE, designated SEQ ID:435, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41301] Another function of GAM2071 is therefore inhibition of FLJ37543 (Accession NP_775938.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37543.

[41302] FLJ37940 (Accession NP_848629.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ37940

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37940, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37940 BINDING SITE, designated SEQ ID:7849, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41303] Another function of GAM2071 is therefore inhibition of FLJ37940 (Accession NP_848629.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37940.

[41304] FLJ38149 (Accession XP_091919.5) is another GAM2071 target gene, herein designated TARGET GENE. FLJ38149 BINDING SITE1 through FLJ38149 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by FLJ38149, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38149 BINDING SITE1 through FLJ38149 BINDING SITE4, designated SEQ ID:6194, SEQ ID:11661, SEQ ID:12581 and SEQ ID:2644 respectively, to

the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41305] Another function of GAM2071 is therefore inhibition of FLJ38149 (Accession XP_091919.5) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38149.

[41306] FLJ38281 (Accession NP_689814.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ38281 BINDING SITE1 and FLJ38281 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38281, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38281 BINDING SITE1 and FLJ38281 BINDING SITE2, designated SEQ ID:17962 and SEQ ID:19457 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41307] Another function of GAM2071 is therefore inhibition of FLJ38281 (Accession NP_689814.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ38281.

[41308] FLJ38607 (Accession NP_689867.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ38607 BINDING SITE1 and FLJ38607 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38607, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38607 BINDING SITE1 and FLJ38607 BINDING SITE2, designated SEQ ID:18917 and SEQ ID:3109 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41309] Another function of GAM2071 is therefore inhibition of FLJ38607 (Accession NP_689867.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38607.

[41310] FLJ38705 (Accession NP_776193.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ38705 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38705, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38705 BINDING SITE, designated SEQ ID:6867, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41311] Another function of GAM2071 is therefore inhibition of FLJ38705 (Accession NP_776193.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38705.

[41312] FLJ38792 (Accession NP_848615.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ38792 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38792, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38792 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41313] Another function of GAM2071 is therefore inhibition of FLJ38792 (Accession NP_848615.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ38792.

[41314] FLJ38819 (Accession NP_665872.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ38819 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38819, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38819 BINDING SITE, designated SEQ ID:3726, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41315] Another function of GAM2071 is therefore inhibition of FLJ38819 (Accession NP_665872.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38819.

[41316] FLJ38991 (Accession NP_776188.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ38991 BINDING SITE1 and FLJ38991 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38991, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38991 BINDING SITE1 and FLJ38991 BINDING SITE2, designated SEQ ID:5383 and SEQ ID:7191 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41317] Another function of GAM2071 is therefore inhibition of FLJ38991 (Accession NP_776188.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38991.

[41318] FLJ39415 (Accession NP_775952.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ39415 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39415, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39415 BINDING SITE, designated SEQ ID:17781, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41319] Another function of GAM2071 is therefore inhibition of FLJ39415 (Accession NP_775952.1) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39415.

[41320] FLJ39426 (Accession NP_775880.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ39426 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ39426, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39426 BINDING SITE, designated SEQ ID:5369, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41321] Another function of GAM2071 is therefore inhibition of FLJ39426 (Accession NP_775880.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39426.

[41322] FLJ39599 (Accession NP_776164.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ39599 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39599, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39599 BINDING SITE, designated SEQ ID:7948, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41323] Another function of GAM2071 is therefore inhibition of FLJ39599 (Accession NP_776164.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39599.

[41324] FLJ39639 (Accession XP_290687.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ39639 BINDING SITE1 and FLJ39639 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ39639, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39639 BINDING SITE1 and FLJ39639 BINDING SITE2, designated SEQ ID:13371 and SEQ ID:7663 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41325] Another function of GAM2071 is therefore inhibition of

FLJ39639 (Accession XP_290687.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39639.

[41326] FLJ39821 (Accession NP_775971.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ39821 BINDING SITE1 and FLJ39821 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ39821, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39821 BINDING SITE1 and FLJ39821 BINDING SITE2, designated SEQ ID:14284 and SEQ ID:8171 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41327] Another function of GAM2071 is therefore inhibition of FLJ39821 (Accession NP_775971.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39821.

[41328] FLJ90231 (Accession NP_775852.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ90231

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90231, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90231 BINDING SITE, designated SEQ ID:18854, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41329] Another function of GAM2071 is therefore inhibition of FLJ90231 (Accession NP_775852.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90231.

[41330] FLJ90723 (Accession NP_787115.1) is another GAM2071 target gene, herein designated TARGET GENE. FLJ90723 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90723, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90723 BINDING SITE, designated SEQ ID:16986, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41331] Another function of GAM2071 is therefore inhibition of FLJ90723 (Accession NP_787115.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90723.

[41332] Formin binding protein 1 (FNBP1, Accession XP_052666.3) is another GAM2071 target gene, herein designated TARGET GENE. FNBP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FNBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FNBP1 BINDING SITE, designated SEQ ID:8560, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41333] Another function of GAM2071 is therefore inhibition of Formin binding protein 1 (FNBP1, Accession XP_052666.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FNBP1.

[41334] Fsh primary response (lrpr1 homolog, rat) 1 (FSHPRH1, Accession NP_006724.1) is another GAM2071 target gene,

herein designated TARGET GENE. FSHPRH1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FSHPRH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FSHPRH1 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41335] Another function of GAM2071 is therefore inhibition of Fsh primary response (lrpr1 homolog, rat) 1 (FSHPRH1, Accession NP_006724.1), a gene which is involved in the response of gonadal tissues to follicle- stimulating hormone. and therefore may be associated with Hyperg- onadotropic ovarian dysgenesis (odg), x- linked disorders of gonadal development. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Hypergonadotropic ovarian dysgenesis (odg), x- linked disorders of gonadal development, and of other diseases and clinical conditions associated with FSHPRH1.

[41336] The function of FSHPRH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM189.1.Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) is another GAM2071 target gene, herein designated TARGET GENE. FUT1 BINDING SITE1 and FUT1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FUT1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FUT1 BINDING SITE1 and FUT1 BINDING SITE2, designated SEQ ID:3102 and SEQ ID:7472 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41337] Another function of GAM2071 is therefore inhibition of Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUT1.

[41338] Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075010.1) is another GAM2071 target gene,

herein designated TARGET GENE. G1P3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by G1P3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G1P3 BINDING SITE, designated SEQ ID:14496, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41339] Another function of GAM2071 is therefore inhibition of Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075010.1), a gene which is an interferon-stimulated gene (ISG). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G1P3.

[41340] The function of G1P3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075011.1) is another GAM2071 target gene, herein designated TARGET GENE. G1P3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA en-

coded by G1P3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G1P3 BINDING SITE, designated SEQ ID:14496, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41341] Another function of GAM2071 is therefore inhibition of Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_075011.1), a gene which is an interferon-stimulated gene (ISG). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G1P3.

[41342] The function of G1P3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_002029.3) is another GAM2071 target gene, herein designated TARGET GENE. G1P3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by G1P3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G1P3 BINDING SITE, designated SEQ ID:14496, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41343] Another function of GAM2071 is therefore inhibition of Interferon, alpha-inducible protein (clone ifi-6-16) (G1P3, Accession NP_002029.3), a gene which is an interferon-stimulated gene (ISG). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G1P3.

[41344] The function of G1P3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Glucose-6-phosphatase, catalytic (glycogen storage disease type i, von gierke disease) (G6PC, Accession NP_000142.1) is another GAM2071 target gene, herein designated TARGET GENE. G6PC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G6PC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G6PC BINDING SITE,

designated SEQ ID:8902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41345] Another function of GAM2071 is therefore inhibition of Glucose-6-phosphatase, catalytic (glycogen storage disease type i, von gierke disease) (G6PC, Accession NP_000142.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G6PC.

[41346] GAL3ST-4 (Accession NP_078913.3) is another GAM2071 target gene, herein designated TARGET GENE. GAL3ST-4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAL3ST-4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAL3ST-4 BINDING SITE, designated SEQ ID:13405, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41347] Another function of GAM2071 is therefore inhibition of GAL3ST-4 (Accession NP_078913.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

GAL3ST-4.

[41348] GBP4 (Accession NP_443173.2) is another GAM2071 target gene, herein designated TARGET GENE. GBP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GBP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GBP4 BINDING SITE, designated SEQ ID:12569, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41349] Another function of GAM2071 is therefore inhibition of GBP4 (Accession NP_443173.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GBP4.

[41350] GDEP (Accession NP_477516.1) is another GAM2071 target gene, herein designated TARGET GENE. GDEP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GDEP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GDEP BINDING SITE, designated SEQ ID:14396, to the nucleotide se-

quence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41351] Another function of GAM2071 is therefore inhibition of GDEP (Accession NP_477516.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GDEP.

[41352] Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) is another GAM2071 target gene, herein designated TARGET GENE. GGA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE, designated SEQ ID:520, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41353] Another function of GAM2071 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[41354] Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) is another GAM2071 target gene, herein designated TARGET GENE. GGA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE, designated SEQ ID:520, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41355] Another function of GAM2071 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[41356] Gm2 ganglioside activator protein (GM2A, Accession NP_000396.1) is another GAM2071 target gene, herein designated TARGET GENE. GM2A BINDING SITE1 and GM2A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GM2A, corresponding to target binding sites such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GM2A BINDING SITE1 and GM2A BINDING SITE2, designated SEQ ID:17118 and SEQ ID:2518 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41357] Another function of GAM2071 is therefore inhibition of Gm2 ganglioside activator protein (GM2A, Accession NP_000396.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GM2A.

[41358] GNE (Accession NP_005467.1) is another GAM2071 target gene, herein designated TARGET GENE. GNE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNE BINDING SITE, designated SEQ ID:7151, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41359] Another function of GAM2071 is therefore inhibition of GNE (Accession NP_005467.1), a gene which has roles in

sialic acid biosynthesis and regulates cell surface sialylation. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNE.

[41360] The function of GNE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Guanine nucleotide binding protein (g protein), gamma 4 (GNG4, Accession NP_004476.1) is another GAM2071 target gene, herein designated TARGET GENE. GNG4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNG4 BINDING SITE, designated SEQ ID:11336, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41361] Another function of GAM2071 is therefore inhibition of Guanine nucleotide binding protein (g protein), gamma 4 (GNG4, Accession NP_004476.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNG4.

[41362] GNPNAT1 (Accession XP_085119.1) is another GAM2071 target gene, herein designated TARGET GENE. GNPNAT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNPNAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNPNAT1 BINDING SITE, designated SEQ ID:19027, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41363] Another function of GAM2071 is therefore inhibition of GNPNAT1 (Accession XP_085119.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNPNAT1.

[41364] GNRPX (Accession NP_060519.1) is another GAM2071 target gene, herein designated TARGET GENE. GNRPX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNRPX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNRPX BINDING SITE, designated SEQ ID:17848, to the nucleotide

sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41365] Another function of GAM2071 is therefore inhibition of GNRPX (Accession NP_060519.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNRPX.

[41366] Golgi autoantigen, golgin subfamily a, 3 (GOLGA3, Accession NP_005886.2) is another GAM2071 target gene, herein designated TARGET GENE. GOLGA3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GOLGA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GOLGA3 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41367] Another function of GAM2071 is therefore inhibition of Golgi autoantigen, golgin subfamily a, 3 (GOLGA3, Accession NP_005886.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLGA3.

[41368] GPR128 (Accession NP_116176.1) is another GAM2071

target gene, herein designated TARGET GENE. GPR128 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GPR128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR128 BINDING SITE, designated SEQ ID:6503, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41369] Another function of GAM2071 is therefore inhibition of GPR128 (Accession NP_116176.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR128.

[41370] G protein-coupled receptor 4 (GPR4, Accession NP_005273.1) is another GAM2071 target gene, herein designated TARGET GENE. GPR4 BINDING SITE1 and GPR4 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GPR4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR4 BINDING SITE1 and GPR4 BINDING SITE2, designated SEQ

ID:15917 and SEQ ID:16936 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41371] Another function of GAM2071 is therefore inhibition of G protein-coupled receptor 4 (GPR4, Accession NP_005273.1), a gene which stimulates to produce increased calcium by both SPC and LPC . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR4.

[41372] The function of GPR4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.G protein-coupled receptor 56 (GPR56, Accession NP_005673.2) is another GAM2071 target gene, herein designated TARGET GENE. GPR56 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GPR56, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR56 BINDING SITE, designated SEQ ID:6235, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[41373] Another function of GAM2071 is therefore inhibition of G protein-coupled receptor 56 (GPR56, Accession NP_005673.2), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR56.

[41374] The function of GPR56 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.G protein-coupled receptor 66 (GPR66, Accession NP_006047.2) is another GAM2071 target gene, herein designated TARGET GENE. GPR66 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR66, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR66 BINDING SITE, designated SEQ ID:4149, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41375] Another function of GAM2071 is therefore inhibition of G

protein-coupled receptor 66 (GPR66, Accession NP_006047.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR66.

[41376] G protein-coupled receptor 81 (GPR81, Accession NP_115943.1) is another GAM2071 target gene, herein designated TARGET GENE. GPR81 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR81, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR81 BINDING SITE, designated SEQ ID:9012, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41377] Another function of GAM2071 is therefore inhibition of G protein-coupled receptor 81 (GPR81, Accession NP_115943.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR81.

[41378] GR6 (Accession NP_031380.1) is another GAM2071 target gene, herein designated TARGET GENE. GR6 BINDING SITE is a target binding site found in the 5` untranslated re-

gion of mRNA encoded by GR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GR6 BINDING SITE, designated SEQ ID:11621, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41379] Another function of GAM2071 is therefore inhibition of GR6 (Accession NP_031380.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GR6.

[41380] GRAF (Accession NP_055886.1) is another GAM2071 target gene, herein designated TARGET GENE. GRAF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRAF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRAF BINDING SITE, designated SEQ ID:18118, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41381] Another function of GAM2071 is therefore inhibition of GRAF (Accession NP_055886.1), a gene which ia a GTPase

activating protein for p21- rac and therefore may be associated with Juvenile myelomonocytic leukemia. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Juvenile myelomonocytic leukemia, and of other diseases and clinical conditions associated with GRAF.

[41382] The function of GRAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.GREB1 (Accession NP_055483.2) is another GAM2071 target gene, herein designated TARGET GENE. GREB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GREB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GREB1 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41383] Another function of GAM2071 is therefore inhibition of GREB1 (Accession NP_055483.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with GREB1.

[41384] Glutamate receptor, ionotropic, n-methyl d-aspartate-like 1a (GRINL1A, Accession NP_056347.1) is another GAM2071 target gene, herein designated TARGET GENE. GRINL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRINL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRINL1A BINDING SITE, designated SEQ ID:17379, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41385] Another function of GAM2071 is therefore inhibition of Glutamate receptor, ionotropic, n-methyl d-aspartate-like 1a (GRINL1A, Accession NP_056347.1), a gene which plays a role in the development and function of the mammalian brain. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRINL1A.

[41386] The function of GRINL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Glutamate receptor, metabotropic 6 (GRM6,

Accession NP_000834.1) is another GAM2071 target gene, herein designated TARGET GENE. GRM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRM6 BINDING SITE, designated SEQ ID:5942, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41387] Another function of GAM2071 is therefore inhibition of Glutamate receptor, metabotropic 6 (GRM6, Accession NP_000834.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRM6.

[41388] GRWD (Accession NP_113673.2) is another GAM2071 target gene, herein designated TARGET GENE. GRWD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRWD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRWD BINDING SITE, designated SEQ ID:6811, to the nucleotide

sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41389] Another function of GAM2071 is therefore inhibition of GRWD (Accession NP_113673.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRWD.

[41390] GSDM (Accession XP_209009.1) is another GAM2071 target gene, herein designated TARGET GENE. GSDM BINDING SITE1 and GSDM BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by GSDM, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSDM BINDING SITE1 and GSDM BINDING SITE2, designated SEQ ID:13197 and SEQ ID:3037 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41391] Another function of GAM2071 is therefore inhibition of GSDM (Accession XP_209009.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSDM.

[41392] GTF2IRD2 (Accession NP_775808.1) is another GAM2071

target gene, herein designated TARGET GENE. GTF2IRD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GTF2IRD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2IRD2 BINDING SITE, designated SEQ ID:3107, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41393] Another function of GAM2071 is therefore inhibition of GTF2IRD2 (Accession NP_775808.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2IRD2.

[41394] GTF2IRD2 (Accession NP_115579.3) is another GAM2071 target gene, herein designated TARGET GENE. GTF2IRD2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GTF2IRD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2IRD2 BINDING SITE, designated

SEQ ID:3107, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41395] Another function of GAM2071 is therefore inhibition of GTF2IRD2 (Accession NP_115579.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2IRD2.

[41396] GTPBG3 (Accession NP_116009.1) is another GAM2071 target gene, herein designated TARGET GENE. GTPBG3 BINDING SITE1 and GTPBG3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GTPBG3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTPBG3 BINDING SITE1 and GTPBG3 BINDING SITE2, designated SEQ ID:15596 and SEQ ID:7742 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41397] Another function of GAM2071 is therefore inhibition of GTPBG3 (Accession NP_116009.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with GTPBG3.

[41398] H-plk (Accession NP_056936.1) is another GAM2071 target gene, herein designated TARGET GENE. H-plk BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by H-plk, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H-plk BINDING SITE, designated SEQ ID:8288, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41399] Another function of GAM2071 is therefore inhibition of H-plk (Accession NP_056936.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H-plk.

[41400] H2AV (Accession NP_619541.1) is another GAM2071 target gene, herein designated TARGET GENE. H2AV BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H2AV, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of H2AV BINDING SITE, designated SEQ ID:11005, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41401] Another function of GAM2071 is therefore inhibition of H2AV (Accession NP_619541.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H2AV.

[41402] HECA (Accession NP_057301.1) is another GAM2071 target gene, herein designated TARGET GENE. HECA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HECA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HECA BINDING SITE, designated SEQ ID:6145, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41403] Another function of GAM2071 is therefore inhibition of HECA (Accession NP_057301.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HECA.

[41404] HEMK (Accession NP_057257.1) is another GAM2071 target gene, herein designated TARGET GENE. HEMK BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HEMK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HEMK BINDING SITE, designated SEQ ID:12517, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41405] Another function of GAM2071 is therefore inhibition of HEMK (Accession NP_057257.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEMK.

[41406] HIP1R (Accession XP_290592.1) is another GAM2071 target gene, herein designated TARGET GENE. HIP1R BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HIP1R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIP1R BINDING SITE, designated SEQ ID:4431, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41407] Another function of GAM2071 is therefore inhibition of

HIP1R (Accession XP_290592.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIP1R.

[41408] Holocarboxylase synthetase (biotin-[proprionyl-coenzyme a-carboxylase (atp-hydrolysing)] ligase) (HLCS, Accession NP_000402.2) is another GAM2071 target gene, herein designated TARGET GENE. HLCS BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HLCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:10628, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41409] Another function of GAM2071 is therefore inhibition of Holocarboxylase synthetase (biotin-[proprionyl-coenzyme a-carboxylase (atp-hydrolysing)] ligase) (HLCS, Accession NP_000402.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLCS.

[41410] High-mobility group 20a (HMG20A, Accession NP_060670.1) is another GAM2071 target gene, herein

designated TARGET GENE. HMG20A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HMG20A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HMG20A BINDING SITE, designated SEQ ID:19141, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41411] Another function of GAM2071 is therefore inhibition of High-mobility group 20a (HMG20A, Accession NP_060670.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMG20A.

[41412] Histamine receptor h4 (HRH4, Accession NP_067637.2) is another GAM2071 target gene, herein designated TARGET GENE. HRH4 BINDING SITE1 and HRH4 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HRH4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HRH4 BINDING SITE1 and HRH4 BINDING SITE2, designated SEQ ID:12079 and SEQ

ID:5920 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41413] Another function of GAM2071 is therefore inhibition of Histamine receptor h4 (HRH4, Accession NP_067637.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRH4.

[41414] Heparan sulfate (glucosamine) 3-o-sulfotransferase 4 (HS3ST4, Accession XP_056254.4) is another GAM2071 target gene, herein designated TARGET GENE. HS3ST4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HS3ST4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HS3ST4 BINDING SITE, designated SEQ ID:2420, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41415] Another function of GAM2071 is therefore inhibition of Heparan sulfate (glucosamine) 3-o-sulfotransferase 4 (HS3ST4, Accession XP_056254.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with HS3ST4.

[41416] HSA250839 (Accession NP_060871.1) is another GAM2071 target gene, herein designated TARGET GENE. HSA250839 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSA250839, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSA250839 BINDING SITE, designated SEQ ID:588, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41417] Another function of GAM2071 is therefore inhibition of HSA250839 (Accession NP_060871.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSA250839.

[41418] HSD3B7 (Accession NP_079469.2) is another GAM2071 target gene, herein designated TARGET GENE. HSD3B7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSD3B7, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSD3B7 BINDING SITE, designated SEQ ID:16293, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41419] Another function of GAM2071 is therefore inhibition of HSD3B7 (Accession NP_079469.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSD3B7.

[41420] HSNOV1 (Accession NP_059985.2) is another GAM2071 target gene, herein designated TARGET GENE. HSNOV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSNOV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSNOV1 BINDING SITE, designated SEQ ID:1150, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41421] Another function of GAM2071 is therefore inhibition of HSNOV1 (Accession NP_059985.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with HSNOV1.

[41422] HSPC065 (Accession NP_054876.2) is another GAM2071 target gene, herein designated TARGET GENE. HSPC065 BINDING SITE1 and HSPC065 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by HSPC065, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPC065 BINDING SITE1 and HSPC065 BINDING SITE2, designated SEQ ID:10877 and SEQ ID:7511 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41423] Another function of GAM2071 is therefore inhibition of HSPC065 (Accession NP_054876.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC065.

[41424] 5-hydroxytryptamine (serotonin) receptor 1d (HTR1D, Accession NP_000855.1) is another GAM2071 target gene, herein designated TARGET GENE. HTR1D BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by HTR1D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR1D BINDING SITE, designated SEQ ID:14604, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41425] Another function of GAM2071 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 1d (HTR1D, Accession NP_000855.1), a gene which belongs to g- protein coupled receptor. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR1D.

[41426] The function of HTR1D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.5-hydroxytryptamine (serotonin) receptor 1e (HTR1E, Accession NP_000856.1) is another GAM2071 target gene, herein designated TARGET GENE. HTR1E BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR1E, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of HTR1E BINDING SITE, designated SEQ ID:9063, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41427] Another function of GAM2071 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 1e (HTR1E, Accession NP_000856.1), a gene which belongs to g- protein coupled receptors. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR1E.

[41428] The function of HTR1E and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Hormonally upregulated neu-associated kinase (HUNK, Accession NP_055401.1) is another GAM2071 target gene, herein designated TARGET GENE. HUNK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HUNK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUNK BINDING SITE, designated SEQ ID:1413, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41429] Another function of GAM2071 is therefore inhibition of Hormonally upregulated neu-associated kinase (HUNK, Accession NP_055401.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUNK.

[41430] Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1) is another GAM2071 target gene, herein designated TARGET GENE. HUS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HUS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUS1 BINDING SITE, designated SEQ ID:11161, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41431] Another function of GAM2071 is therefore inhibition of Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1), a gene which May form DNA damage- responsive protein complex . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUS1.

[41432] The function of HUS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Hyaluronoglucosaminidase 4 (HYAL4, Accession NP_036401.1) is another GAM2071 target gene, herein designated TARGET GENE. HYAL4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HYAL4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HYAL4 BINDING SITE, designated SEQ ID:19431, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41433] Another function of GAM2071 is therefore inhibition of Hyaluronoglucosaminidase 4 (HYAL4, Accession NP_036401.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HYAL4.

[41434] HYPC (Accession NP_036404.1) is another GAM2071 target gene, herein designated TARGET GENE. HYPC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HYPC, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HYPC BINDING SITE, designated SEQ ID:10529, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41435] Another function of GAM2071 is therefore inhibition of HYPC (Accession NP_036404.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HYPC.

[41436] Intercellular adhesion molecule 1 (cd54), human rhinovirus receptor (ICAM1, Accession NP_000192.1) is another GAM2071 target gene, herein designated TARGET GENE. ICAM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ICAM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICAM1 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41437] Another function of GAM2071 is therefore inhibition of Intercellular adhesion molecule 1 (cd54), human rhi-

novirus receptor (ICAM1, Accession NP_000192.1), a gene which binds the integrin LFA- 1 (ITGB2) and promotes adhesion; member of the immunoglobulin superfamily and therefore may be associated with Malaria, cerebral, susceptibility to. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Malaria, cerebral, susceptibility to, and of other diseases and clinical conditions associated with ICAM1.

[41438] The function of ICAM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.ICK (Accession NP_057597.2) is another GAM2071 target gene, herein designated TARGET GENE. ICK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ICK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:3106, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41439] Another function of GAM2071 is therefore inhibition of ICK (Accession NP_057597.2) . Accordingly, utilities of

GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK.

[41440] ICK (Accession NP_055735.1) is another GAM2071 target gene, herein designated TARGET GENE. ICK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ICK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:3106, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41441] Another function of GAM2071 is therefore inhibition of ICK (Accession NP_055735.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK.

[41442] Insulin-like growth factor 1 (somatomedin c) (IGF1, Accession NP_000609.1) is another GAM2071 target gene, herein designated TARGET GENE. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of IGF1 BINDING SITE, designated SEQ ID:8230, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41443] Another function of GAM2071 is therefore inhibition of Insulin-like growth factor 1 (somatomedin c) (IGF1, Accession NP_000609.1), a gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore may be associated with Growth retardation with sensorineural deafness and mental retardation. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Growth retardation with sensorineural deafness and mental retardation, and of other diseases and clinical conditions associated with IGF1.

[41444] The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Interleukin 11 (IL11, Accession NP_000632.1) is another GAM2071 target gene, herein designated TARGET GENE. IL11 BINDING SITE1 and IL11 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by IL11, corresponding to target binding

sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL11 BINDING SITE1 and IL11 BINDING SITE2, designated SEQ ID:6919 and SEQ ID:17785 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41445] Another function of GAM2071 is therefore inhibition of Interleukin 11 (IL11, Accession NP_000632.1), a gene which stimulates the proliferation of hematopoietic stem cells and megakaryocyte progenitor cells and induces megakaryocyte maturation. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL11.

[41446] The function of IL11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM41.1.Interleukin 20 receptor, alpha (IL20RA, Accession NP_055247.2) is another GAM2071 target gene, herein designated TARGET GENE. IL20RA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL20RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL20RA BINDING SITE, designated SEQ ID:9137, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41447] Another function of GAM2071 is therefore inhibition of Interleukin 20 receptor, alpha (IL20RA, Accession NP_055247.2), a gene which is the receptor for interleukin- 20 . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL20RA.

[41448] The function of IL20RA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM316.1.Interleukin 28 receptor, alpha (IL28RA, Accession NP_775087.1) is another GAM2071 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:17486, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41449] Another function of GAM2071 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_775087.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[41450] Interleukin 28 receptor, alpha (IL28RA, Accession NP_734464.1) is another GAM2071 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:17486, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41451] Another function of GAM2071 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_734464.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[41452] Interleukin 28 receptor, alpha (IL28RA, Accession NP_775088.1) is another GAM2071 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:17486, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41453] Another function of GAM2071 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_775088.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[41454] IMPACT (Accession NP_060909.1) is another GAM2071 target gene, herein designated TARGET GENE. IMPACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IMPACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

IMPACT BINDING SITE, designated SEQ ID:19846, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41455] Another function of GAM2071 is therefore inhibition of IMPACT (Accession NP_060909.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMPACT.

[41456] INHBE (Accession NP_113667.1) is another GAM2071 target gene, herein designated TARGET GENE. INHBE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INHBE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INHBE BINDING SITE, designated SEQ ID:9633, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41457] Another function of GAM2071 is therefore inhibition of INHBE (Accession NP_113667.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INHBE.

[41458] Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) is another GAM2071 target gene, herein

designated TARGET GENE. INMT BINDING SITE1 and INMT BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by INMT, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INMT BINDING SITE1 and INMT BINDING SITE2, designated SEQ ID:3109 and SEQ ID:1421 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41459] Another function of GAM2071 is therefore inhibition of Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INMT.

[41460] IPO13 (Accession NP_055467.1) is another GAM2071 target gene, herein designated TARGET GENE. IPO13 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IPO13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IPO13 BINDING SITE, designated SEQ ID:6877, to the nucleotide se-

quence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41461] Another function of GAM2071 is therefore inhibition of IPO13 (Accession NP_055467.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IPO13.

[41462] Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) is another GAM2071 target gene, herein designated TARGET GENE. IRF4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IRF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRF4 BINDING SITE, designated SEQ ID:16311, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41463] Another function of GAM2071 is therefore inhibition of Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRF4.

[41464] Integrin, alpha l (antigen cd11a (p180), lymphocyte func-

tion-associated antigen 1; alpha polypeptide) (ITGAL, Accession NP_002200.1) is another GAM2071 target gene, herein designated TARGET GENE. ITGAL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITGAL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITGAL BINDING SITE, designated SEQ ID:17682, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41465] Another function of GAM2071 is therefore inhibition of Integrin, alpha l (antigen cd11a (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL, Accession NP_002200.1), a gene which s a receptor for icam1, icam2, icam3 and icam4. it is involved in a variety of immune phenomena including leukocyte- endothelial cell interaction, cytotoxic t- cell mediated killing, and antibody dependent killing by granulocytes and monocytes. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAL.

[41466] The function of ITGAL and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM148.1.Integrin, alpha x (antigen cd11c (p150), alpha polypeptide) (ITGAX, Accession NP_000878.1) is another GAM2071 target gene, herein designated TARGET GENE. ITGAX BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITGAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITGAX BINDING SITE, designated SEQ ID:11336, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41467] Another function of GAM2071 is therefore inhibition of Integrin, alpha x (antigen cd11c (p150), alpha polypeptide) (ITGAX, Accession NP_000878.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAX.

[41468] Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3, Accession NP_000206.1) is another GAM2071 target gene, herein designated TARGET GENE. JAK3 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by JAK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JAK3 BINDING SITE, designated SEQ ID:6262, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41469] Another function of GAM2071 is therefore inhibition of Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3, Accession NP_000206.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAK3.

[41470] JM11 (Accession NP_296375.1) is another GAM2071 target gene, herein designated TARGET GENE. JM11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JM11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JM11 BINDING SITE, designated SEQ ID:15361, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41471] Another function of GAM2071 is therefore inhibition of

JM11 (Accession NP_296375.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JM11.

[41472] Jerky homolog (mouse) (JRK, Accession NP_003715.1) is another GAM2071 target gene, herein designated TARGET GENE. JRK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JRK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JRK BINDING SITE, designated SEQ ID:1529, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41473] Another function of GAM2071 is therefore inhibition of Jerky homolog (mouse) (JRK, Accession NP_003715.1), a gene which might function as a DNA- binding protein. and therefore may be associated with Absence epilepsy. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Absence epilepsy, and of other diseases and clinical conditions associated with JRK.

[41474] The function of JRK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM65.2.Potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5, Accession NP_002225.2) is another GAM2071 target gene, herein designated TARGET GENE. KCNA5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KCNA5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNA5 BINDING SITE, designated SEQ ID:18957, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41475] Another function of GAM2071 is therefore inhibition of Potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5, Accession NP_002225.2), a gene which mediates the voltage- dependent potassium ion permeability of excitable membranes. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNA5.

[41476] The function of KCNA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM391.1.Potassium voltage-gated channel, isk-related family, member 3 (KCNE3, Accession NP_005463.1) is another GAM2071 target gene, herein designated TARGET GENE. KCNE3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KCNE3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNE3 BINDING SITE, designated SEQ ID:6918, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41477] Another function of GAM2071 is therefore inhibition of Potassium voltage-gated channel, isk-related family, member 3 (KCNE3, Accession NP_005463.1), a gene which ancillary protein that co- assemble with a potassium channel alpha- subunit to modulate the gating kinetics and enhance stability of the multimeric complex (by similarity). and therefore may be associated with Hypokalemic periodic paralysis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Hypokalemic periodic paralysis, and of other diseases and clinical conditions associated with KCNE3.

[41478] The function of KCNE3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Potassium inwardly-rectifying channel, subfamily j, member 11 (KCNJ11, Accession NP_000516.2) is another GAM2071 target gene, herein designated TARGET GENE. KCNJ11 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KCNJ11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ11 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41479] Another function of GAM2071 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 11 (KCNJ11, Accession NP_000516.2), a gene which is controlled by g proteins. inward rectifier k+ channels are characterized by a greater tendancy to allow potassium to flow into the cell rather than out of it. and therefore is associated with Persistent hyperinsulinemic hypoglycemia of infancy. Accordingly, utilities of GAM2071 include diagno-

sis, prevention and treatment of Persistent hyperinsulinemic hypoglycemia of infancy, and of other diseases and clinical conditions associated with KCNJ11.

[41480] The function of KCNJ11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.KENAE (Accession NP_789786.1) is another GAM2071 target gene, herein designated TARGET GENE. KENAE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KENAE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KENAE BINDING SITE, designated SEQ ID:18180, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41481] Another function of GAM2071 is therefore inhibition of KENAE (Accession NP_789786.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KENAE.

[41482] KIAA0053 (Accession NP_055697.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0053 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA0053, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0053 BINDING SITE, designated SEQ ID:16223, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41483] Another function of GAM2071 is therefore inhibition of KIAA0053 (Accession NP_055697.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0053.

[41484] KIAA0087 (Accession NP_055584.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0087 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0087, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0087 BINDING SITE, designated SEQ ID:14875, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41485] Another function of GAM2071 is therefore inhibition of

KIAA0087 (Accession NP_055584.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0087.

[41486] KIAA0117 (Accession XP_290939.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0117 BINDING SITE, designated SEQ ID:1353, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41487] Another function of GAM2071 is therefore inhibition of KIAA0117 (Accession XP_290939.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0117.

[41488] KIAA0186 (Accession NP_066545.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0186, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0186 BINDING SITE, designated SEQ ID:6841, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41489] Another function of GAM2071 is therefore inhibition of KIAA0186 (Accession NP_066545.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0186.

[41490] KIAA0205 (Accession NP_055688.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0205 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0205, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0205 BINDING SITE, designated SEQ ID:17371, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41491] Another function of GAM2071 is therefore inhibition of KIAA0205 (Accession NP_055688.1) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0205.

[41492] KIAA0350 (Accession XP_290667.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0350 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0350, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0350 BINDING SITE, designated SEQ ID:12671, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41493] Another function of GAM2071 is therefore inhibition of KIAA0350 (Accession XP_290667.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0350.

[41494] KIAA0435 (Accession NP_055616.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0435 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0435, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0435 BINDING SITE, designated SEQ ID:14441, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41495] Another function of GAM2071 is therefore inhibition of KIAA0435 (Accession NP_055616.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0435.

[41496] KIAA0446 (Accession XP_044155.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0446 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0446, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0446 BINDING SITE, designated SEQ ID:20115, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41497] Another function of GAM2071 is therefore inhibition of KIAA0446 (Accession XP_044155.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA0446.

[41498] KIAA0459 (Accession XP_027862.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:3442, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41499] Another function of GAM2071 is therefore inhibition of KIAA0459 (Accession XP_027862.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459.

[41500] KIAA0469 (Accession NP_055666.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0469 BINDING SITE1 and KIAA0469 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0469, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0469 BINDING SITE1 and KIAA0469 BINDING SITE2, designated SEQ ID:14283 and SEQ ID:1413 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41501] Another function of GAM2071 is therefore inhibition of KIAA0469 (Accession NP_055666.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469.

[41502] KIAA0471 (Accession NP_055672.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0471 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0471, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0471 BINDING SITE, designated SEQ ID:16265, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41503] Another function of GAM2071 is therefore inhibition of KIAA0471 (Accession NP_055672.1) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0471.

[41504] KIAA0475 (Accession NP_055679.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0475 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:7946, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41505] Another function of GAM2071 is therefore inhibition of KIAA0475 (Accession NP_055679.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475.

[41506] KIAA0478 (Accession NP_055685.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0478, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0478 BINDING SITE, designated SEQ ID:11512, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41507] Another function of GAM2071 is therefore inhibition of KIAA0478 (Accession NP_055685.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0478.

[41508] KIAA0493 (Accession XP_034717.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0493 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0493 BINDING SITE, designated SEQ ID:6597, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41509] Another function of GAM2071 is therefore inhibition of KIAA0493 (Accession XP_034717.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA0493.

[41510] KIAA0495 (Accession XP_031397.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0495 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0495, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0495 BINDING SITE, designated SEQ ID:5452, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41511] Another function of GAM2071 is therefore inhibition of KIAA0495 (Accession XP_031397.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0495.

[41512] KIAA0513 (Accession NP_055547.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0513 BINDING SITE1 through KIAA0513 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by KIAA0513, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE1 through KIAA0513 BINDING SITE3, designated SEQ ID:11210, SEQ ID:7613 and SEQ ID:12742 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41513] Another function of GAM2071 is therefore inhibition of KIAA0513 (Accession NP_055547.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513.

[41514] KIAA0527 (Accession XP_171054.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0527 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0527, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0527 BINDING SITE, designated SEQ ID:19044, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41515] Another function of GAM2071 is therefore inhibition of KIAA0527 (Accession XP_171054.1) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0527.

[41516] KIAA0532 (Accession XP_047659.6) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0532 BINDING SITE, designated SEQ ID:483, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41517] Another function of GAM2071 is therefore inhibition of KIAA0532 (Accession XP_047659.6) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0532.

[41518] KIAA0557 (Accession XP_085507.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0557 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0557, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0557 BINDING SITE, designated SEQ ID:16200, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41519] Another function of GAM2071 is therefore inhibition of KIAA0557 (Accession XP_085507.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0557.

[41520] KIAA0561 (Accession XP_038150.2) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0561 BINDING SITE1 and KIAA0561 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0561, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0561 BINDING SITE1 and KIAA0561 BINDING SITE2, designated SEQ ID:11513 and SEQ ID:12972 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41521] Another function of GAM2071 is therefore inhibition of

KIAA0561 (Accession XP_038150.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0561.

[41522] KIAA0562 (Accession NP_055519.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0562 BINDING SITE, designated SEQ ID:10458, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41523] Another function of GAM2071 is therefore inhibition of KIAA0562 (Accession NP_055519.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0562.

[41524] KIAA0563 (Accession NP_055649.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0563 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0563, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0563 BINDING SITE, designated SEQ ID:19679, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41525] Another function of GAM2071 is therefore inhibition of KIAA0563 (Accession NP_055649.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0563.

[41526] KIAA0605 (Accession NP_055509.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0605 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0605, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0605 BINDING SITE, designated SEQ ID:11045, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41527] Another function of GAM2071 is therefore inhibition of KIAA0605 (Accession NP_055509.1) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0605.

[41528] KIAA0682 (Accession NP_055667.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0682 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA0682, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0682 BINDING SITE, designated SEQ ID:2671, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41529] Another function of GAM2071 is therefore inhibition of KIAA0682 (Accession NP_055667.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0682.

[41530] KIAA0831 (Accession NP_055739.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0831 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0831, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0831 BINDING SITE, designated SEQ ID:16264, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41531] Another function of GAM2071 is therefore inhibition of KIAA0831 (Accession NP_055739.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0831.

[41532] KIAA0841 (Accession XP_049237.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0841 BINDING SITE1 and KIAA0841 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0841, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0841 BINDING SITE1 and KIAA0841 BINDING SITE2, designated SEQ ID:901 and SEQ ID:1519 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41533] Another function of GAM2071 is therefore inhibition of KIAA0841 (Accession XP_049237.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0841.

[41534] KIAA0861 (Accession NP_055893.2) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0861 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0861, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0861 BINDING SITE, designated SEQ ID:10629, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41535] Another function of GAM2071 is therefore inhibition of KIAA0861 (Accession NP_055893.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0861.

[41536] KIAA0924 (Accession NP_055712.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0924 BINDING SITE1 and KIAA0924 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by KIAA0924, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0924 BINDING SITE1 and KIAA0924 BINDING SITE2, designated SEQ ID:19935 and SEQ ID:864 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41537] Another function of GAM2071 is therefore inhibition of KIAA0924 (Accession NP_055712.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0924.

[41538] KIAA0931 (Accession XP_041191.2) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0931 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0931, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0931 BINDING SITE, designated SEQ ID:8504, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41539] Another function of GAM2071 is therefore inhibition of KIAA0931 (Accession XP_041191.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0931.

[41540] KIAA0935 (Accession XP_052620.6) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0935 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0935, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0935 BINDING SITE, designated SEQ ID:10957, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41541] Another function of GAM2071 is therefore inhibition of KIAA0935 (Accession XP_052620.6) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0935.

[41542] KIAA0937 (Accession XP_166213.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA0937

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0937, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0937 BINDING SITE, designated SEQ ID:7974, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41543] Another function of GAM2071 is therefore inhibition of KIAA0937 (Accession XP_166213.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0937.

[41544] KIAA1002 (Accession XP_290584.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1002 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1002, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1002 BINDING SITE, designated SEQ ID:8660, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41545] Another function of GAM2071 is therefore inhibition of KIAA1002 (Accession XP_290584.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1002.

[41546] KIAA1040 (Accession XP_051091.3) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1040 BINDING SITE1 and KIAA1040 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1040, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1040 BINDING SITE1 and KIAA1040 BINDING SITE2, designated SEQ ID:5138 and SEQ ID:5080 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41547] Another function of GAM2071 is therefore inhibition of KIAA1040 (Accession XP_051091.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1040.

[41548] KIAA1041 (Accession NP_055762.1) is another GAM2071

target gene, herein designated TARGET GENE. KIAA1041 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1041, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1041 BINDING SITE, designated SEQ ID:11112, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41549] Another function of GAM2071 is therefore inhibition of KIAA1041 (Accession NP_055762.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1041.

[41550] KIAA1043 (Accession NP_056096.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1043 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1043, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1043 BINDING SITE, designated SEQ ID:18400, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41551] Another function of GAM2071 is therefore inhibition of KIAA1043 (Accession NP_056096.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1043.

[41552] KIAA1045 (Accession XP_048592.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1045 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1045 BINDING SITE, designated SEQ ID:9634, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41553] Another function of GAM2071 is therefore inhibition of KIAA1045 (Accession XP_048592.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1045.

[41554] KIAA1052 (Accession NP_055771.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1052

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1052 BINDING SITE, designated SEQ ID:1530, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41555] Another function of GAM2071 is therefore inhibition of KIAA1052 (Accession NP_055771.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1052.

[41556] KIAA1054 (Accession XP_043493.5) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1054 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1054, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1054 BINDING SITE, designated SEQ ID:7973, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41557] Another function of GAM2071 is therefore inhibition of KIAA1054 (Accession XP_043493.5) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1054.

[41558] KIAA1126 (Accession XP_050325.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1126 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1126, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1126 BINDING SITE, designated SEQ ID:6077, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41559] Another function of GAM2071 is therefore inhibition of KIAA1126 (Accession XP_050325.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1126.

[41560] KIAA1143 (Accession XP_044014.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1143 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1143 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41561] Another function of GAM2071 is therefore inhibition of KIAA1143 (Accession XP_044014.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1143.

[41562] KIAA1155 (Accession XP_030864.2) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1155 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1155, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1155 BINDING SITE, designated SEQ ID:5405, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41563] Another function of GAM2071 is therefore inhibition of

KIAA1155 (Accession XP_030864.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1155.

[41564] KIAA1185 (Accession NP_065761.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1185 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1185, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1185 BINDING SITE, designated SEQ ID:9213, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41565] Another function of GAM2071 is therefore inhibition of KIAA1185 (Accession NP_065761.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1185.

[41566] KIAA1193 (Accession XP_041843.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1193, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1193 BINDING SITE, designated SEQ ID:1683, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41567] Another function of GAM2071 is therefore inhibition of KIAA1193 (Accession XP_041843.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1193.

[41568] KIAA1198 (Accession NP_065765.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE6 are target binding sites found in untranslated regions of mRNA encoded by KIAA1198, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE6, designated SEQ ID:19094, SEQ ID:17786, SEQ ID:8170, SEQ ID:5522, SEQ ID:17617 and SEQ ID:17224 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41569] Another function of GAM2071 is therefore inhibition of KIAA1198 (Accession NP_065765.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1198.

[41570] KIAA1210 (Accession XP_172801.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1210 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1210, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1210 BINDING SITE, designated SEQ ID:1409, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41571] Another function of GAM2071 is therefore inhibition of KIAA1210 (Accession XP_172801.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1210.

[41572] KIAA1257 (Accession XP_031577.2) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1257

BINDING SITE1 and KIAA1257 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1257, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1257 BINDING SITE1 and KIAA1257 BINDING SITE2, designated SEQ ID:14928 and SEQ ID:3109 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41573] Another function of GAM2071 is therefore inhibition of KIAA1257 (Accession XP_031577.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1257.

[41574] KIAA1272 (Accession XP_046600.7) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1272 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1272, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1272 BINDING SITE, designated SEQ ID:15059, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41575] Another function of GAM2071 is therefore inhibition of KIAA1272 (Accession XP_046600.7) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1272.

[41576] KIAA1287 (Accession NP_065799.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1287 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1287, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1287 BINDING SITE, designated SEQ ID:13685, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41577] Another function of GAM2071 is therefore inhibition of KIAA1287 (Accession NP_065799.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1287.

[41578] KIAA1393 (Accession XP_050793.2) is another GAM2071

target gene, herein designated TARGET GENE. KIAA1393 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1393 BINDING SITE, designated SEQ ID:6495, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41579] Another function of GAM2071 is therefore inhibition of KIAA1393 (Accession XP_050793.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1393.

[41580] KIAA1407 (Accession NP_065868.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1407 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1407, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1407 BINDING SITE, designated SEQ ID:15873, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41581] Another function of GAM2071 is therefore inhibition of KIAA1407 (Accession NP_065868.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1407.

[41582] KIAA1456 (Accession XP_040100.3) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1456 BINDING SITE, designated SEQ ID:13974, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41583] Another function of GAM2071 is therefore inhibition of KIAA1456 (Accession XP_040100.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1456.

[41584] KIAA1465 (Accession XP_027396.4) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1465

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1465, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1465 BINDING SITE, designated SEQ ID:13306, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41585] Another function of GAM2071 is therefore inhibition of KIAA1465 (Accession XP_027396.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1465.

[41586] KIAA1508 (Accession XP_290952.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1508 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1508, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1508 BINDING SITE, designated SEQ ID:16911, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41587] Another function of GAM2071 is therefore inhibition of KIAA1508 (Accession XP_290952.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1508.

[41588] KIAA1518 (Accession XP_170889.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1518 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA1518, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1518 BINDING SITE, designated SEQ ID:17375, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41589] Another function of GAM2071 is therefore inhibition of KIAA1518 (Accession XP_170889.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1518.

[41590] KIAA1530 (Accession XP_042661.5) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1530

BINDING SITE1 and KIAA1530 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1530, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1530 BINDING SITE1 and KIAA1530 BINDING SITE2, designated SEQ ID:12872 and SEQ ID:6360 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41591] Another function of GAM2071 is therefore inhibition of KIAA1530 (Accession XP_042661.5) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1530.

[41592] KIAA1553 (Accession XP_166320.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1553 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1553, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1553 BINDING SITE, designated SEQ ID:3650, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41593] Another function of GAM2071 is therefore inhibition of KIAA1553 (Accession XP_166320.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1553.

[41594] KIAA1554 (Accession XP_290768.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1554 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1554, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1554 BINDING SITE, designated SEQ ID:15297, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41595] Another function of GAM2071 is therefore inhibition of KIAA1554 (Accession XP_290768.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1554.

[41596] KIAA1559 (Accession XP_054472.2) is another GAM2071

target gene, herein designated TARGET GENE. KIAA1559 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1559, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1559 BINDING SITE, designated SEQ ID:14408, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41597] Another function of GAM2071 is therefore inhibition of KIAA1559 (Accession XP_054472.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1559.

[41598] KIAA1571 (Accession XP_027744.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1571 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1571, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1571 BINDING SITE, designated SEQ ID:13037, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41599] Another function of GAM2071 is therefore inhibition of KIAA1571 (Accession XP_027744.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1571.

[41600] KIAA1615 (Accession NP_066002.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1615, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2, designated SEQ ID:8578 and SEQ ID:12534 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41601] Another function of GAM2071 is therefore inhibition of KIAA1615 (Accession NP_066002.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1615.

[41602] KIAA1671 (Accession XP_037809.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1671 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1671, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1671 BINDING SITE, designated SEQ ID:17814, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41603] Another function of GAM2071 is therefore inhibition of KIAA1671 (Accession XP_037809.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1671.

[41604] KIAA1727 (Accession XP_034262.4) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1727 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1727, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1727 BINDING SITE, designated SEQ ID:14415, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41605] Another function of GAM2071 is therefore inhibition of KIAA1727 (Accession XP_034262.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1727.

[41606] KIAA1784 (Accession NP_115820.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1784 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1784, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1784 BINDING SITE, designated SEQ ID:18884, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41607] Another function of GAM2071 is therefore inhibition of KIAA1784 (Accession NP_115820.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1784.

[41608] KIAA1827 (Accession XP_290834.1) is another GAM2071

target gene, herein designated TARGET GENE. KIAA1827 BINDING SITE1 and KIAA1827 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1827, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1827 BINDING SITE1 and KIAA1827 BINDING SITE2, designated SEQ ID:2385 and SEQ ID:19431 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41609] Another function of GAM2071 is therefore inhibition of KIAA1827 (Accession XP_290834.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1827.

[41610] KIAA1829 (Accession XP_030378.2) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1829 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1829, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1829 BINDING SITE, designated SEQ ID:12386, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41611] Another function of GAM2071 is therefore inhibition of KIAA1829 (Accession XP_030378.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1829.

[41612] KIAA1836 (Accession XP_114087.2) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1836 BINDING SITE, designated SEQ ID:17519, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41613] Another function of GAM2071 is therefore inhibition of KIAA1836 (Accession XP_114087.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1836.

[41614] KIAA1853 (Accession XP_045184.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1853 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1853, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1853 BINDING SITE, designated SEQ ID:19842, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41615] Another function of GAM2071 is therefore inhibition of KIAA1853 (Accession XP_045184.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1853.

[41616] KIAA1924 (Accession NP_694971.2) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1924 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1924, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1924 BINDING SITE, designated SEQ ID:7825, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41617] Another function of GAM2071 is therefore inhibition of KIAA1924 (Accession NP_694971.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1924.

[41618] KIAA1951 (Accession XP_057401.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1951 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1951, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1951 BINDING SITE, designated SEQ ID:12956, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41619] Another function of GAM2071 is therefore inhibition of KIAA1951 (Accession XP_057401.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1951.

[41620] KIAA1971 (Accession XP_058720.4) is another GAM2071

target gene, herein designated TARGET GENE. KIAA1971 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1971, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1971 BINDING SITE, designated SEQ ID:19552, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41621] Another function of GAM2071 is therefore inhibition of KIAA1971 (Accession XP_058720.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1971.

[41622] KIAA1987 (Accession XP_113870.1) is another GAM2071 target gene, herein designated TARGET GENE. KIAA1987 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1987, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1987 BINDING SITE, designated SEQ ID:18263, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41623] Another function of GAM2071 is therefore inhibition of KIAA1987 (Accession XP_113870.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1987.

[41624] KIAA2028 (Accession XP_059415.2) is another GAM2071 target gene, herein designated TARGET GENE. KIAA2028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA2028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA2028 BINDING SITE, designated SEQ ID:11722, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41625] Another function of GAM2071 is therefore inhibition of KIAA2028 (Accession XP_059415.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2028.

[41626] Kruppel-like factor 5 (intestinal) (KLF5, Accession NP_001721.2) is another GAM2071 target gene, herein

designated TARGET GENE. KLF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KLF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLF5 BINDING SITE, designated SEQ ID:17531, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41627] Another function of GAM2071 is therefore inhibition of Kruppel-like factor 5 (intestinal) (KLF5, Accession NP_001721.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF5.

[41628] Kallikrein 10 (KLK10, Accession NP_665895.1) is another GAM2071 target gene, herein designated TARGET GENE. KLK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLK10 BINDING SITE, designated SEQ ID:6691, to the nucleotide sequence of GAM2071

RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41629] Another function of GAM2071 is therefore inhibition of Kallikrein 10 (KLK10, Accession NP_665895.1), a gene which has a tumor- suppressor role in breast and prostate cancer. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLK10.

[41630] The function of KLK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Kallikrein 10 (KLK10, Accession NP_002767.2) is another GAM2071 target gene, herein designated TARGET GENE. KLK10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLK10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLK10 BINDING SITE, designated SEQ ID:6691, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41631] Another function of GAM2071 is therefore inhibition of

Kallikrein 10 (KLK10, Accession NP_002767.2), a gene which has a tumor- suppressor role in breast and prostate cancer. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLK10.

[41632] The function of KLK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NP_003670.1) is another GAM2071 target gene, herein designated TARGET GENE. KMO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KMO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KMO BINDING SITE, designated SEQ ID:5730, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41633] Another function of GAM2071 is therefore inhibition of Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NP_003670.1), a gene which may play a role in encephalic photoreception. Ac-

cordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KMO.

[41634] The function of KMO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Kinase suppressor of ras (KSR, Accession XP_290793.1) is another GAM2071 target gene, herein designated TARGET GENE. KSR BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KSR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KSR BINDING SITE, designated SEQ ID:15951, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41635] Another function of GAM2071 is therefore inhibition of Kinase suppressor of ras (KSR, Accession XP_290793.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KSR.

[41636] Lysosomal-associated membrane protein 3 (LAMP3, Ac-

cession NP_055213.1) is another GAM2071 target gene, herein designated TARGET GENE. LAMP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAMP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMP3 BINDING SITE, designated SEQ ID:970, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41637] Another function of GAM2071 is therefore inhibition of Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP3.

[41638] LANO (Accession NP_060684.1) is another GAM2071 target gene, herein designated TARGET GENE. LANO BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LANO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LANO BINDING SITE, designated SEQ ID:4507,

to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41639] Another function of GAM2071 is therefore inhibition of LANO (Accession NP_060684.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LANO.

[41640] Lipocalin 7 (LCN7, Accession NP_071447.1) is another GAM2071 target gene, herein designated TARGET GENE. LCN7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCN7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCN7 BINDING SITE, designated SEQ ID:3972, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41641] Another function of GAM2071 is therefore inhibition of Lipocalin 7 (LCN7, Accession NP_071447.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCN7.

[41642] Lymphoid enhancer-binding factor 1 (LEF1, Accession NP_057353.1) is another GAM2071 target gene, herein

designated TARGET GENE. LEF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LEF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LEF1 BINDING SITE, designated SEQ ID:11499, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41643] Another function of GAM2071 is therefore inhibition of Lymphoid enhancer-binding factor 1 (LEF1, Accession NP_057353.1), a gene which plays an essential role in the formation of several organs and structures that require inductive tissue interactions. and therefore may be associated with Colon cancer. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Colon cancer, and of other diseases and clinical conditions associated with LEF1.

[41644] The function of LEF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM272.1.Lipoma hmgic fusion partner (LHFP, Accession NP_005771.1) is another GAM2071 target gene,

herein designated TARGET GENE. LHFP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LHFP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LHFP BINDING SITE, designated SEQ ID:8128, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41645] Another function of GAM2071 is therefore inhibition of Lipoma hmgic fusion partner (LHFP, Accession NP_005771.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHFP.

[41646] LIN-28 (Accession NP_078950.1) is another GAM2071 target gene, herein designated TARGET GENE. LIN-28 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LIN-28, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LIN-28 BINDING SITE, designated SEQ ID:6030, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41647] Another function of GAM2071 is therefore inhibition of LIN-28 (Accession NP_078950.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIN-28.

[41648] LNK (Accession NP_005466.1) is another GAM2071 target gene, herein designated TARGET GENE. LNK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LNK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LNK BINDING SITE, designated SEQ ID:9510, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41649] Another function of GAM2071 is therefore inhibition of LNK (Accession NP_005466.1), a gene which links T- cell receptor activation signal to phospholipase c- gamma- 1, grb- 2 and phosphatidylinositol 3- kinase (by similarity). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNK.

[41650] The function of LNK and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.LOC112687 (Accession XP_053145.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC112687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112687 BINDING SITE, designated SEQ ID:4875, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41651] Another function of GAM2071 is therefore inhibition of LOC112687 (Accession XP_053145.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112687.

[41652] LOC112817 (Accession NP_612422.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC112817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112817, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112817 BINDING SITE, designated SEQ ID:16516, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41653] Another function of GAM2071 is therefore inhibition of LOC112817 (Accession NP_612422.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112817.

[41654] LOC113444 (Accession NP_612437.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC113444 BINDING SITE1 through LOC113444 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC113444, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC113444 BINDING SITE1 through LOC113444 BINDING SITE3, designated SEQ ID:15369, SEQ ID:15847 and SEQ ID:14262 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ

ID:371.

[41655] Another function of GAM2071 is therefore inhibition of LOC113444 (Accession NP_612437.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113444.

[41656] LOC115648 (Accession NP_663299.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC115648 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC115648, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115648 BINDING SITE, designated SEQ ID:6386, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41657] Another function of GAM2071 is therefore inhibition of LOC115648 (Accession NP_663299.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115648.

[41658] LOC116411 (Accession XP_058095.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC116411 BINDING SITE1 and LOC116411 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC116411, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC116411 BINDING SITE1 and LOC116411 BINDING SITE2, designated SEQ ID:1487 and SEQ ID:13193 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41659] Another function of GAM2071 is therefore inhibition of LOC116411 (Accession XP_058095.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116411.

[41660] LOC118490 (Accession XP_060981.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC118490 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC118490, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC118490 BINDING SITE, designated SEQ ID:11022, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41661] Another function of GAM2071 is therefore inhibition of LOC118490 (Accession XP_060981.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118490.

[41662] LOC118812 (Accession XP_058346.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:7879, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41663] Another function of GAM2071 is therefore inhibition of LOC118812 (Accession XP_058346.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC118812.

[41664] LOC118812 (Accession NP_849154.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:7879, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41665] Another function of GAM2071 is therefore inhibition of LOC118812 (Accession NP_849154.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118812.

[41666] LOC120526 (Accession XP_058475.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC120526 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC120526, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC120526 BINDING SITE, designated SEQ ID:14215, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41667] Another function of GAM2071 is therefore inhibition of LOC120526 (Accession XP_058475.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120526.

[41668] LOC121498 (Accession XP_062669.7) is another GAM2071 target gene, herein designated TARGET GENE. LOC121498 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC121498, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC121498 BINDING SITE, designated SEQ ID:1850, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41669] Another function of GAM2071 is therefore inhibition of

LOC121498 (Accession XP_062669.7) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121498.

[41670] LOC121952 (Accession XP_062872.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC121952 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC121952, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC121952 BINDING SITE, designated SEQ ID:17591, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41671] Another function of GAM2071 is therefore inhibition of LOC121952 (Accession XP_062872.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121952.

[41672] LOC125061 (Accession XP_058889.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC125061 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC125061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC125061 BINDING SITE, designated SEQ ID:9098, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41673] Another function of GAM2071 is therefore inhibition of LOC125061 (Accession XP_058889.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125061.

[41674] LOC127602 (Accession XP_059166.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC127602 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC127602, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC127602 BINDING SITE, designated SEQ ID:14354, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[41675] Another function of GAM2071 is therefore inhibition of LOC127602 (Accession XP_059166.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127602.

[41676] LOC130813 (Accession XP_065904.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC130813 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC130813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:16452, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41677] Another function of GAM2071 is therefore inhibition of LOC130813 (Accession XP_065904.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813.

[41678] LOC131963 (Accession XP_067689.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC131963 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC131963, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC131963 BINDING SITE, designated SEQ ID:5289, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41679] Another function of GAM2071 is therefore inhibition of LOC131963 (Accession XP_067689.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC131963.

[41680] LOC132241 (Accession XP_059583.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC132241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC132241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC132241 BINDING SITE, desig-

nated SEQ ID:13281, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41681] Another function of GAM2071 is therefore inhibition of LOC132241 (Accession XP_059583.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132241.

[41682] LOC134466 (Accession XP_068858.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC134466 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC134466, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC134466 BINDING SITE, designated SEQ ID:11536, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41683] Another function of GAM2071 is therefore inhibition of LOC134466 (Accession XP_068858.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC134466.

[41684] LOC135293 (Accession XP_072402.4) is another GAM2071 target gene, herein designated TARGET GENE. LOC135293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135293 BINDING SITE, designated SEQ ID:11660, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41685] Another function of GAM2071 is therefore inhibition of LOC135293 (Accession XP_072402.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135293.

[41686] LOC135763 (Accession NP_612639.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC135763 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135763, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135763 BINDING SITE, designated SEQ ID:14442, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41687] Another function of GAM2071 is therefore inhibition of LOC135763 (Accession NP_612639.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135763.

[41688] LOC139422 (Accession XP_066687.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC139422 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC139422, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC139422 BINDING SITE, designated SEQ ID:17958, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41689] Another function of GAM2071 is therefore inhibition of LOC139422 (Accession XP_066687.2) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139422.

[41690] LOC144248 (Accession XP_084786.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC144248 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144248 BINDING SITE, designated SEQ ID:11361, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41691] Another function of GAM2071 is therefore inhibition of LOC144248 (Accession XP_084786.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144248.

[41692] LOC144404 (Accession XP_084852.6) is another GAM2071 target gene, herein designated TARGET GENE. LOC144404 BINDING SITE1 and LOC144404 BINDING SITE2 are target binding sites found in untranslated re-

gions of mRNA encoded by LOC144404, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144404 BINDING SITE1 and LOC144404 BINDING SITE2, designated SEQ ID:8561 and SEQ ID:11669 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41693] Another function of GAM2071 is therefore inhibition of LOC144404 (Accession XP_084852.6) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144404.

[41694] LOC144481 (Accession XP_096611.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC144481 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144481, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144481 BINDING SITE, designated SEQ ID:17022, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[41695] Another function of GAM2071 is therefore inhibition of LOC144481 (Accession XP_096611.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144481.

[41696] LOC144766 (Accession XP_084963.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC144766 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144766, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144766 BINDING SITE, designated SEQ ID:19847, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41697] Another function of GAM2071 is therefore inhibition of LOC144766 (Accession XP_084963.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144766.

[41698] LOC144817 (Accession XP_084972.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC144817 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144817 BINDING SITE, designated SEQ ID:12382, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41699] Another function of GAM2071 is therefore inhibition of LOC144817 (Accession XP_084972.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144817.

[41700] LOC144871 (Accession XP_096698.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC144871 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144871, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144871 BINDING SITE, desig-

nated SEQ ID:10644, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41701] Another function of GAM2071 is therefore inhibition of LOC144871 (Accession XP_096698.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144871.

[41702] LOC145453 (Accession XP_085120.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC145453 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145453, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145453 BINDING SITE, designated SEQ ID:8486, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41703] Another function of GAM2071 is therefore inhibition of LOC145453 (Accession XP_085120.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC145453.

[41704] LOC145676 (Accession XP_085202.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC145676 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145676, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145676 BINDING SITE, designated SEQ ID:2964, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41705] Another function of GAM2071 is therefore inhibition of LOC145676 (Accession XP_085202.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145676.

[41706] LOC145757 (Accession XP_085227.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC145757 BINDING SITE1 and LOC145757 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC145757, corresponding to target binding sites such as BINDING SITE I, BINDING SITE

II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145757 BINDING SITE1 and LOC145757 BINDING SITE2, designated SEQ ID:13797 and SEQ ID:3109 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41707] Another function of GAM2071 is therefore inhibition of LOC145757 (Accession XP_085227.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145757.

[41708] LOC145783 (Accession XP_085231.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC145783 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145783, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145783 BINDING SITE, designated SEQ ID:6743, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41709] Another function of GAM2071 is therefore inhibition of

LOC145783 (Accession XP_085231.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145783.

[41710] LOC145813 (Accession XP_096873.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC145813 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145813 BINDING SITE, designated SEQ ID:987, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41711] Another function of GAM2071 is therefore inhibition of LOC145813 (Accession XP_096873.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145813.

[41712] LOC145988 (Accession XP_085290.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC145988 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC145988, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145988 BINDING SITE, designated SEQ ID:1945, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41713] Another function of GAM2071 is therefore inhibition of LOC145988 (Accession XP_085290.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145988.

[41714] LOC146177 (Accession NP_778229.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC146177 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146177 BINDING SITE, designated SEQ ID:15157, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[41715] Another function of GAM2071 is therefore inhibition of LOC146177 (Accession NP_778229.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146177.

[41716] LOC146229 (Accession XP_085387.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC146229 BINDING SITE1 and LOC146229 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC146229, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146229 BINDING SITE1 and LOC146229 BINDING SITE2, designated SEQ ID:3109 and SEQ ID:8345 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41717] Another function of GAM2071 is therefore inhibition of LOC146229 (Accession XP_085387.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146229.

[41718] LOC146336 (Accession XP_085421.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC146336 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146336 BINDING SITE, designated SEQ ID:4132, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41719] Another function of GAM2071 is therefore inhibition of LOC146336 (Accession XP_085421.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146336.

[41720] LOC146346 (Accession XP_085430.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC146346 BINDING SITE1 and LOC146346 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC146346, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC146346 BINDING SITE1 and LOC146346 BINDING SITE2, designated SEQ ID:16312 and SEQ ID:6781 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41721] Another function of GAM2071 is therefore inhibition of LOC146346 (Accession XP_085430.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146346.

[41722] LOC146429 (Accession XP_096998.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC146429 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146429, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146429 BINDING SITE, designated SEQ ID:8579, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41723] Another function of GAM2071 is therefore inhibition of LOC146429 (Accession XP_096998.2) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146429.

[41724] LOC146443 (Accession XP_085461.6) is another GAM2071 target gene, herein designated TARGET GENE. LOC146443 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146443, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146443 BINDING SITE, designated SEQ ID:5238, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41725] Another function of GAM2071 is therefore inhibition of LOC146443 (Accession XP_085461.6) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146443.

[41726] LOC146603 (Accession XP_085514.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC146603 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC146603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146603 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41727] Another function of GAM2071 is therefore inhibition of LOC146603 (Accession XP_085514.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146603.

[41728] LOC146784 (Accession XP_085588.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC146784 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146784, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146784 BINDING SITE, designated SEQ ID:13452, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41729] Another function of GAM2071 is therefore inhibition of LOC146784 (Accession XP_085588.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146784.

[41730] LOC146839 (Accession XP_097107.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC146839 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146839, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146839 BINDING SITE, designated SEQ ID:11661, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41731] Another function of GAM2071 is therefore inhibition of LOC146839 (Accession XP_097107.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146839.

[41732] LOC146894 (Accession NP_660316.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC146894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146894 BINDING SITE, designated SEQ ID:2386, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41733] Another function of GAM2071 is therefore inhibition of LOC146894 (Accession NP_660316.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146894.

[41734] LOC146895 (Accession XP_097120.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC146895 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146895, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146895 BINDING SITE, designated SEQ ID:8862, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41735] Another function of GAM2071 is therefore inhibition of LOC146895 (Accession XP_097120.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146895.

[41736] LOC146901 (Accession XP_097121.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC146901 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146901, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146901 BINDING SITE, designated SEQ ID:12152, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41737] Another function of GAM2071 is therefore inhibition of LOC146901 (Accession XP_097121.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146901.

[41738] LOC146909 (Accession XP_085634.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC146909 BINDING SITE1 and LOC146909 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC146909, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146909 BINDING SITE1 and LOC146909 BINDING SITE2, designated SEQ ID:14280 and SEQ ID:20010 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41739] Another function of GAM2071 is therefore inhibition of LOC146909 (Accession XP_085634.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146909.

[41740] LOC147080 (Accession XP_097182.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC147080 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147080, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147080 BINDING SITE, designated SEQ ID:18093, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41741] Another function of GAM2071 is therefore inhibition of LOC147080 (Accession XP_097182.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147080.

[41742] LOC147166 (Accession XP_085722.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC147166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147166 BINDING SITE, designated SEQ ID:546, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41743] Another function of GAM2071 is therefore inhibition of LOC147166 (Accession XP_085722.2) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147166.

[41744] LOC147343 (Accession XP_097225.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC147343 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147343, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147343 BINDING SITE, designated SEQ ID:14957, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41745] Another function of GAM2071 is therefore inhibition of LOC147343 (Accession XP_097225.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147343.

[41746] LOC147407 (Accession XP_084000.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC147407 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC147407, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147407 BINDING SITE, designated SEQ ID:12382, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41747] Another function of GAM2071 is therefore inhibition of LOC147407 (Accession XP_084000.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147407.

[41748] LOC147622 (Accession XP_097255.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC147622 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147622, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147622 BINDING SITE, designated SEQ ID:10349, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41749] Another function of GAM2071 is therefore inhibition of LOC147622 (Accession XP_097255.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147622.

[41750] LOC147817 (Accession XP_085903.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC147817 BINDING SITE1 and LOC147817 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC147817, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147817 BINDING SITE1 and LOC147817 BINDING SITE2, designated SEQ ID:14003 and SEQ ID:11085 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41751] Another function of GAM2071 is therefore inhibition of LOC147817 (Accession XP_085903.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147817.

[41752] LOC147841 (Accession XP_085924.2) is another

GAM2071 target gene, herein designated TARGET GENE. LOC147841 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147841, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147841 BINDING SITE, designated SEQ ID:18175, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41753] Another function of GAM2071 is therefore inhibition of LOC147841 (Accession XP_085924.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147841.

[41754] LOC147947 (Accession XP_085974.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC147947 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147947, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147947 BINDING SITE, desig-

nated SEQ ID:438, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41755] Another function of GAM2071 is therefore inhibition of LOC147947 (Accession XP_085974.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147947.

[41756] LOC148137 (Accession NP_653293.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC148137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148137 BINDING SITE, designated SEQ ID:13130, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41757] Another function of GAM2071 is therefore inhibition of LOC148137 (Accession NP_653293.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC148137.

[41758] LOC148708 (Accession XP_086286.4) is another GAM2071 target gene, herein designated TARGET GENE. LOC148708 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148708 BINDING SITE, designated SEQ ID:18164, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41759] Another function of GAM2071 is therefore inhibition of LOC148708 (Accession XP_086286.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148708.

[41760] LOC148709 (Accession XP_086281.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC148709 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148709, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148709 BINDING SITE, designated SEQ ID:8427, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41761] Another function of GAM2071 is therefore inhibition of LOC148709 (Accession XP_086281.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148709.

[41762] LOC149134 (Accession XP_097594.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC149134 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149134, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149134 BINDING SITE, designated SEQ ID:16592, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41763] Another function of GAM2071 is therefore inhibition of LOC149134 (Accession XP_097594.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149134.

[41764] LOC149149 (Accession XP_097598.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC149149 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149149 BINDING SITE, designated SEQ ID:9725, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41765] Another function of GAM2071 is therefore inhibition of LOC149149 (Accession XP_097598.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149149.

[41766] LOC149371 (Accession NP_787072.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC149371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC149371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149371 BINDING SITE, designated SEQ ID:14762, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41767] Another function of GAM2071 is therefore inhibition of LOC149371 (Accession NP_787072.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149371.

[41768] LOC149478 (Accession XP_086536.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC149478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149478, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149478 BINDING SITE, designated SEQ ID:2514, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41769] Another function of GAM2071 is therefore inhibition of LOC149478 (Accession XP_086536.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149478.

[41770] LOC149506 (Accession XP_097661.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC149506 BINDING SITE1 and LOC149506 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC149506, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE1 and LOC149506 BINDING SITE2, designated SEQ ID:17503 and SEQ ID:5777 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41771] Another function of GAM2071 is therefore inhibition of LOC149506 (Accession XP_097661.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149506.

[41772] LOC149692 (Accession XP_097706.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC149692 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149692, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149692 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41773] Another function of GAM2071 is therefore inhibition of LOC149692 (Accession XP_097706.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149692.

[41774] LOC149703 (Accession XP_097719.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC149703 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149703, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149703 BINDING SITE, desig-

nated SEQ ID:19805, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41775] Another function of GAM2071 is therefore inhibition of LOC149703 (Accession XP_097719.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149703.

[41776] LOC150054 (Accession XP_097797.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC150054 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150054, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150054 BINDING SITE, designated SEQ ID:18175, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41777] Another function of GAM2071 is therefore inhibition of LOC150054 (Accession XP_097797.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC150054.

[41778] LOC150225 (Accession XP_097870.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC150225 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150225, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150225 BINDING SITE, designated SEQ ID:1664, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41779] Another function of GAM2071 is therefore inhibition of LOC150225 (Accession XP_097870.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150225.

[41780] LOC150407 (Accession XP_086906.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC150407 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150407, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150407 BINDING SITE, designated SEQ ID:2430, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41781] Another function of GAM2071 is therefore inhibition of LOC150407 (Accession XP_086906.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150407.

[41782] LOC150587 (Accession XP_097917.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC150587 BINDING SITE1 and LOC150587 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC150587, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150587 BINDING SITE1 and LOC150587 BINDING SITE2, designated SEQ ID:15619 and SEQ ID:8861 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41783] Another function of GAM2071 is therefore inhibition of

LOC150587 (Accession XP_097917.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150587.

[41784] LOC151057 (Accession XP_097998.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC151057 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151057, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151057 BINDING SITE, designated SEQ ID:5519, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41785] Another function of GAM2071 is therefore inhibition of LOC151057 (Accession XP_097998.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151057.

[41786] LOC151201 (Accession XP_098021.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC151201 BINDING SITE1 and LOC151201 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC151201, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE1 and LOC151201 BINDING SITE2, designated SEQ ID:3299 and SEQ ID:11934 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41787] Another function of GAM2071 is therefore inhibition of LOC151201 (Accession XP_098021.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151201.

[41788] LOC151475 (Accession XP_098063.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC151475 BINDING SITE1 and LOC151475 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC151475, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151475 BINDING SITE1 and LOC151475 BINDING SITE2, desig-

nated SEQ ID:7086 and SEQ ID:15680 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41789] Another function of GAM2071 is therefore inhibition of LOC151475 (Accession XP_098063.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151475.

[41790] LOC151636 (Accession NP_612144.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC151636 BINDING SITE1 through LOC151636 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC151636, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151636 BINDING SITE1 through LOC151636 BINDING SITE3, designated SEQ ID:2479, SEQ ID:896 and SEQ ID:19982 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41791] Another function of GAM2071 is therefore inhibition of LOC151636 (Accession NP_612144.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC151636.

[41792] LOC152245 (Accession XP_098182.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC152245 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152245, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152245 BINDING SITE, designated SEQ ID:19257, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41793] Another function of GAM2071 is therefore inhibition of LOC152245 (Accession XP_098182.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152245.

[41794] LOC152445 (Accession XP_098231.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC152445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152445, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE, designated SEQ ID:13905, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41795] Another function of GAM2071 is therefore inhibition of LOC152445 (Accession XP_098231.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152445.

[41796] LOC152620 (Accession XP_011108.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC152620 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152620, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152620 BINDING SITE, designated SEQ ID:13870, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41797] Another function of GAM2071 is therefore inhibition of

LOC152620 (Accession XP_011108.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152620.

[41798] LOC152719 (Accession XP_098257.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC152719 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152719 BINDING SITE, designated SEQ ID:1141, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41799] Another function of GAM2071 is therefore inhibition of LOC152719 (Accession XP_098257.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152719.

[41800] LOC152794 (Accession XP_087525.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC152794 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152794, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152794 BINDING SITE, designated SEQ ID:3556, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41801] Another function of GAM2071 is therefore inhibition of LOC152794 (Accession XP_087525.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152794.

[41802] LOC152804 (Accession XP_098266.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC152804 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152804, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC152804 BINDING SITE, designated SEQ ID:8155, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41803] Another function of GAM2071 is therefore inhibition of LOC152804 (Accession XP_098266.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152804.

[41804] LOC153077 (Accession XP_098307.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC153077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153077 BINDING SITE, designated SEQ ID:19370, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41805] Another function of GAM2071 is therefore inhibition of LOC153077 (Accession XP_098307.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC153077.

[41806] LOC153811 (Accession XP_087779.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC153811 BINDING SITE1 through LOC153811 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC153811, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153811 BINDING SITE1 through LOC153811 BINDING SITE3, designated SEQ ID:6031, SEQ ID:14281 and SEQ ID:15030 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41807] Another function of GAM2071 is therefore inhibition of LOC153811 (Accession XP_087779.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153811.

[41808] LOC153883 (Accession XP_087798.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC153883 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC153883, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153883 BINDING SITE, designated SEQ ID:3293, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41809] Another function of GAM2071 is therefore inhibition of LOC153883 (Accession XP_087798.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153883.

[41810] LOC153910 (Accession XP_087801.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC153910 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153910, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153910 BINDING SITE, designated SEQ ID:7292, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41811] Another function of GAM2071 is therefore inhibition of LOC153910 (Accession XP_087801.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153910.

[41812] LOC154282 (Accession XP_098505.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC154282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154282 BINDING SITE, designated SEQ ID:14848, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41813] Another function of GAM2071 is therefore inhibition of LOC154282 (Accession XP_098505.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154282.

[41814] LOC154822 (Accession XP_098618.3) is another GAM2071 target gene, herein designated TARGET GENE.

LOC154822 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154822 BINDING SITE, designated SEQ ID:3008, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41815] Another function of GAM2071 is therefore inhibition of LOC154822 (Accession XP_098618.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154822.

[41816] LOC154877 (Accession XP_098626.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC154877 BINDING SITE1 through LOC154877 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC154877, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE1 through LOC154877 BINDING SITE3, des-

ignated SEQ ID:15947, SEQ ID:3038 and SEQ ID:14342 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41817] Another function of GAM2071 is therefore inhibition of LOC154877 (Accession XP_098626.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877.

[41818] LOC158014 (Accession XP_088442.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC158014 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158014, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158014 BINDING SITE, designated SEQ ID:12285, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41819] Another function of GAM2071 is therefore inhibition of LOC158014 (Accession XP_088442.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC158014.

[41820] LOC158310 (Accession XP_098919.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC158310 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158310, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158310 BINDING SITE, designated SEQ ID:18175, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41821] Another function of GAM2071 is therefore inhibition of LOC158310 (Accession XP_098919.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158310.

[41822] LOC158402 (Accession XP_098936.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC158402 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158402, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158402 BINDING SITE, designated SEQ ID:1414, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41823] Another function of GAM2071 is therefore inhibition of LOC158402 (Accession XP_098936.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158402.

[41824] LOC158436 (Accession XP_098942.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC158436 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158436 BINDING SITE, designated SEQ ID:7071, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41825] Another function of GAM2071 is therefore inhibition of LOC158436 (Accession XP_098942.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158436.

[41826] LOC158476 (Accession XP_098955.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC158476 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158476, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158476 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41827] Another function of GAM2071 is therefore inhibition of LOC158476 (Accession XP_098955.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158476.

[41828] LOC158563 (Accession XP_088606.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC158563 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC158563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158563 BINDING SITE, designated SEQ ID:9685, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41829] Another function of GAM2071 is therefore inhibition of LOC158563 (Accession XP_088606.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158563.

[41830] LOC160897 (Accession XP_090573.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC160897 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC160897, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC160897 BINDING SITE, designated SEQ ID:14437, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41831] Another function of GAM2071 is therefore inhibition of LOC160897 (Accession XP_090573.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160897.

[41832] LOC162083 (Accession XP_091339.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC162083 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC162083, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162083 BINDING SITE, designated SEQ ID:17143, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41833] Another function of GAM2071 is therefore inhibition of LOC162083 (Accession XP_091339.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162083.

[41834] LOC162427 (Accession XP_091549.3) is another GAM2071 target gene, herein designated TARGET GENE.

LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC162427, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2, designated SEQ ID:1761 and SEQ ID:12386 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41835] Another function of GAM2071 is therefore inhibition of LOC162427 (Accession XP_091549.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162427.

[41836] LOC162427 (Accession NP_835227.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC162427, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162427 BINDING SITE1 and LOC162427 BINDING SITE2, designated SEQ ID:1761 and SEQ ID:12386 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41837] Another function of GAM2071 is therefore inhibition of LOC162427 (Accession NP_835227.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162427.

[41838] LOC162967 (Accession XP_091890.6) is another GAM2071 target gene, herein designated TARGET GENE. LOC162967 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC162967, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162967 BINDING SITE, designated SEQ ID:3050, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41839] Another function of GAM2071 is therefore inhibition of

LOC162967 (Accession XP_091890.6) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162967.

[41840] LOC163227 (Accession NP_775802.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC163227, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2, designated SEQ ID:1413 and SEQ ID:9582 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41841] Another function of GAM2071 is therefore inhibition of LOC163227 (Accession NP_775802.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163227.

[41842] LOC168451 (Accession XP_095114.2) is another GAM2071 target gene, herein designated TARGET GENE.

LOC168451 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC168451, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC168451 BINDING SITE, designated SEQ ID:7426, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41843] Another function of GAM2071 is therefore inhibition of LOC168451 (Accession XP_095114.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168451.

[41844] LOC170409 (Accession XP_096330.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC170409 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC170409, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC170409 BINDING SITE, designated SEQ ID:7616, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41845] Another function of GAM2071 is therefore inhibition of LOC170409 (Accession XP_096330.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170409.

[41846] LOC196264 (Accession XP_113683.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC196264 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196264, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196264 BINDING SITE, designated SEQ ID:8574, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41847] Another function of GAM2071 is therefore inhibition of LOC196264 (Accession XP_113683.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196264.

[41848] LOC196993 (Accession XP_116971.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC196993 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC196993, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196993 BINDING SITE, designated SEQ ID:7905, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41849] Another function of GAM2071 is therefore inhibition of LOC196993 (Accession XP_116971.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196993.

[41850] LOC197336 (Accession NP_660337.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC197336 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC197336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC197336 BINDING SITE, designated SEQ ID:18551, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41851] Another function of GAM2071 is therefore inhibition of LOC197336 (Accession NP_660337.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197336.

[41852] LOC197358 (Accession XP_113872.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC197358 BINDING SITE1 and LOC197358 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC197358, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC197358 BINDING SITE1 and LOC197358 BINDING SITE2, designated SEQ ID:3887 and SEQ ID:5402 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41853] Another function of GAM2071 is therefore inhibition of LOC197358 (Accession XP_113872.2) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197358.

[41854] LOC199906 (Accession XP_114052.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC199906 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC199906, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199906 BINDING SITE, designated SEQ ID:11637, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41855] Another function of GAM2071 is therefore inhibition of LOC199906 (Accession XP_114052.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199906.

[41856] LOC200169 (Accession XP_117200.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC200169 BINDING SITE1 and LOC200169 BINDING SITE2 are target binding sites found in untranslated re-

gions of multiple transcripts of mRNA encoded by LOC200169, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200169 BINDING SITE1 and LOC200169 BINDING SITE2, designated SEQ ID:6517 and SEQ ID:5066 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41857] Another function of GAM2071 is therefore inhibition of LOC200169 (Accession XP_117200.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200169.

[41858] LOC200860 (Accession XP_117289.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC200860 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200860, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200860 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41859] Another function of GAM2071 is therefore inhibition of LOC200860 (Accession XP_117289.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200860.

[41860] LOC200895 (Accession NP_789785.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC200895 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200895, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200895 BINDING SITE, designated SEQ ID:3376, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41861] Another function of GAM2071 is therefore inhibition of LOC200895 (Accession NP_789785.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200895.

[41862] LOC200916 (Accession XP_114317.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC200916 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200916, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200916 BINDING SITE, designated SEQ ID:873, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41863] Another function of GAM2071 is therefore inhibition of LOC200916 (Accession XP_114317.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200916.

[41864] LOC201164 (Accession NP_849158.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC201164 BINDING SITE1 and LOC201164 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC201164, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201164 BINDING SITE1 and LOC201164 BINDING SITE2, designated SEQ ID:18118 and SEQ ID:13530 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41865] Another function of GAM2071 is therefore inhibition of LOC201164 (Accession NP_849158.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201164.

[41866] LOC201292 (Accession NP_775818.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC201292 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201292, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201292 BINDING SITE, designated SEQ ID:14592, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41867] Another function of GAM2071 is therefore inhibition of

LOC201292 (Accession NP_775818.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201292.

[41868] LOC201510 (Accession XP_113972.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC201510 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201510, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201510 BINDING SITE, designated SEQ ID:4316, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41869] Another function of GAM2071 is therefore inhibition of LOC201510 (Accession XP_113972.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201510.

[41870] LOC201562 (Accession XP_114343.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC201562 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC201562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201562 BINDING SITE, designated SEQ ID:9102, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41871] Another function of GAM2071 is therefore inhibition of LOC201562 (Accession XP_114343.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201562.

[41872] LOC201725 (Accession XP_114370.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC201725 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201725 BINDING SITE, designated SEQ ID:18941, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[41873] Another function of GAM2071 is therefore inhibition of LOC201725 (Accession XP_114370.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201725.

[41874] LOC202400 (Accession XP_117397.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC202400 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC202400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202400 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41875] Another function of GAM2071 is therefore inhibition of LOC202400 (Accession XP_117397.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202400.

[41876] LOC202404 (Accession XP_114481.4) is another

GAM2071 target gene, herein designated TARGET GENE. LOC202404 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC202404, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202404 BINDING SITE, designated SEQ ID:15206, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41877] Another function of GAM2071 is therefore inhibition of LOC202404 (Accession XP_114481.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202404.

[41878] LOC202460 (Accession XP_114493.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC202460 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC202460, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202460 BINDING SITE, desig-

nated SEQ ID:1278, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41879] Another function of GAM2071 is therefore inhibition of LOC202460 (Accession XP_114493.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202460.

[41880] LOC202934 (Accession XP_117486.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC202934 BINDING SITE1 and LOC202934 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC202934, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE1 and LOC202934 BINDING SITE2, designated SEQ ID:9097 and SEQ ID:6782 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41881] Another function of GAM2071 is therefore inhibition of LOC202934 (Accession XP_117486.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC202934.

[41882] LOC203427 (Accession NP_660348.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC203427 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC203427, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC203427 BINDING SITE, designated SEQ ID:11590, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41883] Another function of GAM2071 is therefore inhibition of LOC203427 (Accession NP_660348.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203427.

[41884] LOC203547 (Accession XP_114719.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC203547 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC203547, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC203547 BINDING SITE, designated SEQ ID:10631, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41885] Another function of GAM2071 is therefore inhibition of LOC203547 (Accession XP_114719.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203547.

[41886] LOC219293 (Accession XP_166599.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC219293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219293 BINDING SITE, designated SEQ ID:12080, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41887] Another function of GAM2071 is therefore inhibition of

LOC219293 (Accession XP_166599.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219293.

[41888] LOC219731 (Accession XP_167596.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC219731 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC219731, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219731 BINDING SITE, designated SEQ ID:3320, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41889] Another function of GAM2071 is therefore inhibition of LOC219731 (Accession XP_167596.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219731.

[41890] LOC219735 (Accession XP_167601.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC219735 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC219735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219735 BINDING SITE, designated SEQ ID:3675, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41891] Another function of GAM2071 is therefore inhibition of LOC219735 (Accession XP_167601.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219735.

[41892] LOC219894 (Accession XP_167782.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC219894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219894 BINDING SITE, designated SEQ ID:7138, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[41893] Another function of GAM2071 is therefore inhibition of LOC219894 (Accession XP_167782.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219894.

[41894] LOC220074 (Accession NP_660352.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC220074 BINDING SITE1 through LOC220074 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC220074, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220074 BINDING SITE1 through LOC220074 BINDING SITE3, designated SEQ ID:1413, SEQ ID:2086 and SEQ ID:4396 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41895] Another function of GAM2071 is therefore inhibition of LOC220074 (Accession NP_660352.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220074.

[41896] LOC220594 (Accession NP_665808.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC220594 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC220594, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220594 BINDING SITE, designated SEQ ID:6273, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41897] Another function of GAM2071 is therefore inhibition of LOC220594 (Accession NP_665808.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220594.

[41898] LOC221663 (Accession XP_168131.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC221663 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC221663 BINDING SITE, designated SEQ ID:10616, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41899] Another function of GAM2071 is therefore inhibition of LOC221663 (Accession XP_168131.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221663.

[41900] LOC221683 (Accession XP_168089.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC221683 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221683, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221683 BINDING SITE, designated SEQ ID:1313, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41901] Another function of GAM2071 is therefore inhibition of LOC221683 (Accession XP_168089.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC221683.

[41902] LOC221814 (Accession XP_168226.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC221814 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221814, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221814 BINDING SITE, designated SEQ ID:6429, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41903] Another function of GAM2071 is therefore inhibition of LOC221814 (Accession XP_168226.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221814.

[41904] LOC221946 (Accession XP_168340.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC221946 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221946, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221946 BINDING SITE, designated SEQ ID:3294, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41905] Another function of GAM2071 is therefore inhibition of LOC221946 (Accession XP_168340.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221946.

[41906] LOC222057 (Accession XP_166594.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC222057 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222057, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222057 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41907] Another function of GAM2071 is therefore inhibition of

LOC222057 (Accession XP_166594.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222057.

[41908] LOC222068 (Accession XP_166556.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC222068 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC222068, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222068 BINDING SITE, designated SEQ ID:6331, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41909] Another function of GAM2071 is therefore inhibition of LOC222068 (Accession XP_166556.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222068.

[41910] LOC252983 (Accession XP_170858.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC252983 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC252983, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC252983 BINDING SITE, designated SEQ ID:8882, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41911] Another function of GAM2071 is therefore inhibition of LOC252983 (Accession XP_170858.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC252983.

[41912] LOC253216 (Accession XP_170765.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC253216 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC253216, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253216 BINDING SITE, designated SEQ ID:14534, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[41913] Another function of GAM2071 is therefore inhibition of LOC253216 (Accession XP_170765.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253216.

[41914] LOC253612 (Accession XP_172985.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC253612 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253612, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253612 BINDING SITE, designated SEQ ID:19268, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41915] Another function of GAM2071 is therefore inhibition of LOC253612 (Accession XP_172985.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253612.

[41916] LOC253805 (Accession XP_172854.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC253805 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC253805, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253805 BINDING SITE, designated SEQ ID:7275, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41917] Another function of GAM2071 is therefore inhibition of LOC253805 (Accession XP_172854.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253805.

[41918] LOC255031 (Accession XP_173187.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC255031 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC255031, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255031 BINDING SITE, desig-

nated SEQ ID:11416, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41919] Another function of GAM2071 is therefore inhibition of LOC255031 (Accession XP_173187.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255031.

[41920] LOC255488 (Accession XP_172581.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC255488 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC255488, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255488 BINDING SITE, designated SEQ ID:18594, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41921] Another function of GAM2071 is therefore inhibition of LOC255488 (Accession XP_172581.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC255488.

[41922] LOC255975 (Accession XP_171083.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC255975 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255975 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41923] Another function of GAM2071 is therefore inhibition of LOC255975 (Accession XP_171083.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255975.

[41924] LOC256614 (Accession XP_172864.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC256614 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC256614, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256614 BINDING SITE, designated SEQ ID:3106, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41925] Another function of GAM2071 is therefore inhibition of LOC256614 (Accession XP_172864.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256614.

[41926] LOC282905 (Accession XP_212606.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC282905 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282905, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282905 BINDING SITE, designated SEQ ID:8939, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41927] Another function of GAM2071 is therefore inhibition of LOC282905 (Accession XP_212606.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282905.

[41928] LOC282943 (Accession XP_212647.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC282943 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282943, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282943 BINDING SITE, designated SEQ ID:8939, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41929] Another function of GAM2071 is therefore inhibition of LOC282943 (Accession XP_212647.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282943.

[41930] LOC282987 (Accession XP_210845.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC282987 BINDING SITE1 and LOC282987 BINDING SITE2 are target binding sites found in untranslated re-

gions of mRNA encoded by LOC282987, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282987 BINDING SITE1 and LOC282987 BINDING SITE2, designated SEQ ID:12386 and SEQ ID:10460 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41931] Another function of GAM2071 is therefore inhibition of LOC282987 (Accession XP_210845.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282987.

[41932] LOC283031 (Accession XP_210859.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283031 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283031, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283031 BINDING SITE, designated SEQ ID:654, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[41933] Another function of GAM2071 is therefore inhibition of LOC283031 (Accession XP_210859.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283031.

[41934] LOC283061 (Accession XP_210875.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283061 BINDING SITE, designated SEQ ID:18916, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41935] Another function of GAM2071 is therefore inhibition of LOC283061 (Accession XP_210875.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283061.

[41936] LOC283067 (Accession XP_208501.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC283067 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283067, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283067 BINDING SITE, designated SEQ ID:18641, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41937] Another function of GAM2071 is therefore inhibition of LOC283067 (Accession XP_208501.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283067.

[41938] LOC283087 (Accession XP_208509.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283087 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283087, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283087 BINDING SITE, desig-

nated SEQ ID:6936, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41939] Another function of GAM2071 is therefore inhibition of LOC283087 (Accession XP_208509.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283087.

[41940] LOC283089 (Accession XP_210885.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283089 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283089, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283089 BINDING SITE, designated SEQ ID:6866, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41941] Another function of GAM2071 is therefore inhibition of LOC283089 (Accession XP_210885.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283089.

[41942] LOC283119 (Accession XP_210895.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283119 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283119, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283119 BINDING SITE, designated SEQ ID:1505, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41943] Another function of GAM2071 is therefore inhibition of LOC283119 (Accession XP_210895.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283119.

[41944] LOC283130 (Accession XP_208525.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC283130 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283130, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283130 BINDING SITE, designated SEQ ID:469, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41945] Another function of GAM2071 is therefore inhibition of LOC283130 (Accession XP_208525.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283130.

[41946] LOC283143 (Accession XP_210920.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283143 BINDING SITE, designated SEQ ID:14843, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41947] Another function of GAM2071 is therefore inhibition of LOC283143 (Accession XP_210920.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283143.

[41948] LOC283152 (Accession XP_210917.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC283152 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283152, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283152 BINDING SITE, designated SEQ ID:17431, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41949] Another function of GAM2071 is therefore inhibition of LOC283152 (Accession XP_210917.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283152.

[41950] LOC283170 (Accession XP_208535.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC283170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283170 BINDING SITE, designated SEQ ID:19643, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41951] Another function of GAM2071 is therefore inhibition of LOC283170 (Accession XP_208535.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283170.

[41952] LOC283199 (Accession XP_210929.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283199 BINDING SITE1 and LOC283199 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283199, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283199 BINDING SITE1 and LOC283199 BINDING SITE2, designated SEQ ID:20110 and SEQ ID:4762 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[41953] Another function of GAM2071 is therefore inhibition of LOC283199 (Accession XP_210929.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283199.

[41954] LOC283215 (Accession XP_208555.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC283215 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283215, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283215 BINDING SITE, designated SEQ ID:14997, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41955] Another function of GAM2071 is therefore inhibition of LOC283215 (Accession XP_208555.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283215.

[41956] LOC283241 (Accession NP_787089.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC283241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283241 BINDING SITE, designated SEQ ID:10625, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41957] Another function of GAM2071 is therefore inhibition of LOC283241 (Accession NP_787089.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283241.

[41958] LOC283293 (Accession XP_210962.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283293 BINDING SITE, desig-

nated SEQ ID:438, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41959] Another function of GAM2071 is therefore inhibition of LOC283293 (Accession XP_210962.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283293.

[41960] LOC283329 (Accession XP_210978.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283329 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283329 BINDING SITE, designated SEQ ID:6052, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41961] Another function of GAM2071 is therefore inhibition of LOC283329 (Accession XP_210978.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283329.

[41962] LOC283335 (Accession XP_210981.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283335 BINDING SITE1 and LOC283335 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283335, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283335 BINDING SITE1 and LOC283335 BINDING SITE2, designated SEQ ID:10626 and SEQ ID:9238 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41963] Another function of GAM2071 is therefore inhibition of LOC283335 (Accession XP_210981.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283335.

[41964] LOC283377 (Accession XP_208647.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283377 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283377, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283377 BINDING SITE, designated SEQ ID:8862, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41965] Another function of GAM2071 is therefore inhibition of LOC283377 (Accession XP_208647.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283377.

[41966] LOC283395 (Accession XP_211020.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283395 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283395, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283395 BINDING SITE, designated SEQ ID:13838, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41967] Another function of GAM2071 is therefore inhibition of

LOC283395 (Accession XP_211020.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283395.

[41968] LOC283432 (Accession XP_211032.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283432 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283432, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283432 BINDING SITE, designated SEQ ID:6836, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41969] Another function of GAM2071 is therefore inhibition of LOC283432 (Accession XP_211032.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283432.

[41970] LOC283434 (Accession XP_211034.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283434 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC283434, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283434 BINDING SITE, designated SEQ ID:16416, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41971] Another function of GAM2071 is therefore inhibition of LOC283434 (Accession XP_211034.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283434.

[41972] LOC283445 (Accession XP_211044.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283445 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283445 BINDING SITE, designated SEQ ID:9159, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[41973] Another function of GAM2071 is therefore inhibition of LOC283445 (Accession XP_211044.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283445.

[41974] LOC283452 (Accession XP_208679.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283452 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283452 BINDING SITE, designated SEQ ID:17791, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41975] Another function of GAM2071 is therefore inhibition of LOC283452 (Accession XP_208679.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283452.

[41976] LOC283454 (Accession XP_211049.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC283454 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283454, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283454 BINDING SITE, designated SEQ ID:12385, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41977] Another function of GAM2071 is therefore inhibition of LOC283454 (Accession XP_211049.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283454.

[41978] LOC283475 (Accession XP_211056.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283475 BINDING SITE1 and LOC283475 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283475, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283475

BINDING SITE1 and LOC283475 BINDING SITE2, designated SEQ ID:8583 and SEQ ID:12806 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41979] Another function of GAM2071 is therefore inhibition of LOC283475 (Accession XP_211056.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283475.

[41980] LOC283507 (Accession XP_211075.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283507 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283507 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41981] Another function of GAM2071 is therefore inhibition of LOC283507 (Accession XP_211075.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283507.

[41982] LOC283534 (Accession XP_211083.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283534 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283534, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283534 BINDING SITE, designated SEQ ID:13197, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41983] Another function of GAM2071 is therefore inhibition of LOC283534 (Accession XP_211083.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283534.

[41984] LOC283565 (Accession XP_211100.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283565 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283565, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283565 BINDING SITE, designated SEQ ID:6104, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41985] Another function of GAM2071 is therefore inhibition of LOC283565 (Accession XP_211100.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283565.

[41986] LOC283585 (Accession XP_294741.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283585 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283585, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283585 BINDING SITE, designated SEQ ID:3904, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41987] Another function of GAM2071 is therefore inhibition of

LOC283585 (Accession XP_294741.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283585.

[41988] LOC283588 (Accession NP_787093.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283588 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283588, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283588 BINDING SITE, designated SEQ ID:14938, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41989] Another function of GAM2071 is therefore inhibition of LOC283588 (Accession NP_787093.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283588.

[41990] LOC283624 (Accession XP_211126.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283624 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC283624, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283624 BINDING SITE, designated SEQ ID:13972, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41991] Another function of GAM2071 is therefore inhibition of LOC283624 (Accession XP_211126.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283624.

[41992] LOC283637 (Accession XP_211134.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283637 BINDING SITE1 and LOC283637 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283637, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283637 BINDING SITE1 and LOC283637 BINDING SITE2, designated SEQ ID:12382 and SEQ ID:3786 respectively, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41993] Another function of GAM2071 is therefore inhibition of LOC283637 (Accession XP_211134.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283637.

[41994] LOC283641 (Accession XP_208764.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283641 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283641, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283641 BINDING SITE, designated SEQ ID:435, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41995] Another function of GAM2071 is therefore inhibition of LOC283641 (Accession XP_208764.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283641.

[41996] LOC283664 (Accession XP_208773.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283664 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283664, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283664 BINDING SITE, designated SEQ ID:11292, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41997] Another function of GAM2071 is therefore inhibition of LOC283664 (Accession XP_208773.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283664.

[41998] LOC283679 (Accession XP_211157.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283679 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283679, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC283679 BINDING SITE, designated SEQ ID:18582, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[41999] Another function of GAM2071 is therefore inhibition of LOC283679 (Accession XP_211157.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283679.

[42000] LOC283687 (Accession NP_787094.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283687 BINDING SITE, designated SEQ ID:5544, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42001] Another function of GAM2071 is therefore inhibition of LOC283687 (Accession NP_787094.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283687.

[42002] LOC283701 (Accession XP_211170.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC283701 BINDING SITE1 and LOC283701 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283701, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283701 BINDING SITE1 and LOC283701 BINDING SITE2, designated SEQ ID:7650 and SEQ ID:777 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42003] Another function of GAM2071 is therefore inhibition of LOC283701 (Accession XP_211170.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283701.

[42004] LOC283706 (Accession XP_208804.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC283706 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC283706, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283706 BINDING SITE, designated SEQ ID:16154, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42005] Another function of GAM2071 is therefore inhibition of LOC283706 (Accession XP_208804.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283706.

[42006] LOC283741 (Accession XP_208115.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283741 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283741, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283741 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42007] Another function of GAM2071 is therefore inhibition of LOC283741 (Accession XP_208115.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283741.

[42008] LOC283778 (Accession XP_211199.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283778 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283778, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283778 BINDING SITE, designated SEQ ID:15679, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42009] Another function of GAM2071 is therefore inhibition of LOC283778 (Accession XP_211199.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283778.

[42010] LOC283801 (Accession XP_208122.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC283801 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283801, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283801 BINDING SITE, designated SEQ ID:11237, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42011] Another function of GAM2071 is therefore inhibition of LOC283801 (Accession XP_208122.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283801.

[42012] LOC283802 (Accession XP_208850.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283802 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283802, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283802 BINDING SITE, designated SEQ ID:16635, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42013] Another function of GAM2071 is therefore inhibition of LOC283802 (Accession XP_208850.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283802.

[42014] LOC283818 (Accession XP_211218.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283818 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283818 BINDING SITE, designated SEQ ID:3834, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42015] Another function of GAM2071 is therefore inhibition of LOC283818 (Accession XP_211218.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283818.

[42016] LOC283851 (Accession XP_211229.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283851 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283851, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283851 BINDING SITE, designated SEQ ID:12708, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42017] Another function of GAM2071 is therefore inhibition of LOC283851 (Accession XP_211229.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283851.

[42018] LOC283861 (Accession NP_787095.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283861 BINDING SITE1 and LOC283861 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283861, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC283861 BINDING SITE1 and LOC283861 BINDING SITE2, designated SEQ ID:10879 and SEQ ID:8996 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42019] Another function of GAM2071 is therefore inhibition of LOC283861 (Accession NP_787095.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283861.

[42020] LOC283887 (Accession XP_211248.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC283887 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283887, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283887 BINDING SITE, designated SEQ ID:9775, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42021] Another function of GAM2071 is therefore inhibition of LOC283887 (Accession XP_211248.2) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283887.

[42022] LOC283889 (Accession XP_208899.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283889 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283889, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283889 BINDING SITE, designated SEQ ID:13686, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42023] Another function of GAM2071 is therefore inhibition of LOC283889 (Accession XP_208899.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283889.

[42024] LOC283928 (Accession XP_208909.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283928 BINDING SITE1 through LOC283928 BINDING SITE3 are target binding sites found in untranslated re-

gions of mRNA encoded by LOC283928, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283928 BINDING SITE1 through LOC283928 BINDING SITE3, designated SEQ ID:3604, SEQ ID:9603 and SEQ ID:13293 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42025] Another function of GAM2071 is therefore inhibition of LOC283928 (Accession XP_208909.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283928.

[42026] LOC283929 (Accession XP_208905.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC283929 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283929, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283929 BINDING SITE, designated SEQ ID:10232, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[42027] Another function of GAM2071 is therefore inhibition of LOC283929 (Accession XP_208905.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283929.

[42028] LOC283932 (Accession NP_787097.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC283932 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283932, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283932 BINDING SITE, designated SEQ ID:15305, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42029] Another function of GAM2071 is therefore inhibition of LOC283932 (Accession NP_787097.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283932.

[42030] LOC283964 (Accession XP_208145.2) is another

GAM2071 target gene, herein designated TARGET GENE. LOC283964 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283964, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283964 BINDING SITE, designated SEQ ID:1384, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42031] Another function of GAM2071 is therefore inhibition of LOC283964 (Accession XP_208145.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283964.

[42032] LOC284001 (Accession XP_208958.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC284001 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284001 BINDING SITE, desig-

nated SEQ ID:6195, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42033] Another function of GAM2071 is therefore inhibition of LOC284001 (Accession XP_208958.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284001.

[42034] LOC284017 (Accession XP_208961.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284017 BINDING SITE, designated SEQ ID:3858, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42035] Another function of GAM2071 is therefore inhibition of LOC284017 (Accession XP_208961.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284017.

[42036] LOC284023 (Accession XP_208983.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC284023 BINDING SITE1 and LOC284023 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284023, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284023 BINDING SITE1 and LOC284023 BINDING SITE2, designated SEQ ID:429 and SEQ ID:5520 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42037] Another function of GAM2071 is therefore inhibition of LOC284023 (Accession XP_208983.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284023.

[42038] LOC284048 (Accession XP_208152.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284048 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284048, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284048 BINDING SITE, designated SEQ ID:17222, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42039] Another function of GAM2071 is therefore inhibition of LOC284048 (Accession XP_208152.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284048.

[42040] LOC284063 (Accession XP_208992.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284063 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284063, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284063 BINDING SITE, designated SEQ ID:17713, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42041] Another function of GAM2071 is therefore inhibition of

LOC284063 (Accession XP_208992.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284063.

[42042] LOC284074 (Accession XP_211321.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284074 BINDING SITE1 and LOC284074 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284074, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284074 BINDING SITE1 and LOC284074 BINDING SITE2, designated SEQ ID:18547 and SEQ ID:5751 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42043] Another function of GAM2071 is therefore inhibition of LOC284074 (Accession XP_211321.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284074.

[42044] LOC284082 (Accession XP_211323.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC284082 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284082, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284082 BINDING SITE, designated SEQ ID:18527, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42045] Another function of GAM2071 is therefore inhibition of LOC284082 (Accession XP_211323.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284082.

[42046] LOC284095 (Accession XP_211324.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284095 BINDING SITE1 and LOC284095 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284095, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284095 BINDING SITE1 and LOC284095 BINDING SITE2, desig-

nated SEQ ID:19595 and SEQ ID:16884 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42047] Another function of GAM2071 is therefore inhibition of LOC284095 (Accession XP_211324.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284095.

[42048] LOC284098 (Accession XP_209008.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC284098 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284098, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284098 BINDING SITE, designated SEQ ID:18178, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42049] Another function of GAM2071 is therefore inhibition of LOC284098 (Accession XP_209008.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284098.

[42050] LOC284102 (Accession XP_211327.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC284102 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284102, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284102 BINDING SITE, designated SEQ ID:17111, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42051] Another function of GAM2071 is therefore inhibition of LOC284102 (Accession XP_211327.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284102.

[42052] LOC284106 (Accession XP_209004.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284106 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284106, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284106 BINDING SITE, designated SEQ ID:11925, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42053] Another function of GAM2071 is therefore inhibition of LOC284106 (Accession XP_209004.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284106.

[42054] LOC284116 (Accession XP_211338.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC284116 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284116, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284116 BINDING SITE, designated SEQ ID:1709, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42055] Another function of GAM2071 is therefore inhibition of LOC284116 (Accession XP_211338.2) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284116.

[42056] LOC284117 (Accession XP_209024.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284117 BINDING SITE, designated SEQ ID:11347, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42057] Another function of GAM2071 is therefore inhibition of LOC284117 (Accession XP_209024.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284117.

[42058] LOC284128 (Accession XP_211342.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284128 BINDING SITE1 and LOC284128 BINDING SITE2 are target binding sites found in untranslated re-

gions of mRNA encoded by LOC284128, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284128 BINDING SITE1 and LOC284128 BINDING SITE2, designated SEQ ID:17271 and SEQ ID:17792 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42059] Another function of GAM2071 is therefore inhibition of LOC284128 (Accession XP_211342.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284128.

[42060] LOC284145 (Accession XP_211353.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284145 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284145, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284145 BINDING SITE, designated SEQ ID:8678, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[42061] Another function of GAM2071 is therefore inhibition of LOC284145 (Accession XP_211353.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284145.

[42062] LOC284171 (Accession XP_209051.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284171 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284171, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284171 BINDING SITE, designated SEQ ID:12420, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42063] Another function of GAM2071 is therefore inhibition of LOC284171 (Accession XP_209051.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284171.

[42064] LOC284186 (Accession XP_209060.2) is another

GAM2071 target gene, herein designated TARGET GENE. LOC284186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284186 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42065] Another function of GAM2071 is therefore inhibition of LOC284186 (Accession XP_209060.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284186.

[42066] LOC284191 (Accession XP_211377.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284191 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284191, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284191 BINDING SITE, desig-

nated SEQ ID:7923, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42067] Another function of GAM2071 is therefore inhibition of LOC284191 (Accession XP_211377.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284191.

[42068] LOC284267 (Accession XP_211411.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284267 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284267, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284267 BINDING SITE, designated SEQ ID:5421, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42069] Another function of GAM2071 is therefore inhibition of LOC284267 (Accession XP_211411.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284267.

[42070] LOC284276 (Accession XP_211412.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284276 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284276, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284276 BINDING SITE, designated SEQ ID:12113, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42071] Another function of GAM2071 is therefore inhibition of LOC284276 (Accession XP_211412.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284276.

[42072] LOC284286 (Accession XP_211419.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284286 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284286, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284286 BINDING SITE, designated SEQ ID:5521, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42073] Another function of GAM2071 is therefore inhibition of LOC284286 (Accession XP_211419.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284286.

[42074] LOC284289 (Accession XP_209105.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284289 BINDING SITE, designated SEQ ID:7635, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42075] Another function of GAM2071 is therefore inhibition of LOC284289 (Accession XP_209105.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284289.

[42076] LOC284304 (Accession XP_211426.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284304 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284304, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284304 BINDING SITE, designated SEQ ID:16163, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42077] Another function of GAM2071 is therefore inhibition of LOC284304 (Accession XP_211426.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284304.

[42078] LOC284305 (Accession XP_211425.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284305 BINDING SITE1 and LOC284305 BINDING SITE2 are target binding sites found in untranslated re-

gions of mRNA encoded by LOC284305, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284305 BINDING SITE1 and LOC284305 BINDING SITE2, designated SEQ ID:15706 and SEQ ID:12588 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42079] Another function of GAM2071 is therefore inhibition of LOC284305 (Accession XP_211425.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284305.

[42080] LOC284317 (Accession XP_209162.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284317 BINDING SITE1 and LOC284317 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284317, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284317 BINDING SITE1 and LOC284317 BINDING SITE2, designated SEQ ID:5320 and SEQ ID:11486 respectively, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42081] Another function of GAM2071 is therefore inhibition of LOC284317 (Accession XP_209162.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284317.

[42082] LOC284321 (Accession XP_211432.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284321 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284321, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284321 BINDING SITE, designated SEQ ID:11129, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42083] Another function of GAM2071 is therefore inhibition of LOC284321 (Accession XP_211432.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284321.

[42084] LOC284325 (Accession XP_209143.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284325 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284325, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284325 BINDING SITE, designated SEQ ID:11657, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42085] Another function of GAM2071 is therefore inhibition of LOC284325 (Accession XP_209143.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284325.

[42086] LOC284362 (Accession XP_211435.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284362 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284362, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284362 BINDING SITE, designated SEQ ID:10666, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42087] Another function of GAM2071 is therefore inhibition of LOC284362 (Accession XP_211435.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284362.

[42088] LOC284375 (Accession XP_209154.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284375 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284375, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284375 BINDING SITE, designated SEQ ID:13618, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42089] Another function of GAM2071 is therefore inhibition of LOC284375 (Accession XP_209154.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284375.

[42090] LOC284376 (Accession XP_209157.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284376 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284376, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284376 BINDING SITE, designated SEQ ID:9328, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42091] Another function of GAM2071 is therefore inhibition of LOC284376 (Accession XP_209157.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284376.

[42092] LOC284379 (Accession XP_209163.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284379 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284379, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284379 BINDING SITE, designated SEQ ID:2198, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42093] Another function of GAM2071 is therefore inhibition of LOC284379 (Accession XP_209163.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284379.

[42094] LOC284405 (Accession XP_209183.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC284405 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284405, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284405 BINDING SITE, designated SEQ ID:3894, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42095] Another function of GAM2071 is therefore inhibition of

LOC284405 (Accession XP_209183.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284405.

[42096] LOC284421 (Accession XP_209200.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284421 BINDING SITE1 and LOC284421 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284421, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284421 BINDING SITE1 and LOC284421 BINDING SITE2, designated SEQ ID:2985 and SEQ ID:15524 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42097] Another function of GAM2071 is therefore inhibition of LOC284421 (Accession XP_209200.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284421.

[42098] LOC284426 (Accession XP_209198.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC284426 BINDING SITE1 and LOC284426 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284426, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284426 BINDING SITE1 and LOC284426 BINDING SITE2, designated SEQ ID:19419 and SEQ ID:932 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42099] Another function of GAM2071 is therefore inhibition of LOC284426 (Accession XP_209198.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284426.

[42100] LOC284436 (Accession XP_290862.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284436 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284436 BINDING SITE, desig-

nated SEQ ID:6140, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42101] Another function of GAM2071 is therefore inhibition of LOC284436 (Accession XP_290862.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284436.

[42102] LOC284440 (Accession XP_209210.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284440 BINDING SITE, designated SEQ ID:12050, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42103] Another function of GAM2071 is therefore inhibition of LOC284440 (Accession XP_209210.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284440.

[42104] LOC284454 (Accession XP_209216.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284454 BINDING SITE1 and LOC284454 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284454, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284454 BINDING SITE1 and LOC284454 BINDING SITE2, designated SEQ ID:3963 and SEQ ID:18896 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42105] Another function of GAM2071 is therefore inhibition of LOC284454 (Accession XP_209216.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284454.

[42106] LOC284456 (Accession XP_211470.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284456 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284456, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284456 BINDING SITE, designated SEQ ID:10594, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42107] Another function of GAM2071 is therefore inhibition of LOC284456 (Accession XP_211470.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284456.

[42108] LOC284459 (Accession XP_290826.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284459 BINDING SITE, designated SEQ ID:1740, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42109] Another function of GAM2071 is therefore inhibition of

LOC284459 (Accession XP_290826.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284459.

[42110] LOC284471 (Accession XP_209225.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284471 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284471, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284471 BINDING SITE, designated SEQ ID:4926, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42111] Another function of GAM2071 is therefore inhibition of LOC284471 (Accession XP_209225.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284471.

[42112] LOC284486 (Accession XP_209231.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284486 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC284486, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284486 BINDING SITE, designated SEQ ID:10824, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42113] Another function of GAM2071 is therefore inhibition of LOC284486 (Accession XP_209231.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284486.

[42114] LOC284513 (Accession XP_211502.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284513 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284513, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284513 BINDING SITE, designated SEQ ID:19066, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[42115] Another function of GAM2071 is therefore inhibition of LOC284513 (Accession XP_211502.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284513.

[42116] LOC284531 (Accession XP_211513.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284531 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284531, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284531 BINDING SITE, designated SEQ ID:2846, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42117] Another function of GAM2071 is therefore inhibition of LOC284531 (Accession XP_211513.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284531.

[42118] LOC284551 (Accession XP_211515.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC284551 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284551, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284551 BINDING SITE, designated SEQ ID:17959, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42119] Another function of GAM2071 is therefore inhibition of LOC284551 (Accession XP_211515.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284551.

[42120] LOC284577 (Accession XP_211522.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284577 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284577, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284577 BINDING SITE, desig-

nated SEQ ID:11682, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42121] Another function of GAM2071 is therefore inhibition of LOC284577 (Accession XP_211522.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284577.

[42122] LOC284587 (Accession XP_209278.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC284587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284587 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42123] Another function of GAM2071 is therefore inhibition of LOC284587 (Accession XP_209278.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284587.

[42124] LOC284611 (Accession XP_211552.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284611 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284611, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284611 BINDING SITE, designated SEQ ID:11652, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42125] Another function of GAM2071 is therefore inhibition of LOC284611 (Accession XP_211552.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284611.

[42126] LOC284675 (Accession XP_209319.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284675 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284675, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284675 BINDING SITE, designated SEQ ID:8487, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42127] Another function of GAM2071 is therefore inhibition of LOC284675 (Accession XP_209319.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284675.

[42128] LOC284701 (Accession XP_294994.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284701 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284701, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284701 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42129] Another function of GAM2071 is therefore inhibition of LOC284701 (Accession XP_294994.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284701.

[42130] LOC284723 (Accession XP_211602.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284723 BINDING SITE1 and LOC284723 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284723, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284723 BINDING SITE1 and LOC284723 BINDING SITE2, designated SEQ ID:6492 and SEQ ID:17106 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42131] Another function of GAM2071 is therefore inhibition of LOC284723 (Accession XP_211602.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284723.

[42132] LOC284805 (Accession XP_209371.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284805 BINDING SITE1 and LOC284805 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284805, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284805 BINDING SITE1 and LOC284805 BINDING SITE2, designated SEQ ID:18781 and SEQ ID:11447 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42133] Another function of GAM2071 is therefore inhibition of LOC284805 (Accession XP_209371.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284805.

[42134] LOC284845 (Accession XP_211663.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284845 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284845, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284845 BINDING SITE, designated SEQ ID:15141, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42135] Another function of GAM2071 is therefore inhibition of LOC284845 (Accession XP_211663.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284845.

[42136] LOC284856 (Accession XP_302835.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284856 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC284856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284856 BINDING SITE, designated SEQ ID:3436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42137] Another function of GAM2071 is therefore inhibition of LOC284856 (Accession XP_302835.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284856.

[42138] LOC284856 (Accession XP_211668.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC284856 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC284856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284856 BINDING SITE, designated SEQ ID:3436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42139] Another function of GAM2071 is therefore inhibition of LOC284856 (Accession XP_211668.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284856.

[42140] LOC284874 (Accession XP_209394.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284874 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284874, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284874 BINDING SITE, designated SEQ ID:2751, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42141] Another function of GAM2071 is therefore inhibition of LOC284874 (Accession XP_209394.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284874.

[42142] LOC284934 (Accession XP_211696.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284934 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284934, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284934 BINDING SITE, designated SEQ ID:17477, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42143] Another function of GAM2071 is therefore inhibition of LOC284934 (Accession XP_211696.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284934.

[42144] LOC284950 (Accession XP_211703.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284950 BINDING SITE1 and LOC284950 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284950, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284950 BINDING SITE1 and LOC284950 BINDING SITE2, designated SEQ ID:1362 and SEQ ID:6753 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42145] Another function of GAM2071 is therefore inhibition of LOC284950 (Accession XP_211703.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284950.

[42146] LOC284965 (Accession XP_209425.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284965 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC284965, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284965 BINDING SITE, designated SEQ ID:6801, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42147] Another function of GAM2071 is therefore inhibition of LOC284965 (Accession XP_209425.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284965.

[42148] LOC284976 (Accession XP_211714.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC284976 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284976, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284976 BINDING SITE, designated SEQ ID:5711, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42149] Another function of GAM2071 is therefore inhibition of LOC284976 (Accession XP_211714.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284976.

[42150] LOC285026 (Accession XP_209440.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285026 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285026, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285026 BINDING SITE, designated SEQ ID:14276, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42151] Another function of GAM2071 is therefore inhibition of LOC285026 (Accession XP_209440.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285026.

[42152] LOC285052 (Accession XP_211751.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC285052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285052 BINDING SITE, designated SEQ ID:5968, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42153] Another function of GAM2071 is therefore inhibition of LOC285052 (Accession XP_211751.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285052.

[42154] LOC285058 (Accession XP_211753.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285058 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285058 BINDING SITE, designated SEQ ID:10836, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42155] Another function of GAM2071 is therefore inhibition of LOC285058 (Accession XP_211753.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285058.

[42156] LOC285083 (Accession XP_209464.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285083 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285083, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285083 BINDING SITE, designated SEQ ID:18085, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42157] Another function of GAM2071 is therefore inhibition of LOC285083 (Accession XP_209464.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285083.

[42158] LOC285094 (Accession XP_209471.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285094 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285094, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285094 BINDING SITE, designated SEQ ID:2931, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42159] Another function of GAM2071 is therefore inhibition of LOC285094 (Accession XP_209471.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285094.

[42160] LOC285127 (Accession XP_211771.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285127 BINDING SITE1 and LOC285127 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285127, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC285127 BINDING SITE1 and LOC285127 BINDING SITE2, designated SEQ ID:19204 and SEQ ID:3106 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42161] Another function of GAM2071 is therefore inhibition of LOC285127 (Accession XP_211771.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285127.

[42162] LOC285176 (Accession XP_209500.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285176 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285176, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285176 BINDING SITE, designated SEQ ID:12167, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42163] Another function of GAM2071 is therefore inhibition of LOC285176 (Accession XP_209500.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285176.

[42164] LOC285193 (Accession XP_209509.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285193, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285193 BINDING SITE, designated SEQ ID:13870, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42165] Another function of GAM2071 is therefore inhibition of LOC285193 (Accession XP_209509.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285193.

[42166] LOC285221 (Accession XP_209521.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285221 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC285221, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285221 BINDING SITE, designated SEQ ID:15365, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42167] Another function of GAM2071 is therefore inhibition of LOC285221 (Accession XP_209521.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285221.

[42168] LOC285231 (Accession XP_211813.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285231 BINDING SITE1 through LOC285231 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC285231, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285231 BINDING SITE1 through LOC285231 BINDING SITE3, designated SEQ ID:3632, SEQ ID:11238 and SEQ ID:13069 respectively, to the nucleotide sequence of GAM2071 RNA,

herein designated GAM RNA, also designated SEQ ID:371.

[42169] Another function of GAM2071 is therefore inhibition of LOC285231 (Accession XP_211813.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285231.

[42170] LOC285281 (Accession XP_211829.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285281 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285281, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285281 BINDING SITE, designated SEQ ID:7766, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42171] Another function of GAM2071 is therefore inhibition of LOC285281 (Accession XP_211829.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285281.

[42172] LOC285299 (Accession XP_209554.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC285299 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285299, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285299 BINDING SITE, designated SEQ ID:15961, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42173] Another function of GAM2071 is therefore inhibition of LOC285299 (Accession XP_209554.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285299.

[42174] LOC285345 (Accession XP_211854.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285345 BINDING SITE1 and LOC285345 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285345, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285345

BINDING SITE1 and LOC285345 BINDING SITE2, designated SEQ ID:11821 and SEQ ID:13276 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42175] Another function of GAM2071 is therefore inhibition of LOC285345 (Accession XP_211854.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285345.

[42176] LOC285366 (Accession XP_209581.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285366 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285366, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285366 BINDING SITE, designated SEQ ID:4019, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42177] Another function of GAM2071 is therefore inhibition of LOC285366 (Accession XP_209581.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285366.

[42178] LOC285369 (Accession XP_211861.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC285369 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285369, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285369 BINDING SITE, designated SEQ ID:19816, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42179] Another function of GAM2071 is therefore inhibition of LOC285369 (Accession XP_211861.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285369.

[42180] LOC285370 (Accession XP_211869.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285370 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285370, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285370 BINDING SITE, designated SEQ ID:5624, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42181] Another function of GAM2071 is therefore inhibition of LOC285370 (Accession XP_211869.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285370.

[42182] LOC285389 (Accession XP_211873.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285389 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285389, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285389 BINDING SITE, designated SEQ ID:7025, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42183] Another function of GAM2071 is therefore inhibition of

LOC285389 (Accession XP_211873.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285389.

[42184] LOC285392 (Accession XP_211879.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285392 BINDING SITE1 and LOC285392 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285392, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285392 BINDING SITE1 and LOC285392 BINDING SITE2, designated SEQ ID:436 and SEQ ID:6034 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42185] Another function of GAM2071 is therefore inhibition of LOC285392 (Accession XP_211879.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285392.

[42186] LOC285398 (Accession XP_209593.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC285398 BINDING SITE1 and LOC285398 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285398, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285398 BINDING SITE1 and LOC285398 BINDING SITE2, designated SEQ ID:3701 and SEQ ID:4020 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42187] Another function of GAM2071 is therefore inhibition of LOC285398 (Accession XP_209593.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285398.

[42188] LOC285400 (Accession XP_209596.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285400 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285400 BINDING SITE, desig-

nated SEQ ID:3267, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42189] Another function of GAM2071 is therefore inhibition of LOC285400 (Accession XP_209596.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285400.

[42190] LOC285409 (Accession XP_209600.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285409 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285409, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285409 BINDING SITE, designated SEQ ID:1914, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42191] Another function of GAM2071 is therefore inhibition of LOC285409 (Accession XP_209600.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285409.

[42192] LOC285429 (Accession XP_209607.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC285429 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285429, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285429 BINDING SITE, designated SEQ ID:4870, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42193] Another function of GAM2071 is therefore inhibition of LOC285429 (Accession XP_209607.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285429.

[42194] LOC285488 (Accession XP_211914.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285488 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285488, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285488 BINDING SITE, designated SEQ ID:11093, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42195] Another function of GAM2071 is therefore inhibition of LOC285488 (Accession XP_211914.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285488.

[42196] LOC285491 (Accession XP_211917.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285491 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285491, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285491 BINDING SITE, designated SEQ ID:8951, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42197] Another function of GAM2071 is therefore inhibition of LOC285491 (Accession XP_211917.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285491.

[42198] LOC285509 (Accession XP_211923.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285509 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285509, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285509 BINDING SITE, designated SEQ ID:11997, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42199] Another function of GAM2071 is therefore inhibition of LOC285509 (Accession XP_211923.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285509.

[42200] LOC285540 (Accession XP_209654.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285540 BINDING SITE1 and LOC285540 BINDING SITE2 are target binding sites found in untranslated re-

gions of mRNA encoded by LOC285540, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285540 BINDING SITE1 and LOC285540 BINDING SITE2, designated SEQ ID:19426 and SEQ ID:5384 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42201] Another function of GAM2071 is therefore inhibition of LOC285540 (Accession XP_209654.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285540.

[42202] LOC285589 (Accession XP_209671.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285589 BINDING SITE1 and LOC285589 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285589, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285589 BINDING SITE1 and LOC285589 BINDING SITE2, designated SEQ ID:14069 and SEQ ID:3782 respectively, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42203] Another function of GAM2071 is therefore inhibition of LOC285589 (Accession XP_209671.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285589.

[42204] LOC285594 (Accession XP_211946.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC285594 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285594, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285594 BINDING SITE, designated SEQ ID:9271, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42205] Another function of GAM2071 is therefore inhibition of LOC285594 (Accession XP_211946.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285594.

[42206] LOC285608 (Accession XP_211952.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285608 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285608, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285608 BINDING SITE, designated SEQ ID:15956, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42207] Another function of GAM2071 is therefore inhibition of LOC285608 (Accession XP_211952.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285608.

[42208] LOC285638 (Accession XP_209693.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285638 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285638, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC285638 BINDING SITE, designated SEQ ID:13619, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42209] Another function of GAM2071 is therefore inhibition of LOC285638 (Accession XP_209693.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285638.

[42210] LOC285641 (Accession XP_209697.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285641 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285641, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285641 BINDING SITE, designated SEQ ID:3501, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42211] Another function of GAM2071 is therefore inhibition of LOC285641 (Accession XP_209697.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285641.

[42212] LOC285679 (Accession XP_209719.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC285679 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285679, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285679 BINDING SITE, designated SEQ ID:15031, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42213] Another function of GAM2071 is therefore inhibition of LOC285679 (Accession XP_209719.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285679.

[42214] LOC285683 (Accession XP_211980.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285683 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285683, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285683 BINDING SITE, designated SEQ ID:5151, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42215] Another function of GAM2071 is therefore inhibition of LOC285683 (Accession XP_211980.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285683.

[42216] LOC285687 (Accession XP_211985.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285687 BINDING SITE, designated SEQ ID:10580, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42217] Another function of GAM2071 is therefore inhibition of

LOC285687 (Accession XP_211985.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285687.

[42218] LOC285693 (Accession XP_211981.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285693 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285693, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285693 BINDING SITE, designated SEQ ID:7946, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42219] Another function of GAM2071 is therefore inhibition of LOC285693 (Accession XP_211981.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285693.

[42220] LOC285722 (Accession XP_211997.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285722 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC285722, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285722 BINDING SITE, designated SEQ ID:19494, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42221] Another function of GAM2071 is therefore inhibition of LOC285722 (Accession XP_211997.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285722.

[42222] LOC285744 (Accession XP_209743.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285744 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285744, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285744 BINDING SITE, designated SEQ ID:11603, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[42223] Another function of GAM2071 is therefore inhibition of LOC285744 (Accession XP_209743.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285744.

[42224] LOC285747 (Accession XP_209742.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285747 BINDING SITE1 and LOC285747 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285747, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285747 BINDING SITE1 and LOC285747 BINDING SITE2, designated SEQ ID:13800 and SEQ ID:9553 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42225] Another function of GAM2071 is therefore inhibition of LOC285747 (Accession XP_209742.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285747.

[42226] LOC285812 (Accession XP_212055.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285812 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285812 BINDING SITE, designated SEQ ID:13275, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42227] Another function of GAM2071 is therefore inhibition of LOC285812 (Accession XP_212055.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285812.

[42228] LOC285813 (Accession XP_212036.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285813 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC285813 BINDING SITE, designated SEQ ID:17617, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42229] Another function of GAM2071 is therefore inhibition of LOC285813 (Accession XP_212036.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285813.

[42230] LOC285821 (Accession XP_209789.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285821 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285821, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285821 BINDING SITE, designated SEQ ID:7849, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42231] Another function of GAM2071 is therefore inhibition of LOC285821 (Accession XP_209789.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285821.

[42232] LOC285822 (Accession XP_209777.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285822 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285822 BINDING SITE, designated SEQ ID:6011, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42233] Another function of GAM2071 is therefore inhibition of LOC285822 (Accession XP_209777.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285822.

[42234] LOC285830 (Accession XP_212043.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285830 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285830, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285830 BINDING SITE, designated SEQ ID:8939, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42235] Another function of GAM2071 is therefore inhibition of LOC285830 (Accession XP_212043.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285830.

[42236] LOC285840 (Accession XP_208353.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285840 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285840, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285840 BINDING SITE, designated SEQ ID:15519, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42237] Another function of GAM2071 is therefore inhibition of

LOC285840 (Accession XP_208353.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285840.

[42238] LOC285843 (Accession XP_212034.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285843 BINDING SITE1 and LOC285843 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285843, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285843 BINDING SITE1 and LOC285843 BINDING SITE2, designated SEQ ID:1414 and SEQ ID:11782 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42239] Another function of GAM2071 is therefore inhibition of LOC285843 (Accession XP_212034.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285843.

[42240] LOC285847 (Accession XP_212045.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC285847 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285847, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285847 BINDING SITE, designated SEQ ID:7212, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42241] Another function of GAM2071 is therefore inhibition of LOC285847 (Accession XP_212045.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285847.

[42242] LOC285872 (Accession XP_212061.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285872 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285872, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285872 BINDING SITE, designated SEQ ID:7986, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42243] Another function of GAM2071 is therefore inhibition of LOC285872 (Accession XP_212061.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285872.

[42244] LOC285896 (Accession XP_209806.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285896 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285896, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285896 BINDING SITE, designated SEQ ID:4795, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42245] Another function of GAM2071 is therefore inhibition of LOC285896 (Accession XP_209806.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285896.

[42246] LOC285922 (Accession XP_209822.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285922 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285922 BINDING SITE, designated SEQ ID:4795, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42247] Another function of GAM2071 is therefore inhibition of LOC285922 (Accession XP_209822.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285922.

[42248] LOC285923 (Accession XP_212104.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285923 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285923, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC285923 BINDING SITE, designated SEQ ID:16934, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42249] Another function of GAM2071 is therefore inhibition of LOC285923 (Accession XP_212104.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285923.

[42250] LOC285930 (Accession XP_209818.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285930 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285930, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285930 BINDING SITE, designated SEQ ID:3828, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42251] Another function of GAM2071 is therefore inhibition of LOC285930 (Accession XP_209818.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285930.

[42252] LOC285945 (Accession XP_212092.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285945 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285945, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285945 BINDING SITE, designated SEQ ID:12385, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42253] Another function of GAM2071 is therefore inhibition of LOC285945 (Accession XP_212092.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285945.

[42254] LOC285952 (Accession XP_209821.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285952 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285952, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285952 BINDING SITE, designated SEQ ID:2758, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42255] Another function of GAM2071 is therefore inhibition of LOC285952 (Accession XP_209821.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285952.

[42256] LOC285961 (Accession XP_209833.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285961 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285961, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285961 BINDING SITE, designated SEQ ID:11621, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42257] Another function of GAM2071 is therefore inhibition of

LOC285961 (Accession XP_209833.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285961.

[42258] LOC285972 (Accession XP_212105.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285972 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285972 BINDING SITE, designated SEQ ID:8156, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42259] Another function of GAM2071 is therefore inhibition of LOC285972 (Accession XP_212105.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285972.

[42260] LOC285979 (Accession XP_212117.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC285979 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC285979, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285979 BINDING SITE, designated SEQ ID:3889, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42261] Another function of GAM2071 is therefore inhibition of LOC285979 (Accession XP_212117.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285979.

[42262] LOC286029 (Accession XP_209866.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286029 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286029, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286029 BINDING SITE, designated SEQ ID:14224, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[42263] Another function of GAM2071 is therefore inhibition of LOC286029 (Accession XP_209866.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286029.

[42264] LOC286032 (Accession XP_209867.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC286032 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286032, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286032 BINDING SITE, designated SEQ ID:1208, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42265] Another function of GAM2071 is therefore inhibition of LOC286032 (Accession XP_209867.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286032.

[42266] LOC286052 (Accession XP_212152.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC286052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286052 BINDING SITE, designated SEQ ID:14748, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42267] Another function of GAM2071 is therefore inhibition of LOC286052 (Accession XP_212152.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286052.

[42268] LOC286077 (Accession XP_209892.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286077 BINDING SITE, desig-

nated SEQ ID:3388, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42269] Another function of GAM2071 is therefore inhibition of LOC286077 (Accession XP_209892.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286077.

[42270] LOC286078 (Accession XP_212163.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286078 BINDING SITE1 and LOC286078 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC286078, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286078 BINDING SITE1 and LOC286078 BINDING SITE2, designated SEQ ID:8139 and SEQ ID:12045 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42271] Another function of GAM2071 is therefore inhibition of LOC286078 (Accession XP_212163.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC286078.

[42272] LOC286103 (Accession NP_848630.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286103 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC286103, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286103 BINDING SITE, designated SEQ ID:15670, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42273] Another function of GAM2071 is therefore inhibition of LOC286103 (Accession NP_848630.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286103.

[42274] LOC286103 (Accession XP_209897.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286103 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC286103, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286103 BINDING SITE, designated SEQ ID:15670, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42275] Another function of GAM2071 is therefore inhibition of LOC286103 (Accession XP_209897.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286103.

[42276] LOC286121 (Accession XP_212184.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC286121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286121 BINDING SITE, designated SEQ ID:19438, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42277] Another function of GAM2071 is therefore inhibition of

LOC286121 (Accession XP_212184.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286121.

[42278] LOC286126 (Accession XP_212185.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286126 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286126, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286126 BINDING SITE, designated SEQ ID:8950, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42279] Another function of GAM2071 is therefore inhibition of LOC286126 (Accession XP_212185.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286126.

[42280] LOC286132 (Accession XP_212194.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286132 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC286132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286132 BINDING SITE, designated SEQ ID:2266, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42281] Another function of GAM2071 is therefore inhibition of LOC286132 (Accession XP_212194.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286132.

[42282] LOC286166 (Accession XP_209925.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286166 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286166 BINDING SITE, designated SEQ ID:1529, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[42283] Another function of GAM2071 is therefore inhibition of LOC286166 (Accession XP_209925.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286166.

[42284] LOC286186 (Accession XP_212219.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286186 BINDING SITE1 and LOC286186 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC286186, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286186 BINDING SITE1 and LOC286186 BINDING SITE2, designated SEQ ID:15317 and SEQ ID:13117 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42285] Another function of GAM2071 is therefore inhibition of LOC286186 (Accession XP_212219.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286186.

[42286] LOC286207 (Accession XP_209941.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286207 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286207, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286207 BINDING SITE, designated SEQ ID:16987, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42287] Another function of GAM2071 is therefore inhibition of LOC286207 (Accession XP_209941.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286207.

[42288] LOC286208 (Accession XP_212230.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286208 BINDING SITE1 and LOC286208 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC286208, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC286208 BINDING SITE1 and LOC286208 BINDING SITE2, designated SEQ ID:16222 and SEQ ID:14347 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42289] Another function of GAM2071 is therefore inhibition of LOC286208 (Accession XP_212230.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286208.

[42290] LOC286215 (Accession XP_212228.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286215 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286215, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286215 BINDING SITE, designated SEQ ID:14899, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42291] Another function of GAM2071 is therefore inhibition of LOC286215 (Accession XP_212228.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286215.

[42292] LOC286245 (Accession XP_212244.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286245 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286245, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286245 BINDING SITE, designated SEQ ID:4711, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42293] Another function of GAM2071 is therefore inhibition of LOC286245 (Accession XP_212244.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286245.

[42294] LOC286341 (Accession XP_212278.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286341 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC286341, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286341 BINDING SITE, designated SEQ ID:14403, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42295] Another function of GAM2071 is therefore inhibition of LOC286341 (Accession XP_212278.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286341.

[42296] LOC286356 (Accession XP_212290.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286356 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286356 BINDING SITE, designated SEQ ID:13800, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42297] Another function of GAM2071 is therefore inhibition of LOC286356 (Accession XP_212290.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286356.

[42298] LOC286357 (Accession XP_212285.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286357 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286357, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286357 BINDING SITE, designated SEQ ID:13894, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42299] Another function of GAM2071 is therefore inhibition of LOC286357 (Accession XP_212285.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286357.

[42300] LOC286441 (Accession XP_212319.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC286441 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286441, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286441 BINDING SITE, designated SEQ ID:643, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42301] Another function of GAM2071 is therefore inhibition of LOC286441 (Accession XP_212319.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286441.

[42302] LOC286553 (Accession XP_212340.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC286553 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286553, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286553 BINDING SITE, designated SEQ ID:17107, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42303] Another function of GAM2071 is therefore inhibition of LOC286553 (Accession XP_212340.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286553.

[42304] LOC338562 (Accession XP_294654.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC338562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338562 BINDING SITE, designated SEQ ID:17586, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42305] Another function of GAM2071 is therefore inhibition of LOC338562 (Accession XP_294654.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338562.

[42306] LOC338579 (Accession XP_290472.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC338579 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338579, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338579 BINDING SITE, designated SEQ ID:18756, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42307] Another function of GAM2071 is therefore inhibition of LOC338579 (Accession XP_290472.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338579.

[42308] LOC338709 (Accession XP_211595.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC338709 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338709, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC338709 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42309] Another function of GAM2071 is therefore inhibition of LOC338709 (Accession XP_211595.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338709.

[42310] LOC338739 (Accession XP_294690.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC338739 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338739, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338739 BINDING SITE, designated SEQ ID:11661, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42311] Another function of GAM2071 is therefore inhibition of LOC338739 (Accession XP_294690.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC338739.

[42312] LOC338773 (Accession XP_290570.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC338773 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338773, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338773 BINDING SITE, designated SEQ ID:17388, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42313] Another function of GAM2071 is therefore inhibition of LOC338773 (Accession XP_290570.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338773.

[42314] LOC338817 (Accession XP_290588.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC338817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338817, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338817 BINDING SITE, designated SEQ ID:11448, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42315] Another function of GAM2071 is therefore inhibition of LOC338817 (Accession XP_290588.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338817.

[42316] LOC338899 (Accession XP_294740.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC338899 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338899 BINDING SITE, designated SEQ ID:8888, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42317] Another function of GAM2071 is therefore inhibition of

LOC338899 (Accession XP_294740.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338899.

[42318] LOC338923 (Accession XP_294742.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC338923 BINDING SITE1 and LOC338923 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC338923, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338923 BINDING SITE1 and LOC338923 BINDING SITE2, designated SEQ ID:14847 and SEQ ID:3243 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42319] Another function of GAM2071 is therefore inhibition of LOC338923 (Accession XP_294742.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338923.

[42320] LOC339078 (Accession XP_290692.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC339078 BINDING SITE1 and LOC339078 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339078, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339078 BINDING SITE1 and LOC339078 BINDING SITE2, designated SEQ ID:7937 and SEQ ID:19426 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42321] Another function of GAM2071 is therefore inhibition of LOC339078 (Accession XP_290692.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339078.

[42322] LOC339146 (Accession XP_294825.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339146 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339146 BINDING SITE, desig-

nated SEQ ID:822, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42323] Another function of GAM2071 is therefore inhibition of LOC339146 (Accession XP_294825.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339146.

[42324] LOC339178 (Accession XP_290742.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339178 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339178, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339178 BINDING SITE, designated SEQ ID:16519, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42325] Another function of GAM2071 is therefore inhibition of LOC339178 (Accession XP_290742.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC339178.

[42326] LOC339201 (Accession XP_290756.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339201 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339201 BINDING SITE, designated SEQ ID:11830, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42327] Another function of GAM2071 is therefore inhibition of LOC339201 (Accession XP_290756.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339201.

[42328] LOC339298 (Accession XP_294903.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339298 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339298, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339298 BINDING SITE, designated SEQ ID:3121, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42329] Another function of GAM2071 is therefore inhibition of LOC339298 (Accession XP_294903.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339298.

[42330] LOC339318 (Accession XP_290835.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339318 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339318 BINDING SITE, designated SEQ ID:10660, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42331] Another function of GAM2071 is therefore inhibition of LOC339318 (Accession XP_290835.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339318.

[42332] LOC339325 (Accession XP_290830.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339325 BINDING SITE1 and LOC339325 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339325, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339325 BINDING SITE1 and LOC339325 BINDING SITE2, designated SEQ ID:13290 and SEQ ID:7946 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42333] Another function of GAM2071 is therefore inhibition of LOC339325 (Accession XP_290830.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339325.

[42334] LOC339417 (Accession XP_294944.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339417 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC339417, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339417 BINDING SITE, designated SEQ ID:4497, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42335] Another function of GAM2071 is therefore inhibition of LOC339417 (Accession XP_294944.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339417.

[42336] LOC339448 (Accession XP_290902.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339448 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339448, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339448 BINDING SITE, designated SEQ ID:19680, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[42337] Another function of GAM2071 is therefore inhibition of LOC339448 (Accession XP_290902.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339448.

[42338] LOC339458 (Accession XP_290911.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339458 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339458, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339458 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42339] Another function of GAM2071 is therefore inhibition of LOC339458 (Accession XP_290911.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339458.

[42340] LOC339459 (Accession XP_290907.2) is another

GAM2071 target gene, herein designated TARGET GENE. LOC339459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339459 BINDING SITE, designated SEQ ID:13345, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42341] Another function of GAM2071 is therefore inhibition of LOC339459 (Accession XP_290907.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339459.

[42342] LOC339492 (Accession XP_290919.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339492 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339492, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339492 BINDING SITE, desig-

nated SEQ ID:13601, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42343] Another function of GAM2071 is therefore inhibition of LOC339492 (Accession XP_290919.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339492.

[42344] LOC339568 (Accession XP_295008.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339568 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339568, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339568 BINDING SITE, designated SEQ ID:15942, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42345] Another function of GAM2071 is therefore inhibition of LOC339568 (Accession XP_295008.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC339568.

[42346] LOC339577 (Accession XP_295005.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339577 BINDING SITE1 and LOC339577 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339577, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339577 BINDING SITE1 and LOC339577 BINDING SITE2, designated SEQ ID:9239 and SEQ ID:18182 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42347] Another function of GAM2071 is therefore inhibition of LOC339577 (Accession XP_295005.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339577.

[42348] LOC339600 (Accession XP_295014.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339600 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339600, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339600 BINDING SITE, designated SEQ ID:15466, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42349] Another function of GAM2071 is therefore inhibition of LOC339600 (Accession XP_295014.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339600.

[42350] LOC339622 (Accession XP_295016.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339622 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339622, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339622 BINDING SITE, designated SEQ ID:15723, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42351] Another function of GAM2071 is therefore inhibition of

LOC339622 (Accession XP_295016.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339622.

[42352] LOC339663 (Accession XP_295028.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339663 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339663 BINDING SITE, designated SEQ ID:1438, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42353] Another function of GAM2071 is therefore inhibition of LOC339663 (Accession XP_295028.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339663.

[42354] LOC339685 (Accession XP_295032.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339685 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC339685, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339685 BINDING SITE, designated SEQ ID:7793, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42355] Another function of GAM2071 is therefore inhibition of LOC339685 (Accession XP_295032.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339685.

[42356] LOC339711 (Accession XP_295038.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339711 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339711, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339711 BINDING SITE, designated SEQ ID:3106, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[42357] Another function of GAM2071 is therefore inhibition of LOC339711 (Accession XP_295038.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339711.

[42358] LOC339720 (Accession XP_295041.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339720 BINDING SITE1 and LOC339720 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339720, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339720 BINDING SITE1 and LOC339720 BINDING SITE2, designated SEQ ID:7943 and SEQ ID:17652 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42359] Another function of GAM2071 is therefore inhibition of LOC339720 (Accession XP_295041.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339720.

[42360] LOC339803 (Accession XP_295072.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339803 BINDING SITE, designated SEQ ID:2943, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42361] Another function of GAM2071 is therefore inhibition of LOC339803 (Accession XP_295072.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339803.

[42362] LOC339809 (Accession XP_291020.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339809 BINDING SITE1 and LOC339809 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339809, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC339809 BINDING SITE1 and LOC339809 BINDING SITE2, designated SEQ ID:8744 and SEQ ID:9098 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42363] Another function of GAM2071 is therefore inhibition of LOC339809 (Accession XP_291020.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339809.

[42364] LOC339813 (Accession XP_295074.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339813 BINDING SITE1 and LOC339813 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339813, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339813 BINDING SITE1 and LOC339813 BINDING SITE2, designated SEQ ID:10731 and SEQ ID:13432 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42365] Another function of GAM2071 is therefore inhibition of

LOC339813 (Accession XP_295074.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339813.

[42366] LOC339833 (Accession XP_291031.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339833 BINDING SITE1 and LOC339833 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339833, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339833 BINDING SITE1 and LOC339833 BINDING SITE2, designated SEQ ID:8180 and SEQ ID:10061 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42367] Another function of GAM2071 is therefore inhibition of LOC339833 (Accession XP_291031.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339833.

[42368] LOC339834 (Accession XP_291033.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC339834 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC339834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339834 BINDING SITE, designated SEQ ID:2474, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42369] Another function of GAM2071 is therefore inhibition of LOC339834 (Accession XP_291033.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339834.

[42370] LOC339834 (Accession NP_835467.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339834 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC339834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339834 BINDING SITE, designated SEQ ID:2474, to the nucleotide

sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42371] Another function of GAM2071 is therefore inhibition of LOC339834 (Accession NP_835467.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339834.

[42372] LOC339872 (Accession XP_291050.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339872 BINDING SITE1 through LOC339872 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC339872, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339872 BINDING SITE1 through LOC339872 BINDING SITE3, designated SEQ ID:15990, SEQ ID:10908 and SEQ ID:6179 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42373] Another function of GAM2071 is therefore inhibition of LOC339872 (Accession XP_291050.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC339872.

[42374] LOC339894 (Accession XP_295095.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339894 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339894 BINDING SITE, designated SEQ ID:11426, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42375] Another function of GAM2071 is therefore inhibition of LOC339894 (Accession XP_295095.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339894.

[42376] LOC339907 (Accession XP_291065.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339907 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339907, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339907 BINDING SITE, designated SEQ ID:1531, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42377] Another function of GAM2071 is therefore inhibition of LOC339907 (Accession XP_291065.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339907.

[42378] LOC339909 (Accession XP_291069.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339909 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339909, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339909 BINDING SITE, designated SEQ ID:9102, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42379] Another function of GAM2071 is therefore inhibition of LOC339909 (Accession XP_291069.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339909.

[42380] LOC339970 (Accession XP_291095.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC339970 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339970, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339970 BINDING SITE, designated SEQ ID:8858, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42381] Another function of GAM2071 is therefore inhibition of LOC339970 (Accession XP_291095.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339970.

[42382] LOC340125 (Accession XP_291150.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC340125 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC340125, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340125 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42383] Another function of GAM2071 is therefore inhibition of LOC340125 (Accession XP_291150.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340125.

[42384] LOC340138 (Accession XP_291153.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC340138 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340138 BINDING SITE, designated SEQ ID:2442, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42385] Another function of GAM2071 is therefore inhibition of LOC340138 (Accession XP_291153.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340138.

[42386] LOC340156 (Accession XP_291158.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC340156 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340156, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340156 BINDING SITE, designated SEQ ID:8575, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42387] Another function of GAM2071 is therefore inhibition of LOC340156 (Accession XP_291158.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340156.

[42388] LOC340227 (Accession XP_291203.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC340227 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340227, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340227 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42389] Another function of GAM2071 is therefore inhibition of LOC340227 (Accession XP_291203.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340227.

[42390] LOC340249 (Accession XP_291211.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC340249 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340249, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340249 BINDING SITE, designated SEQ ID:8336, to the nucleotide sequence of

GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42391] Another function of GAM2071 is therefore inhibition of LOC340249 (Accession XP_291211.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340249.

[42392] LOC340290 (Accession XP_291214.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC340290 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340290, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340290 BINDING SITE, designated SEQ ID:15164, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42393] Another function of GAM2071 is therefore inhibition of LOC340290 (Accession XP_291214.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340290.

[42394] LOC340318 (Accession XP_290401.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC340318 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340318 BINDING SITE, designated SEQ ID:3251, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42395] Another function of GAM2071 is therefore inhibition of LOC340318 (Accession XP_290401.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340318.

[42396] LOC340414 (Accession XP_295240.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC340414 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340414, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC340414 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42397] Another function of GAM2071 is therefore inhibition of LOC340414 (Accession XP_295240.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340414.

[42398] LOC340450 (Accession XP_295252.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC340450 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340450, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340450 BINDING SITE, designated SEQ ID:4971, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42399] Another function of GAM2071 is therefore inhibition of LOC340450 (Accession XP_295252.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC340450.

[42400] LOC342926 (Accession XP_292790.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC342926 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC342926, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC342926 BINDING SITE, designated SEQ ID:1413, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42401] Another function of GAM2071 is therefore inhibition of LOC342926 (Accession XP_292790.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC342926.

[42402] LOC344805 (Accession XP_293599.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC344805 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC344805, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC344805 BINDING SITE, designated SEQ ID:11441, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42403] Another function of GAM2071 is therefore inhibition of LOC344805 (Accession XP_293599.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC344805.

[42404] LOC345275 (Accession NP_835236.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC345275 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC345275, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC345275 BINDING SITE, designated SEQ ID:14511, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42405] Another function of GAM2071 is therefore inhibition of

LOC345275 (Accession NP_835236.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC345275.

[42406] LOC347803 (Accession XP_302604.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC347803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC347803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347803 BINDING SITE, designated SEQ ID:12975, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42407] Another function of GAM2071 is therefore inhibition of LOC347803 (Accession XP_302604.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347803.

[42408] LOC347918 (Accession XP_300565.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC347918 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC347918, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347918 BINDING SITE, designated SEQ ID:983, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42409] Another function of GAM2071 is therefore inhibition of LOC347918 (Accession XP_300565.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347918.

[42410] LOC348024 (Accession XP_300592.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348024 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348024 BINDING SITE, designated SEQ ID:3526, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[42411] Another function of GAM2071 is therefore inhibition of LOC348024 (Accession XP_300592.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348024.

[42412] LOC348071 (Accession XP_300620.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348071 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348071, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348071 BINDING SITE, designated SEQ ID:16154, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42413] Another function of GAM2071 is therefore inhibition of LOC348071 (Accession XP_300620.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348071.

[42414] LOC348075 (Accession XP_302653.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC348075 BINDING SITE1 and LOC348075 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348075, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348075 BINDING SITE1 and LOC348075 BINDING SITE2, designated SEQ ID:7650 and SEQ ID:777 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42415] Another function of GAM2071 is therefore inhibition of LOC348075 (Accession XP_302653.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348075.

[42416] LOC348115 (Accession XP_300626.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348115 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348115, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC348115 BINDING SITE, designated SEQ ID:12601, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42417] Another function of GAM2071 is therefore inhibition of LOC348115 (Accession XP_300626.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348115.

[42418] LOC348261 (Accession XP_302704.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348261 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348261, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348261 BINDING SITE, designated SEQ ID:19539, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42419] Another function of GAM2071 is therefore inhibition of LOC348261 (Accession XP_302704.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348261.

[42420] LOC348262 (Accession XP_300683.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348262 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348262 BINDING SITE, designated SEQ ID:7914, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42421] Another function of GAM2071 is therefore inhibition of LOC348262 (Accession XP_300683.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348262.

[42422] LOC348314 (Accession XP_302716.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348314 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348314, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348314 BINDING SITE, designated SEQ ID:9161, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42423] Another function of GAM2071 is therefore inhibition of LOC348314 (Accession XP_302716.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348314.

[42424] LOC348326 (Accession XP_300696.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348326 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348326, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348326 BINDING SITE, designated SEQ ID:1995, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42425] Another function of GAM2071 is therefore inhibition of

LOC348326 (Accession XP_300696.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348326.

[42426] LOC348327 (Accession XP_030209.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC348327 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348327, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348327 BINDING SITE, designated SEQ ID:16911, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42427] Another function of GAM2071 is therefore inhibition of LOC348327 (Accession XP_030209.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348327.

[42428] LOC348393 (Accession XP_302741.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348393 BINDING SITE1 and LOC348393 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348393, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348393 BINDING SITE1 and LOC348393 BINDING SITE2, designated SEQ ID:16960 and SEQ ID:20185 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42429] Another function of GAM2071 is therefore inhibition of LOC348393 (Accession XP_302741.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348393.

[42430] LOC348396 (Accession XP_300729.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348396 BINDING SITE1 through LOC348396 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC348396, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348396 BINDING SITE1 through LOC348396 BINDING SITE3, des-

ignated SEQ ID:5596, SEQ ID:1615 and SEQ ID:10631 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42431] Another function of GAM2071 is therefore inhibition of LOC348396 (Accession XP_300729.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348396.

[42432] LOC348402 (Accession XP_300730.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348402 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348402, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348402 BINDING SITE, designated SEQ ID:13601, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42433] Another function of GAM2071 is therefore inhibition of LOC348402 (Accession XP_300730.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC348402.

[42434] LOC348445 (Accession XP_300738.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348445 BINDING SITE, designated SEQ ID:1995, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42435] Another function of GAM2071 is therefore inhibition of LOC348445 (Accession XP_300738.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348445.

[42436] LOC348455 (Accession XP_302760.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348455 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348455, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348455 BINDING SITE, designated SEQ ID:9100, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42437] Another function of GAM2071 is therefore inhibition of LOC348455 (Accession XP_302760.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348455.

[42438] LOC348460 (Accession XP_300743.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348460 BINDING SITE1 and LOC348460 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348460, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348460 BINDING SITE1 and LOC348460 BINDING SITE2, designated SEQ ID:442 and SEQ ID:8756 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42439] Another function of GAM2071 is therefore inhibition of

LOC348460 (Accession XP_300743.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348460.

[42440] LOC348474 (Accession XP_209299.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC348474 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348474, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348474 BINDING SITE, designated SEQ ID:6597, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42441] Another function of GAM2071 is therefore inhibition of LOC348474 (Accession XP_209299.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348474.

[42442] LOC348494 (Accession XP_302789.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348494 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC348494, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348494 BINDING SITE, designated SEQ ID:6743, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42443] Another function of GAM2071 is therefore inhibition of LOC348494 (Accession XP_302789.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348494.

[42444] LOC348503 (Accession XP_300762.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348503 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348503, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348503 BINDING SITE, designated SEQ ID:12080, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:371.

[42445] Another function of GAM2071 is therefore inhibition of LOC348503 (Accession XP_300762.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348503.

[42446] LOC348508 (Accession XP_302806.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348508 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348508, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348508 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42447] Another function of GAM2071 is therefore inhibition of LOC348508 (Accession XP_302806.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348508.

[42448] LOC348525 (Accession XP_300778.1) is another

GAM2071 target gene, herein designated TARGET GENE. LOC348525 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348525, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348525 BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42449] Another function of GAM2071 is therefore inhibition of LOC348525 (Accession XP_300778.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348525.

[42450] LOC348532 (Accession XP_302818.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348532 BINDING SITE1 and LOC348532 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348532, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348532

BINDING SITE1 and LOC348532 BINDING SITE2, designated SEQ ID:16960 and SEQ ID:20185 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42451] Another function of GAM2071 is therefore inhibition of LOC348532 (Accession XP_302818.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348532.

[42452] LOC348702 (Accession XP_300808.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348702 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348702, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348702 BINDING SITE, designated SEQ ID:3103, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42453] Another function of GAM2071 is therefore inhibition of LOC348702 (Accession XP_300808.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348702.

[42454] LOC348790 (Accession XP_300843.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348790 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348790, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348790 BINDING SITE, designated SEQ ID:11124, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42455] Another function of GAM2071 is therefore inhibition of LOC348790 (Accession XP_300843.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348790.

[42456] LOC348797 (Accession XP_302888.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348797 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348797, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348797 BINDING SITE, designated SEQ ID:4796, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42457] Another function of GAM2071 is therefore inhibition of LOC348797 (Accession XP_302888.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348797.

[42458] LOC348798 (Accession XP_300845.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348798 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348798, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348798 BINDING SITE, designated SEQ ID:8736, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42459] Another function of GAM2071 is therefore inhibition of

LOC348798 (Accession XP_300845.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348798.

[42460] LOC348825 (Accession XP_300853.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348825 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348825, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348825 BINDING SITE, designated SEQ ID:2639, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42461] Another function of GAM2071 is therefore inhibition of LOC348825 (Accession XP_300853.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348825.

[42462] LOC348842 (Accession XP_300861.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC348842 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC348842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348842 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42463] Another function of GAM2071 is therefore inhibition of LOC348842 (Accession XP_300861.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348842.

[42464] LOC349024 (Accession XP_300250.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC349024 BINDING SITE1 and LOC349024 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC349024, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349024 BINDING SITE1 and LOC349024 BINDING SITE2, designated SEQ ID:4753 and SEQ ID:11653 respectively, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42465] Another function of GAM2071 is therefore inhibition of LOC349024 (Accession XP_300250.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349024.

[42466] LOC349075 (Accession XP_300932.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC349075 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349075, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349075 BINDING SITE, designated SEQ ID:9465, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42467] Another function of GAM2071 is therefore inhibition of LOC349075 (Accession XP_300932.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349075.

[42468] LOC349114 (Accession XP_302960.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC349114 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349114 BINDING SITE, designated SEQ ID:902, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42469] Another function of GAM2071 is therefore inhibition of LOC349114 (Accession XP_302960.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349114.

[42470] LOC349170 (Accession XP_300969.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC349170 BINDING SITE1 and LOC349170 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC349170, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC349170 BINDING SITE1 and LOC349170 BINDING SITE2, designated SEQ ID:13839 and SEQ ID:19429 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42471] Another function of GAM2071 is therefore inhibition of LOC349170 (Accession XP_300969.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349170.

[42472] LOC349251 (Accession XP_300251.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC349251 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349251, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349251 BINDING SITE, designated SEQ ID:17649, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42473] Another function of GAM2071 is therefore inhibition of LOC349251 (Accession XP_300251.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349251.

[42474] LOC349282 (Accession XP_301008.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC349282 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349282 BINDING SITE, designated SEQ ID:15530, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42475] Another function of GAM2071 is therefore inhibition of LOC349282 (Accession XP_301008.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349282.

[42476] LOC349313 (Accession XP_301024.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC349313 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC349313, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349313 BINDING SITE, designated SEQ ID:15530, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42477] Another function of GAM2071 is therefore inhibition of LOC349313 (Accession XP_301024.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349313.

[42478] LOC349324 (Accession XP_303030.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC349324 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349324, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349324 BINDING SITE, designated SEQ ID:988, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42479] Another function of GAM2071 is therefore inhibition of LOC349324 (Accession XP_303030.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349324.

[42480] LOC349440 (Accession XP_300513.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC349440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349440 BINDING SITE, designated SEQ ID:19505, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42481] Another function of GAM2071 is therefore inhibition of LOC349440 (Accession XP_300513.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349440.

[42482] LOC351597 (Accession XP_302099.1) is another GAM2071 target gene, herein designated TARGET GENE.

LOC351597 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC351597, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC351597 BINDING SITE, designated SEQ ID:14926, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42483] Another function of GAM2071 is therefore inhibition of LOC351597 (Accession XP_302099.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC351597.

[42484] LOC51193 (Accession NP_057415.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC51193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51193, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51193 BINDING SITE, designated SEQ ID:6858, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[42485] Another function of GAM2071 is therefore inhibition of LOC51193 (Accession NP_057415.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51193.

[42486] LOC51248 (Accession NP_057568.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC51248 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC51248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51248 BINDING SITE, designated SEQ ID:10914, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42487] Another function of GAM2071 is therefore inhibition of LOC51248 (Accession NP_057568.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51248.

[42488] LOC51257 (Accession NP_057580.2) is another GAM2071 target gene, herein designated TARGET GENE. LOC51257

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC51257, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51257 BINDING SITE, designated SEQ ID:18183, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42489] Another function of GAM2071 is therefore inhibition of LOC51257 (Accession NP_057580.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51257.

[42490] LOC51336 (Accession NP_057730.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC51336 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51336 BINDING SITE, designated SEQ ID:18609, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42491] Another function of GAM2071 is therefore inhibition of LOC51336 (Accession NP_057730.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51336.

[42492] LOC55954 (Accession NP_061976.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC55954 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC55954, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC55954 BINDING SITE, designated SEQ ID:17853, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42493] Another function of GAM2071 is therefore inhibition of LOC55954 (Accession NP_061976.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC55954.

[42494] LOC56902 (Accession NP_064528.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC56902 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LOC56902, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC56902 BINDING SITE, designated SEQ ID:8077, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42495] Another function of GAM2071 is therefore inhibition of LOC56902 (Accession NP_064528.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56902.

[42496] LOC90408 (Accession XP_031517.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC90408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC90408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90408 BINDING SITE, designated SEQ ID:2729, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42497] Another function of GAM2071 is therefore inhibition of

LOC90408 (Accession XP_031517.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90408.

[42498] LOC90485 (Accession XP_032059.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC90485 BINDING SITE1 and LOC90485 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC90485, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90485 BINDING SITE1 and LOC90485 BINDING SITE2, designated SEQ ID:15525 and SEQ ID:10103 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42499] Another function of GAM2071 is therefore inhibition of LOC90485 (Accession XP_032059.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90485.

[42500] LOC91056 (Accession NP_612377.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC91056

BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC91056, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91056 BINDING SITE, designated SEQ ID:6693, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42501] Another function of GAM2071 is therefore inhibition of LOC91056 (Accession NP_612377.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91056.

[42502] LOC91115 (Accession XP_036218.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC91115 BINDING SITE1 and LOC91115 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC91115, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91115 BINDING SITE1 and LOC91115 BINDING SITE2, designated SEQ ID:18042

and SEQ ID:6053 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42503] Another function of GAM2071 is therefore inhibition of LOC91115 (Accession XP_036218.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91115.

[42504] LOC91170 (Accession XP_036612.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC91170 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91170 BINDING SITE, designated SEQ ID:3969, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42505] Another function of GAM2071 is therefore inhibition of LOC91170 (Accession XP_036612.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91170.

[42506] LOC91250 (Accession XP_037135.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC91250 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91250, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91250 BINDING SITE, designated SEQ ID:16739, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42507] Another function of GAM2071 is therefore inhibition of LOC91250 (Accession XP_037135.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91250.

[42508] LOC91373 (Accession XP_038063.5) is another GAM2071 target gene, herein designated TARGET GENE. LOC91373 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91373, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91373 BINDING SITE, designated SEQ ID:5516, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42509] Another function of GAM2071 is therefore inhibition of LOC91373 (Accession XP_038063.5) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91373.

[42510] LOC91663 (Accession NP_612382.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC91663 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91663 BINDING SITE, designated SEQ ID:13779, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42511] Another function of GAM2071 is therefore inhibition of LOC91663 (Accession NP_612382.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91663.

[42512] LOC91801 (Accession NP_620130.1) is another GAM2071

target gene, herein designated TARGET GENE. LOC91801 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91801, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91801 BINDING SITE, designated SEQ ID:3586, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42513] Another function of GAM2071 is therefore inhibition of LOC91801 (Accession NP_620130.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91801.

[42514] LOC91893 (Accession XP_041340.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC91893 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91893, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91893 BINDING SITE, designated SEQ ID:9129, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[42515] Another function of GAM2071 is therefore inhibition of LOC91893 (Accession XP_041340.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91893.

[42516] LOC92148 (Accession XP_043160.1) is another GAM2071 target gene, herein designated TARGET GENE. LOC92148 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC92148, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92148 BINDING SITE, designated SEQ ID:16536, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42517] Another function of GAM2071 is therefore inhibition of LOC92148 (Accession XP_043160.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92148.

[42518] LOC92659 (Accession XP_046434.3) is another GAM2071 target gene, herein designated TARGET GENE. LOC92659

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92659, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92659 BINDING SITE, designated SEQ ID:19539, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42519] Another function of GAM2071 is therefore inhibition of LOC92659 (Accession XP_046434.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92659.

[42520] LPHN1 (Accession NP_055736.1) is another GAM2071 target gene, herein designated TARGET GENE. LPHN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LPHN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LPHN1 BINDING SITE, designated SEQ ID:12633, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42521] Another function of GAM2071 is therefore inhibition of LPHN1 (Accession NP_055736.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPHN1.

[42522] Leukotriene b4 receptor (LTB4R, Accession NP_000743.1) is another GAM2071 target gene, herein designated TARGET GENE. LTB4R BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LTB4R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LTB4R BINDING SITE, designated SEQ ID:19595, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42523] Another function of GAM2071 is therefore inhibition of Leukotriene b4 receptor (LTB4R, Accession NP_000743.1), a gene which may be the cardiac p2y receptor involved in the regulation of cardiac muscle contraction through modulation of l- type calcium currents. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LTB4R.

[42524] The function of LTB4R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Lysophospholipase ii (LYPLA2, Accession NP_009191.1) is another GAM2071 target gene, herein designated TARGET GENE. LYPLA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LYPLA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LYPLA2 BINDING SITE, designated SEQ ID:15519, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42525] Another function of GAM2071 is therefore inhibition of Lysophospholipase ii (LYPLA2, Accession NP_009191.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LYPLA2.

[42526] Lysozyme (renal amyloidosis) (LYZ, Accession NP_000230.1) is another GAM2071 target gene, herein designated TARGET GENE. LYZ BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by LYZ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LYZ BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42527] Another function of GAM2071 is therefore inhibition of Lysozyme (renal amyloidosis) (LYZ, Accession NP_000230.1), a gene which a bacteriolytic enzyme. and therefore may be associated with Renal amyloidosis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Renal amyloidosis, and of other diseases and clinical conditions associated with LYZ.

[42528] The function of LYZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Leucine zipper, putative tumor suppressor 1 (LZTS1, Accession NP_066300.1) is another GAM2071 target gene, herein designated TARGET GENE. LZTS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LZTS1, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LZTS1 BINDING SITE, designated SEQ ID:13405, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42529] Another function of GAM2071 is therefore inhibition of Leucine zipper, putative tumor suppressor 1 (LZTS1, Accession NP_066300.1), a gene which is an essential component of the nucleoskeleton. potential role in crosslinking filaments or anchoring other molecules. it is essential for growth. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTS1.

[42530] The function of LZTS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Male germ cell-associated kinase (MAK, Accession NP_005897.1) is another GAM2071 target gene, herein designated TARGET GENE. MAK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of MAK BINDING SITE, designated SEQ ID:11208, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42531] Another function of GAM2071 is therefore inhibition of Male germ cell-associated kinase (MAK, Accession NP_005897.1), a gene which plays an important role in spermatogenesis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAK.

[42532] The function of MAK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.MAPA (Accession NP_660299.1) is another GAM2071 target gene, herein designated TARGET GENE. MAPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPA BINDING SITE, designated SEQ ID:12475, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42533] Another function of GAM2071 is therefore inhibition of MAPA (Accession NP_660299.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPA.

[42534] MCLC (Accession NP_055942.1) is another GAM2071 target gene, herein designated TARGET GENE. MCLC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MCLC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCLC BINDING SITE, designated SEQ ID:4526, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42535] Another function of GAM2071 is therefore inhibition of MCLC (Accession NP_055942.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCLC.

[42536] Mcm10 minichromosome maintenance deficient 10 (s. cerevisiae) (MCM10, Accession NP_060988.2) is another GAM2071 target gene, herein designated TARGET GENE. MCM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MCM10, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCM10 BINDING SITE, designated SEQ ID:4821, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42537] Another function of GAM2071 is therefore inhibition of Mcm10 minichromosome maintenance deficient 10 (s. cerevisiae) (MCM10, Accession NP_060988.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCM10.

[42538] MDC1 (Accession NP_055456.1) is another GAM2071 target gene, herein designated TARGET GENE. MDC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MDC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDC1 BINDING SITE, designated SEQ ID:3945, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42539] Another function of GAM2071 is therefore inhibition of

MDC1 (Accession NP_055456.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDC1.

[42540] Mam domain containing glycosylphosphatidylinositol anchor 1 (MDGA1, Accession NP_705691.1) is another GAM2071 target gene, herein designated TARGET GENE. MDGA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MDGA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDGA1 BINDING SITE, designated SEQ ID:1000, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42541] Another function of GAM2071 is therefore inhibition of Mam domain containing glycosylphosphatidylinositol anchor 1 (MDGA1, Accession NP_705691.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDGA1.

[42542] Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006872.1) is another GAM2071 target gene, herein designated TARGET

GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42543] Another function of GAM2071 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006872.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[42544] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006870.1) is another GAM2071 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42545] Another function of GAM2071 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006870.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[42546] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006871.1) is another GAM2071 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42547] Another function of GAM2071 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006871.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of

Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[42548] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006869.1) is another GAM2071 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42549] Another function of GAM2071 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006869.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may

be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[42550] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_002383.1) is another GAM2071 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42551] Another function of GAM2071 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding

protein (mouse) (MDM2, Accession NP_002383.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[42552] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006873.1) is another GAM2071 target gene, herein designated TARGET GENE. MDM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MDM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDM2 BINDING SITE, designated SEQ ID:6085, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[42553] Another function of GAM2071 is therefore inhibition of Mdm2, transformed 3t3 cell double minute 2, p53 binding protein (mouse) (MDM2, Accession NP_006873.1), a gene which binds to and downmodulates p53 (TP53) and retinoblastoma protein (RB1) function. and therefore may be associated with Tumors (including soft tissue sarcomas, osteosarcomas and gliomas). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Tumors (including soft tissue sarcomas, osteosarcomas and gliomas)., and of other diseases and clinical conditions associated with MDM2.

[42554] The function of MDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mdm4, transformed 3t3 cell double minute 4, p53 binding protein (mouse) (MDM4, Accession NP_002384.1) is another GAM2071 target gene, herein designated TARGET GENE. MDM4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MDM4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of MDM4 BINDING SITE, designated SEQ ID:19527, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42555] Another function of GAM2071 is therefore inhibition of Mdm4, transformed 3t3 cell double minute 4, p53 binding protein (mouse) (MDM4, Accession NP_002384.1), a gene which Strongly similar to murine Mdm4; may interact with p53. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDM4.

[42556] The function of MDM4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Mediterranean fever (MEFV, Accession NP_000234.1) is another GAM2071 target gene, herein designated TARGET GENE. MEFV BINDING SITE1 and MEFV BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MEFV, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MEFV BINDING SITE1 and MEFV BINDING SITE2, designated SEQ

ID:12284 and SEQ ID:17376 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42557] Another function of GAM2071 is therefore inhibition of Mediterranean fever (MEFV, Accession NP_000234.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEFV.

[42558] MFTC (Accession NP_110407.2) is another GAM2071 target gene, herein designated TARGET GENE. MFTC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MFTC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MFTC BINDING SITE, designated SEQ ID:10459, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42559] Another function of GAM2071 is therefore inhibition of MFTC (Accession NP_110407.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MFTC.

[42560] Mannosyl (alpha-1,6-)-glycoprotein beta-

1,2-n-acetylglucosaminyltransferase (MGAT2, Accession NP_079374.1) is another GAM2071 target gene, herein designated TARGET GENE. MGAT2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MGAT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGAT2 BINDING SITE, designated SEQ ID:18270, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42561] Another function of GAM2071 is therefore inhibition of Mannosyl (alpha-1,6-)-glycoprotein beta-1,2-n-acetylglucosaminyltransferase (MGAT2, Accession NP_079374.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAT2.

[42562] MGC10200 (Accession NP_659497.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC10200 BINDING SITE1 and MGC10200 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC10200, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10200 BINDING SITE1 and MGC10200 BINDING SITE2, designated SEQ ID:1700 and SEQ ID:13048 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42563] Another function of GAM2071 is therefore inhibition of MGC10200 (Accession NP_659497.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10200.

[42564] MGC11102 (Accession NP_115701.2) is another GAM2071 target gene, herein designated TARGET GENE. MGC11102 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC11102, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC11102 BINDING SITE, designated SEQ ID:14977, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42565] Another function of GAM2071 is therefore inhibition of MGC11102 (Accession NP_115701.2) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11102.

[42566] MGC12262 (Accession NP_116085.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC12262 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC12262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC12262 BINDING SITE, designated SEQ ID:6361, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42567] Another function of GAM2071 is therefore inhibition of MGC12262 (Accession NP_116085.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12262.

[42568] MGC12518 (Accession NP_291026.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC12518 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC12518, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC12518 BINDING SITE, designated SEQ ID:18251, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42569] Another function of GAM2071 is therefore inhibition of MGC12518 (Accession NP_291026.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12518.

[42570] MGC13010 (Accession NP_116076.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC13010 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13010, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13010 BINDING SITE, designated SEQ ID:16983, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42571] Another function of GAM2071 is therefore inhibition of MGC13010 (Accession NP_116076.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC13010.

[42572] MGC13017 (Accession NP_542387.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC13017 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13017, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13017 BINDING SITE, designated SEQ ID:18970, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42573] Another function of GAM2071 is therefore inhibition of MGC13017 (Accession NP_542387.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13017.

[42574] MGC13024 (Accession NP_689501.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC13024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC13024 BINDING SITE, designated SEQ ID:15630, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42575] Another function of GAM2071 is therefore inhibition of MGC13024 (Accession NP_689501.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13024.

[42576] MGC13138 (Accession NP_219363.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC13138 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13138 BINDING SITE, designated SEQ ID:19426, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42577] Another function of GAM2071 is therefore inhibition of MGC13138 (Accession NP_219363.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC13138.

[42578] MGC13204 (Accession NP_113653.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC13204 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13204, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13204 BINDING SITE, designated SEQ ID:17963, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42579] Another function of GAM2071 is therefore inhibition of MGC13204 (Accession NP_113653.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13204.

[42580] MGC14289 (Accession NP_542391.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC14289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC14289 BINDING SITE, designated SEQ ID:1959, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42581] Another function of GAM2071 is therefore inhibition of MGC14289 (Accession NP_542391.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14289.

[42582] MGC14436 (Accession NP_116286.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC14436 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC14436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14436 BINDING SITE, designated SEQ ID:5075, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42583] Another function of GAM2071 is therefore inhibition of MGC14436 (Accession NP_116286.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14436.

[42584] MGC14836 (Accession NP_219480.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC14836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14836 BINDING SITE, designated SEQ ID:9102, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42585] Another function of GAM2071 is therefore inhibition of MGC14836 (Accession NP_219480.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14836.

[42586] MGC15705 (Accession NP_116146.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC15705 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC15705, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15705 BINDING SITE, designated SEQ ID:6734, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42587] Another function of GAM2071 is therefore inhibition of MGC15705 (Accession NP_116146.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15705.

[42588] MGC17839 (Accession NP_777586.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC17839 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC17839, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC17839 BINDING SITE, designated SEQ ID:18441, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42589] Another function of GAM2071 is therefore inhibition of MGC17839 (Accession NP_777586.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC17839.

[42590] MGC1842 (Accession XP_037797.2) is another GAM2071

target gene, herein designated TARGET GENE. MGC1842 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC1842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC1842 BINDING SITE, designated SEQ ID:11658, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42591] Another function of GAM2071 is therefore inhibition of MGC1842 (Accession XP_037797.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC1842.

[42592] MGC2474 (Accession NP_076420.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC2474 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2474, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2474 BINDING SITE, designated SEQ ID:18119, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[42593] Another function of GAM2071 is therefore inhibition of MGC2474 (Accession NP_076420.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2474.

[42594] MGC2477 (Accession NP_077004.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC2477 BINDING SITE1 and MGC2477 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC2477, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2477 BINDING SITE1 and MGC2477 BINDING SITE2, designated SEQ ID:12048 and SEQ ID:3973 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42595] Another function of GAM2071 is therefore inhibition of MGC2477 (Accession NP_077004.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2477.

[42596] MGC2603 (Accession NP_076942.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC2603 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2603, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2603 BINDING SITE, designated SEQ ID:17763, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42597] Another function of GAM2071 is therefore inhibition of MGC2603 (Accession NP_076942.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2603.

[42598] MGC26989 (Accession NP_689976.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC26989 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC26989, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC26989 BINDING SITE, designated SEQ ID:14418, to

the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42599] Another function of GAM2071 is therefore inhibition of MGC26989 (Accession NP_689976.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC26989.

[42600] MGC27345 (Accession XP_300964.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC27345 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MGC27345, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC27345 BINDING SITE, designated SEQ ID:18352, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42601] Another function of GAM2071 is therefore inhibition of MGC27345 (Accession XP_300964.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC27345.

[42602] MGC29891 (Accession NP_653219.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC29891 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC29891, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC29891 BINDING SITE, designated SEQ ID:18179, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42603] Another function of GAM2071 is therefore inhibition of MGC29891 (Accession NP_653219.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29891.

[42604] MGC29898 (Accession NP_659485.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC29898 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC29898, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC29898 BINDING SITE, designated SEQ ID:9164, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42605] Another function of GAM2071 is therefore inhibition of MGC29898 (Accession NP_659485.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29898.

[42606] MGC3113 (Accession NP_076940.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC3113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3113 BINDING SITE, designated SEQ ID:15946, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42607] Another function of GAM2071 is therefore inhibition of MGC3113 (Accession NP_076940.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3113.

[42608] MGC3195 (Accession NP_114111.2) is another GAM2071

target gene, herein designated TARGET GENE. MGC3195 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC3195, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3195 BINDING SITE, designated SEQ ID:15735, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42609] Another function of GAM2071 is therefore inhibition of MGC3195 (Accession NP_114111.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3195.

[42610] MGC3207 (Accession NP_115661.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC3207 BINDING SITE1 and MGC3207 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC3207, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3207 BINDING SITE1 and MGC3207 BINDING SITE2, designated SEQ ID:14723 and

SEQ ID:12382 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42611] Another function of GAM2071 is therefore inhibition of MGC3207 (Accession NP_115661.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3207.

[42612] MGC3248 (Accession NP_115875.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC3248 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3248 BINDING SITE, designated SEQ ID:11953, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42613] Another function of GAM2071 is therefore inhibition of MGC3248 (Accession NP_115875.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3248.

[42614] MGC3329 (Accession NP_076991.2) is another GAM2071 target gene, herein designated TARGET GENE. MGC3329 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3329, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3329 BINDING SITE, designated SEQ ID:4873, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42615] Another function of GAM2071 is therefore inhibition of MGC3329 (Accession NP_076991.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3329.

[42616] MGC33637 (Accession NP_689809.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC33637 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC33637, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC33637 BINDING SITE, designated SEQ ID:12383, to

the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42617] Another function of GAM2071 is therefore inhibition of MGC33637 (Accession NP_689809.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33637.

[42618] MGC34079 (Accession NP_689688.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC34079 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC34079, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34079 BINDING SITE, designated SEQ ID:19879, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42619] Another function of GAM2071 is therefore inhibition of MGC34079 (Accession NP_689688.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34079.

[42620] MGC34132 (Accession XP_291029.1) is another GAM2071

target gene, herein designated TARGET GENE. MGC34132 BINDING SITE1 and MGC34132 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC34132, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34132 BINDING SITE1 and MGC34132 BINDING SITE2, designated SEQ ID:8862 and SEQ ID:9188 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42621] Another function of GAM2071 is therefore inhibition of MGC34132 (Accession XP_291029.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34132.

[42622] MGC35136 (Accession NP_689640.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC35136 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC35136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC35136 BINDING SITE, designated SEQ ID:8783, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42623] Another function of GAM2071 is therefore inhibition of MGC35136 (Accession NP_689640.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35136.

[42624] MGC35440 (Accession NP_694952.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC35440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35440 BINDING SITE, designated SEQ ID:13796, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42625] Another function of GAM2071 is therefore inhibition of MGC35440 (Accession NP_694952.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35440.

[42626] MGC35468 (Accession NP_694976.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC35468 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35468, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35468 BINDING SITE, designated SEQ ID:19258, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42627] Another function of GAM2071 is therefore inhibition of MGC35468 (Accession NP_694976.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35468.

[42628] MGC39320 (Accession NP_689642.2) is another GAM2071 target gene, herein designated TARGET GENE. MGC39320 BINDING SITE1 and MGC39320 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC39320, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC39320 BINDING SITE1

and MGC39320 BINDING SITE2, designated SEQ ID:2691 and SEQ ID:1498 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42629] Another function of GAM2071 is therefore inhibition of MGC39320 (Accession NP_689642.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC39320.

[42630] MGC39558 (Accession NP_689703.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC39558 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC39558, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC39558 BINDING SITE, designated SEQ ID:1145, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42631] Another function of GAM2071 is therefore inhibition of MGC39558 (Accession NP_689703.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC39558.

[42632] MGC40157 (Accession NP_689563.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC40157 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC40157, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC40157 BINDING SITE, designated SEQ ID:13547, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42633] Another function of GAM2071 is therefore inhibition of MGC40157 (Accession NP_689563.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40157.

[42634] MGC40579 (Accession NP_689989.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC40579 BINDING SITE1 and MGC40579 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC40579, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of

the nucleotide sequences of MGC40579 BINDING SITE1 and MGC40579 BINDING SITE2, designated SEQ ID:3759 and SEQ ID:516 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42635] Another function of GAM2071 is therefore inhibition of MGC40579 (Accession NP_689989.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC40579.

[42636] MGC43122 (Accession NP_775784.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC43122 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC43122, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC43122 BINDING SITE, designated SEQ ID:16117, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42637] Another function of GAM2071 is therefore inhibition of MGC43122 (Accession NP_775784.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC43122.

[42638] MGC4415 (Accession NP_113672.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC4415 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC4415, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4415 BINDING SITE, designated SEQ ID:8576, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42639] Another function of GAM2071 is therefore inhibition of MGC4415 (Accession NP_113672.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4415.

[42640] MGC46732 (Accession NP_714925.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC46732 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC46732, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC46732 BINDING SITE, designated SEQ ID:3645, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42641] Another function of GAM2071 is therefore inhibition of MGC46732 (Accession NP_714925.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC46732.

[42642] MGC50337 (Accession NP_848604.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC50337 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC50337, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC50337 BINDING SITE, designated SEQ ID:8882, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42643] Another function of GAM2071 is therefore inhibition of MGC50337 (Accession NP_848604.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC50337.

[42644] MGC50559 (Accession NP_776163.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC50559 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC50559, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC50559 BINDING SITE, designated SEQ ID:7831, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42645] Another function of GAM2071 is therefore inhibition of MGC50559 (Accession NP_776163.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC50559.

[42646] MGC5149 (Accession XP_051200.2) is another GAM2071 target gene, herein designated TARGET GENE. MGC5149 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC5149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC5149 BINDING SITE, designated SEQ ID:17590, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42647] Another function of GAM2071 is therefore inhibition of MGC5149 (Accession XP_051200.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5149.

[42648] MGC9912 (Accession NP_542395.1) is another GAM2071 target gene, herein designated TARGET GENE. MGC9912 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC9912, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC9912 BINDING SITE, designated SEQ ID:11391, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42649] Another function of GAM2071 is therefore inhibition of MGC9912 (Accession NP_542395.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC9912.

[42650] MGRN1 (Accession XP_048119.4) is another GAM2071 target gene, herein designated TARGET GENE. MGRN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGRN1 BINDING SITE, designated SEQ ID:13807, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42651] Another function of GAM2071 is therefore inhibition of MGRN1 (Accession XP_048119.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGRN1.

[42652] Mhc class ii transactivator (MHC2TA, Accession NP_000237.1) is another GAM2071 target gene, herein designated TARGET GENE. MHC2TA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MHC2TA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MHC2TA BINDING SITE, designated SEQ ID:9987, to the nucleotide se-

quence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42653] Another function of GAM2071 is therefore inhibition of Mhc class ii transactivator (MHC2TA, Accession NP_000237.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MHC2TA.

[42654] MIRAB13 (Accession XP_039236.6) is another GAM2071 target gene, herein designated TARGET GENE. MIRAB13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MIRAB13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIRAB13 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42655] Another function of GAM2071 is therefore inhibition of MIRAB13 (Accession XP_039236.6) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIRAB13.

[42656] MIRAB13 (Accession NP_203744.1) is another GAM2071 target gene, herein designated TARGET GENE. MIRAB13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MIRAB13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIRAB13 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42657] Another function of GAM2071 is therefore inhibition of MIRAB13 (Accession NP_203744.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIRAB13.

[42658] MIS12 (Accession NP_076944.1) is another GAM2071 target gene, herein designated TARGET GENE. MIS12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MIS12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIS12

BINDING SITE, designated SEQ ID:3332, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42659] Another function of GAM2071 is therefore inhibition of MIS12 (Accession NP_076944.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIS12.

[42660] Makorin, ring finger protein, 4 (MKRN4, Accession NP_110384.1) is another GAM2071 target gene, herein designated TARGET GENE. MKRN4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MKRN4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MKRN4 BINDING SITE, designated SEQ ID:12385, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42661] Another function of GAM2071 is therefore inhibition of Makorin, ring finger protein, 4 (MKRN4, Accession NP_110384.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKRN4.

[42662] Melanoma-derived leucine zipper, extra-nuclear factor (MLZE, Accession NP_113603.1) is another GAM2071 target gene, herein designated TARGET GENE. MLZE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MLZE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLZE BINDING SITE, designated SEQ ID:11404, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42663] Another function of GAM2071 is therefore inhibition of Melanoma-derived leucine zipper, extra-nuclear factor (MLZE, Accession NP_113603.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLZE.

[42664] Modulator of apoptosis 1 (MOAP1, Accession NP_071434.2) is another GAM2071 target gene, herein designated TARGET GENE. MOAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MOAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of MOAP1 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42665] Another function of GAM2071 is therefore inhibition of Modulator of apoptosis 1 (MOAP1, Accession NP_071434.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOAP1.

[42666] moblak (Accession NP_570719.1) is another GAM2071 target gene, herein designated TARGET GENE. moblak BINDING SITE1 and moblak BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by moblak, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of moblak BINDING SITE1 and moblak BINDING SITE2, designated SEQ ID:2270 and SEQ ID:18353 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42667] Another function of GAM2071 is therefore inhibition of moblak (Accession NP_570719.1) . Accordingly, utilities of

GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with moblak.

[42668] Molybdenum cofactor synthesis 3 (MOCS3, Accession NP_055299.1) is another GAM2071 target gene, herein designated TARGET GENE. MOCS3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MOCS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MOCS3 BINDING SITE, designated SEQ ID:6108, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42669] Another function of GAM2071 is therefore inhibition of Molybdenum cofactor synthesis 3 (MOCS3, Accession NP_055299.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOCS3.

[42670] Myeloproliferative leukemia virus oncogene (MPL, Accession NP_005364.1) is another GAM2071 target gene, herein designated TARGET GENE. MPL BINDING SITE1 and MPL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MPL, correspond-

ing to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPL BINDING SITE1 and MPL BINDING SITE2, designated SEQ ID:11909 and SEQ ID:633 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42671] Another function of GAM2071 is therefore inhibition of Myeloproliferative leukemia virus oncogene (MPL, Accession NP_005364.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPL.

[42672] Mitochondrial ribosomal protein l30 (MRPL30, Accession NP_660213.1) is another GAM2071 target gene, herein designated TARGET GENE. MRPL30 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL30 BINDING SITE, designated SEQ ID:1858, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42673] Another function of GAM2071 is therefore inhibition of Mitochondrial ribosomal protein l30 (MRPL30, Accession NP_660213.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL30.

[42674] Mitochondrial ribosomal protein l35 (MRPL35, Accession NP_057706.2) is another GAM2071 target gene, herein designated TARGET GENE. MRPL35 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL35, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL35 BINDING SITE, designated SEQ ID:10631, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42675] Another function of GAM2071 is therefore inhibition of Mitochondrial ribosomal protein l35 (MRPL35, Accession NP_057706.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL35.

[42676] Mitochondrial ribosomal protein l49 (MRPL49, Accession NP_004918.1) is another GAM2071 target gene, herein

designated TARGET GENE. MRPL49 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPL49, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL49 BINDING SITE, designated SEQ ID:13534, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42677] Another function of GAM2071 is therefore inhibition of Mitochondrial ribosomal protein l49 (MRPL49, Accession NP_004918.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL49.

[42678] Mitochondrial ribosomal protein s27 (MRPS27, Accession NP_055899.1) is another GAM2071 target gene, herein designated TARGET GENE. MRPS27 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPS27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPS27 BINDING SITE, designated SEQ ID:13372, to the nucleotide se-

quence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42679] Another function of GAM2071 is therefore inhibition of Mitochondrial ribosomal protein s27 (MRPS27, Accession NP_055899.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS27.

[42680] MSTP028 (Accession NP_114160.1) is another GAM2071 target gene, herein designated TARGET GENE. MSTP028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MSTP028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MSTP028 BINDING SITE, designated SEQ ID:11359, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42681] Another function of GAM2071 is therefore inhibition of MSTP028 (Accession NP_114160.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSTP028.

[42682] MtFMT (Accession NP_640335.1) is another GAM2071 tar-

get gene, herein designated TARGET GENE. MtFMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MtFMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MtFMT BINDING SITE, designated SEQ ID:2529, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42683] Another function of GAM2071 is therefore inhibition of MtFMT (Accession NP_640335.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MtFMT.

[42684] MTH2 (Accession NP_060753.1) is another GAM2071 target gene, herein designated TARGET GENE. MTH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTH2 BINDING SITE, designated SEQ ID:12462, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42685] Another function of GAM2071 is therefore inhibition of MTH2 (Accession NP_060753.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTH2.

[42686] 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR, Accession NP_000245.1) is another GAM2071 target gene, herein designated TARGET GENE. MTR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTR BINDING SITE, designated SEQ ID:13325, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42687] Another function of GAM2071 is therefore inhibition of 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR, Accession NP_000245.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTR.

[42688] Myosin 5c (MYO5C, Accession NP_061198.1) is another GAM2071 target gene, herein designated TARGET GENE.

MYO5C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYO5C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYO5C BINDING SITE, designated SEQ ID:14846, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42689] Another function of GAM2071 is therefore inhibition of Myosin 5c (MYO5C, Accession NP_061198.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYO5C.

[42690] NAGPA (Accession NP_057340.1) is another GAM2071 target gene, herein designated TARGET GENE. NAGPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NAGPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NAGPA BINDING SITE, designated SEQ ID:8883, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42691] Another function of GAM2071 is therefore inhibition of NAGPA (Accession NP_057340.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAGPA.

[42692] NALP12 (Accession NP_150639.1) is another GAM2071 target gene, herein designated TARGET GENE. NALP12 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NALP12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NALP12 BINDING SITE, designated SEQ ID:12925, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42693] Another function of GAM2071 is therefore inhibition of NALP12 (Accession NP_150639.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NALP12.

[42694] Nanog (Accession NP_079141.1) is another GAM2071 target gene, herein designated TARGET GENE. Nanog BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by Nanog, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Nanog BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42695] Another function of GAM2071 is therefore inhibition of Nanog (Accession NP_079141.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Nanog.

[42696] NCAG1 (Accession NP_115536.1) is another GAM2071 target gene, herein designated TARGET GENE. NCAG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCAG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCAG1 BINDING SITE, designated SEQ ID:11436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42697] Another function of GAM2071 is therefore inhibition of NCAG1 (Accession NP_115536.1) . Accordingly, utilities of

GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCAG1.

[42698] Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1) is another GAM2071 target gene, herein designated TARGET GENE. NCOA6 BINDING SITE1 and NCOA6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCOA6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE1 and NCOA6 BINDING SITE2, designated SEQ ID:5484 and SEQ ID:6181 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42699] Another function of GAM2071 is therefore inhibition of Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1), a gene which activates gene transcription through ligand- dependent association with coactivators. and therefore may be associated with Breast cancer. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Breast cancer., and of other diseases and clinical conditions associated with NCOA6.

[42700] The function of NCOA6 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NP_079107.5) is another GAM2071 target gene, herein designated TARGET GENE. NCOA6IP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCOA6IP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6IP BINDING SITE, designated SEQ ID:3026, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42701] Another function of GAM2071 is therefore inhibition of Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NP_079107.5) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6IP.

[42702] NDP52 (Accession NP_005822.1) is another GAM2071 target gene, herein designated TARGET GENE. NDP52 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDP52, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDP52 BINDING SITE, designated SEQ ID:13886, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42703] Another function of GAM2071 is therefore inhibition of NDP52 (Accession NP_005822.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDP52.

[42704] Ndrg family member 3 (NDRG3, Accession NP_114402.1) is another GAM2071 target gene, herein designated TARGET GENE. NDRG3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NDRG3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDRG3 BINDING SITE, designated SEQ ID:20109, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42705] Another function of GAM2071 is therefore inhibition of Ndrg family member 3 (NDRG3, Accession NP_114402.1) .

Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG3.

[42706] Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) is another GAM2071 target gene, herein designated TARGET GENE. NDUFC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDUFC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDUFC2 BINDING SITE, designated SEQ ID:15362, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42707] Another function of GAM2071 is therefore inhibition of Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDUFC2.

[42708] Sialidase 3 (membrane sialidase) (NEU3, Accession NP_006647.2) is another GAM2071 target gene, herein

designated TARGET GENE. NEU3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NEU3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEU3 BINDING SITE, designated SEQ ID:18182, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42709] Another function of GAM2071 is therefore inhibition of Sialidase 3 (membrane sialidase) (NEU3, Accession NP_006647.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEU3.

[42710] Neurofibromin 2 (bilateral acoustic neuroma) (NF2, Accession NP_057502.1) is another GAM2071 target gene, herein designated TARGET GENE. NF2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by NF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NF2 BINDING SITE, designated SEQ ID:557, to the nu-

cleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42711] Another function of GAM2071 is therefore inhibition of Neurofibromin 2 (bilateral acoustic neuroma) (NF2, Accession NP_057502.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NF2.

[42712] Non-pou domain containing, octamer-binding (NONO, Accession NP_031389.2) is another GAM2071 target gene, herein designated TARGET GENE. NONO BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NONO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NONO BINDING SITE, designated SEQ ID:1412, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42713] Another function of GAM2071 is therefore inhibition of Non-pou domain containing, octamer-binding (NONO, Accession NP_031389.2), a gene which is a nuclear protein which contains RNA recognition motifs. Accordingly, utilities of GAM2071 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with NONO.

[42714] The function of NONO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1) is another GAM2071 target gene, herein designated TARGET GENE. NQO1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NQO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NQO1 BINDING SITE, designated SEQ ID:18183, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42715] Another function of GAM2071 is therefore inhibition of Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1), a gene which is cytochrome b5 reductase which reduces redox dyes and quinones. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NQO1.

[42716] The function of NQO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Neurotensin receptor 2 (NTSR2, Accession NP_036476.1) is another GAM2071 target gene, herein designated TARGET GENE. NTSR2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NTSR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NTSR2 BINDING SITE, designated SEQ ID:4568, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42717] Another function of GAM2071 is therefore inhibition of Neurotensin receptor 2 (NTSR2, Accession NP_036476.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTSR2.

[42718] Nudix (nucleoside diphosphate linked moiety x)-type motif 4 (NUDT4, Accession NP_061967.2) is another GAM2071 target gene, herein designated TARGET GENE. NUDT4 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by NUDT4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUDT4 BINDING SITE, designated SEQ ID:20051, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42719] Another function of GAM2071 is therefore inhibition of Nudix (nucleoside diphosphate linked moiety x)-type motif 4 (NUDT4, Accession NP_061967.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUDT4.

[42720] Nucleoredoxin (NXN, Accession NP_071908.1) is another GAM2071 target gene, herein designated TARGET GENE. NXN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NXN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NXN BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42721] Another function of GAM2071 is therefore inhibition of Nucleoredoxin (NXN, Accession NP_071908.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXN.

[42722] Olfactory receptor, family 51, subfamily e, member 2 (OR51E2, Accession NP_110401.1) is another GAM2071 target gene, herein designated TARGET GENE. OR51E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OR51E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OR51E2 BINDING SITE, designated SEQ ID:8690, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42723] Another function of GAM2071 is therefore inhibition of Olfactory receptor, family 51, subfamily e, member 2 (OR51E2, Accession NP_110401.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OR51E2.

[42724] Origin recognition complex, subunit 1-like (yeast)

(ORC1L, Accession NP_004144.1) is another GAM2071 target gene, herein designated TARGET GENE. ORC1L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ORC1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ORC1L BINDING SITE, designated SEQ ID:436, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42725] Another function of GAM2071 is therefore inhibition of Origin recognition complex, subunit 1-like (yeast) (ORC1L, Accession NP_004144.1), a gene which may be required for initiation of DNA replication. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ORC1L.

[42726] The function of ORC1L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.P15RS (Accession NP_060640.2) is another GAM2071 target gene, herein designated TARGET GENE. P15RS BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by P15RS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P15RS BINDING SITE, designated SEQ ID:1032, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42727] Another function of GAM2071 is therefore inhibition of P15RS (Accession NP_060640.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P15RS.

[42728] Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS, Accession NP_006443.1) is another GAM2071 target gene, herein designated TARGET GENE. PAICS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PAICS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PAICS BINDING SITE, designated SEQ ID:11127, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42729] Another function of GAM2071 is therefore inhibition of Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS, Accession NP_006443.1), a gene which is required for purine biosynthesis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAICS.

[42730] The function of PAICS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.PART1 (Accession NP_057674.1) is another GAM2071 target gene, herein designated TARGET GENE. PART1 BINDING SITE1 and PART1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PART1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PART1 BINDING SITE1 and PART1 BINDING SITE2, designated SEQ ID:19024 and SEQ ID:7026 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42731] Another function of GAM2071 is therefore inhibition of

PART1 (Accession NP_057674.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PART1.

[42732] Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) is another GAM2071 target gene, herein designated TARGET GENE. PASK BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PASK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PASK BINDING SITE, designated SEQ ID:3230, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42733] Another function of GAM2071 is therefore inhibition of Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PASK.

[42734] Protocadherin alpha 9 (PCDHA9, Accession NP_054724.1) is another GAM2071 target gene, herein designated TARGET GENE. PCDHA9 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts

of mRNA encoded by PCDHA9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA9 BINDING SITE, designated SEQ ID:10631, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42735] Another function of GAM2071 is therefore inhibition of Protocadherin alpha 9 (PCDHA9, Accession NP_054724.1), a gene which is a calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA9.

[42736] The function of PCDHA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Protocadherin beta 11 (PCDHB11, Accession NP_061754.1) is another GAM2071 target gene, herein designated TARGET GENE. PCDHB11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of PCDHB11 BINDING SITE, designated SEQ ID:7975, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42737] Another function of GAM2071 is therefore inhibition of Protocadherin beta 11 (PCDHB11, Accession NP_061754.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB11.

[42738] Protocadherin beta 16 (PCDHB16, Accession NP_066008.1) is another GAM2071 target gene, herein designated TARGET GENE. PCDHB16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB16 BINDING SITE, designated SEQ ID:4753, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42739] Another function of GAM2071 is therefore inhibition of Protocadherin beta 16 (PCDHB16, Accession NP_066008.1), a gene which is a potential calcium- de-

pendent cell- adhesion protein. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB16.

[42740] The function of PCDHB16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Protocadherin beta 9 (PCDHB9, Accession NP_061992.2) is another GAM2071 target gene, herein designated TARGET GENE. PCDHB9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB9 BINDING SITE, designated SEQ ID:3109, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42741] Another function of GAM2071 is therefore inhibition of Protocadherin beta 9 (PCDHB9, Accession NP_061992.2), a gene which is a potential calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB9.

[42742] The function of PCDHB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Phosducin-like (PDCL, Accession NP_005379.2) is another GAM2071 target gene, herein designated TARGET GENE. PDCL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDCL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDCL BINDING SITE, designated SEQ ID:14559, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42743] Another function of GAM2071 is therefore inhibition of Phosducin-like (PDCL, Accession NP_005379.2), a gene which may regulate G- protein signaling and similar to phosducins. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDCL.

[42744] The function of PDCL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM30.1.Phosphodiesterase 6b, cgmp-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NP_000274.1) is another GAM2071 target gene, herein designated TARGET GENE. PDE6B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDE6B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDE6B BINDING SITE, designated SEQ ID:18070, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42745] Another function of GAM2071 is therefore inhibition of Phosphodiesterase 6b, cgmp-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NP_000274.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE6B.

[42746] Platelet derived growth factor c (PDGFC, Accession NP_057289.1) is another GAM2071 target gene, herein designated TARGET GENE. PDGFC BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by PDGFC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDGFC BINDING SITE, designated SEQ ID:19767, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42747] Another function of GAM2071 is therefore inhibition of Platelet derived growth factor c (PDGFC, Accession NP_057289.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFC.

[42748] Pdz and lim domain 2 (mystique) (PDLIM2, Accession NP_789847.1) is another GAM2071 target gene, herein designated TARGET GENE. PDLIM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PDLIM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDLIM2 BINDING SITE, designated SEQ ID:4874, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42749] Another function of GAM2071 is therefore inhibition of Pdz and lim domain 2 (mystique) (PDLIM2, Accession NP_789847.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDLIM2.

[42750] Pdz domain containing 1 (PDZK1, Accession NP_002605.2) is another GAM2071 target gene, herein designated TARGET GENE. PDZK1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PDZK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDZK1 BINDING SITE, designated SEQ ID:11598, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42751] Another function of GAM2071 is therefore inhibition of Pdz domain containing 1 (PDZK1, Accession NP_002605.2), a gene which is a contains PDZ interaction domains, interacts with MAP17, a protein involved in control of cell proliferation. and therefore may be associated with Autosomal dominant hypophosphatemic rickets. Accordingly, utilities of GAM2071 include diagnosis, preven-

tion and treatment of Autosomal dominant hypophosphatemic rickets, and of other diseases and clinical conditions associated with PDZK1.

[42752] The function of PDZK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.PDZRN1 (Accession NP_699202.1) is another GAM2071 target gene, herein designated TARGET GENE. PDZRN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDZRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDZRN1 BINDING SITE, designated SEQ ID:17567, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42753] Another function of GAM2071 is therefore inhibition of PDZRN1 (Accession NP_699202.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDZRN1.

[42754] PEGASUS (Accession NP_071911.2) is another GAM2071 target gene, herein designated TARGET GENE. PEGASUS

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PEGASUS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PEGASUS BINDING SITE, designated SEQ ID:13389, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42755] Another function of GAM2071 is therefore inhibition of PEGASUS (Accession NP_071911.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEGASUS.

[42756] Pellino homolog 1 (drosophila) (PELI1, Accession NP_065702.2) is another GAM2071 target gene, herein designated TARGET GENE. PELI1 BINDING SITE1 through PELI1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by PELI1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PELI1 BINDING SITE1 through PELI1 BINDING SITE3, designated SEQ ID:18182, SEQ ID:430 and SEQ ID:13801 re-

spectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42757] Another function of GAM2071 is therefore inhibition of Pellino homolog 1 (drosophila) (PELI1, Accession NP_065702.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PELI1.

[42758] Period homolog 2 (drosophila) (PER2, Accession NP_073728.1) is another GAM2071 target gene, herein designated TARGET GENE. PER2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PER2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PER2 BINDING SITE, designated SEQ ID:6602, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42759] Another function of GAM2071 is therefore inhibition of Period homolog 2 (drosophila) (PER2, Accession NP_073728.1), a gene which Period homolog 2; putative circadian clock protein; has a PAS dimerization domain and therefore may be associated with Familial advanced

sleep- phase syndrome. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Familial advanced sleep- phase syndrome, and of other diseases and clinical conditions associated with PER2.

[42760] The function of PER2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Phosphoribosylformylglycinamidine synthase (fgar amidotransferase) (PFAS, Accession NP_036525.1) is another GAM2071 target gene, herein designated TARGET GENE. PFAS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PFAS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PFAS BINDING SITE, designated SEQ ID:16519, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42761] Another function of GAM2071 is therefore inhibition of Phosphoribosylformylglycinamidine synthase (fgar amidotransferase) (PFAS, Accession NP_036525.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with PFAS.

[42762] Polymeric immunoglobulin receptor (PIGR, Accession NP_002635.2) is another GAM2071 target gene, herein designated TARGET GENE. PIGR BINDING SITE1 and PIGR BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PIGR, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIGR BINDING SITE1 and PIGR BINDING SITE2, designated SEQ ID:5370 and SEQ ID:8350 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42763] Another function of GAM2071 is therefore inhibition of Polymeric immunoglobulin receptor (PIGR, Accession NP_002635.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGR.

[42764] Phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B, Accession NP_002637.2) is another GAM2071 target gene, herein designated TARGET GENE. PIK3C2B BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by PIK3C2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3C2B BINDING SITE, designated SEQ ID:15277, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42765] Another function of GAM2071 is therefore inhibition of Phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B, Accession NP_002637.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3C2B.

[42766] Phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD, Accession NP_005017.2) is another GAM2071 target gene, herein designated TARGET GENE. PIK3CD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3CD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3CD BINDING SITE, designated SEQ ID:4771, to the nucleotide sequence of GAM2071 RNA, herein designated

GAM RNA, also designated SEQ ID:371.

[42767] Another function of GAM2071 is therefore inhibition of Phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD, Accession NP_005017.2), a gene which regulating cell growth. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3CD.

[42768] The function of PIK3CD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.PILRB (Accession NP_778212.2) is another GAM2071 target gene, herein designated TARGET GENE. PILRB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PILRB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PILRB BINDING SITE, designated SEQ ID:15120, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42769] Another function of GAM2071 is therefore inhibition of PILRB (Accession NP_778212.2) . Accordingly, utilities of

GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PILRB.

[42770] PILRB (Accession NP_038468.3) is another GAM2071 target gene, herein designated TARGET GENE. PILRB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PILRB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PILRB BINDING SITE, designated SEQ ID:15120, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42771] Another function of GAM2071 is therefore inhibition of PILRB (Accession NP_038468.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PILRB.

[42772] PILRB (Accession NP_839956.1) is another GAM2071 target gene, herein designated TARGET GENE. PILRB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PILRB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of PILRB BINDING SITE, designated SEQ ID:15120, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42773] Another function of GAM2071 is therefore inhibition of PILRB (Accession NP_839956.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PILRB.

[42774] Phosphatidylinositol-4-phosphate 5-kinase, type i, gamma (PIP5K1C, Accession NP_036530.1) is another GAM2071 target gene, herein designated TARGET GENE. PIP5K1C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PIP5K1C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIP5K1C BINDING SITE, designated SEQ ID:1328, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42775] Another function of GAM2071 is therefore inhibition of Phosphatidylinositol-4-phosphate 5-kinase, type i, gamma (PIP5K1C, Accession NP_036530.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with PIP5K1C.

[42776] Phosphatidylinositol-4-phosphate 5-kinase, type i, gamma (PIP5K1C, Accession XP_047620.2) is another GAM2071 target gene, herein designated TARGET GENE. PIP5K1C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PIP5K1C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIP5K1C BINDING SITE, designated SEQ ID:1328, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42777] Another function of GAM2071 is therefore inhibition of Phosphatidylinositol-4-phosphate 5-kinase, type i, gamma (PIP5K1C, Accession XP_047620.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIP5K1C.

[42778] Phosphotidylinositol transfer protein, beta (PITPNB, Accession NP_036531.1) is another GAM2071 target gene, herein designated TARGET GENE. PITPNB BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by PITPNB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PITPNB BINDING SITE, designated SEQ ID:19285, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42779] Another function of GAM2071 is therefore inhibition of Phosphotidylinositol transfer protein, beta (PITPNB, Accession NP_036531.1), a gene which catalyzes the transfer of ptdins and phosphatidylcholine between membranes. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PITPNB.

[42780] The function of PITPNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.1.Phosphomannomutase 2 (PMM2, Accession NP_000294.1) is another GAM2071 target gene, herein designated TARGET GENE. PMM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMM2, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMM2 BINDING SITE, designated SEQ ID:1676, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42781] Another function of GAM2071 is therefore inhibition of Phosphomannomutase 2 (PMM2, Accession NP_000294.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMM2.

[42782] Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) is another GAM2071 target gene, herein designated TARGET GENE. PNMA2 BINDING SITE1 and PNMA2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PNMA2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PNMA2 BINDING SITE1 and PNMA2 BINDING SITE2, designated SEQ ID:11236 and SEQ ID:11189 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42783] Another function of GAM2071 is therefore inhibition of Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNMA2.

[42784] Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) is another GAM2071 target gene, herein designated TARGET GENE. POFUT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by POFUT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POFUT1 BINDING SITE, designated SEQ ID:1760, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42785] Another function of GAM2071 is therefore inhibition of Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POFUT1.

[42786] Polymerase (dna directed), epsilon 3 (p17 subunit) (POLE3, Accession NP_059139.2) is another GAM2071 target gene,

herein designated TARGET GENE. POLE3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLE3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLE3 BINDING SITE, designated SEQ ID:5665, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42787] Another function of GAM2071 is therefore inhibition of Polymerase (dna directed), epsilon 3 (p17 subunit) (POLE3, Accession NP_059139.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLE3.

[42788] Polymerase (rna) ii (dna directed) polypeptide d (POLR2D, Accession NP_004796.1) is another GAM2071 target gene, herein designated TARGET GENE. POLR2D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLR2D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLR2D BINDING SITE, designated SEQ ID:11282, to the nucleotide se-

quence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42789] Another function of GAM2071 is therefore inhibition of Polymerase (rna) ii (dna directed) polypeptide d (POLR2D, Accession NP_004796.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLR2D.

[42790] Paraoxonase 1 (PON1, Accession NP_000437.3) is another GAM2071 target gene, herein designated TARGET GENE. PON1 BINDING SITE1 and PON1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PON1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PON1 BINDING SITE1 and PON1 BINDING SITE2, designated SEQ ID:19429 and SEQ ID:1117 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42791] Another function of GAM2071 is therefore inhibition of Paraoxonase 1 (PON1, Accession NP_000437.3), a gene which hydrolyzes the toxic metabolites of a variety of organophosphorus insecticides. Accordingly, utilities of

GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PON1.

[42792] The function of PON1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Pou domain, class 2, transcription factor 3 (POU2F3, Accession NP_055167.1) is another GAM2071 target gene, herein designated TARGET GENE. POU2F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POU2F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POU2F3 BINDING SITE, designated SEQ ID:7036, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42793] Another function of GAM2071 is therefore inhibition of Pou domain, class 2, transcription factor 3 (POU2F3, Accession NP_055167.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU2F3.

[42794] Ptprf interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1, Accession NP_003613.2) is another GAM2071

target gene, herein designated TARGET GENE. PPFIBP1 BINDING SITE1 and PPFIBP1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PPFIBP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPFIBP1 BINDING SITE1 and PPFIBP1 BINDING SITE2, designated SEQ ID:8861 and SEQ ID:5523 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42795] Another function of GAM2071 is therefore inhibition of Ptprf interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1, Accession NP_003613.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPFIBP1.

[42796] Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession NP_005029.1) is another GAM2071 target gene, herein designated TARGET GENE. PPID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPID BINDING SITE, designated SEQ ID:3110, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42797] Another function of GAM2071 is therefore inhibition of Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession NP_005029.1), a gene which catalyzes the cis- trans isomerization of proline imidic peptide bonds in oligopeptides. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPID.

[42798] The function of PPID and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) is another GAM2071 target gene, herein designated TARGET GENE. PPIL2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPIL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of PPIL2 BINDING SITE, designated SEQ ID:18677, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42799] Another function of GAM2071 is therefore inhibition of Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPIL2.

[42800] Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_115288.1) is another GAM2071 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE, designated SEQ ID:14820, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42801] Another function of GAM2071 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_115288.1) . Accordingly, utili-

ties of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[42802] Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) is another GAM2071 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE, designated SEQ ID:14820, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42803] Another function of GAM2071 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[42804] Protein phosphatase 2 (formerly 2a), regulatory subunit a (pr 65), beta isoform (PPP2R1B, Accession NP_002707.2)

is another GAM2071 target gene, herein designated TARGET GENE. PPP2R1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPP2R1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP2R1B BINDING SITE, designated SEQ ID:8962, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42805] Another function of GAM2071 is therefore inhibition of Protein phosphatase 2 (formerly 2a), regulatory subunit a (pr 65), beta isoform (PPP2R1B, Accession NP_002707.2), a gene which is necessary for interaction of the catalytic PP2A- C and variable PP2A- B subunits. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R1B.

[42806] The function of PPP2R1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.PRDX6 (Accession NP_004896.1) is another GAM2071 target gene, herein designated TARGET GENE.

PRDX6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRDX6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRDX6 BINDING SITE, designated SEQ ID:19006, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42807] Another function of GAM2071 is therefore inhibition of PRDX6 (Accession NP_004896.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDX6.

[42808] Primase, polypeptide 2a, 58kda (PRIM2A, Accession NP_000938.1) is another GAM2071 target gene, herein designated TARGET GENE. PRIM2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRIM2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRIM2A BINDING SITE, designated SEQ ID:12707, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42809] Another function of GAM2071 is therefore inhibition of Primase, polypeptide 2a, 58kda (PRIM2A, Accession NP_000938.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRIM2A.

[42810] Protein kinase, lysine deficient 3 (PRKWNK3, Accession NP_065973.1) is another GAM2071 target gene, herein designated TARGET GENE. PRKWNK3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKWNK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKWNK3 BINDING SITE, designated SEQ ID:5524, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42811] Another function of GAM2071 is therefore inhibition of Protein kinase, lysine deficient 3 (PRKWNK3, Accession NP_065973.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKWNK3.

[42812] Protein kinase, y-linked (PRKY, Accession NP_002751.1) is another GAM2071 target gene, herein designated TARGET

GENE. PRKY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKY BINDING SITE, designated SEQ ID:1958, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42813] Another function of GAM2071 is therefore inhibition of Protein kinase, y-linked (PRKY, Accession NP_002751.1), a gene which is a putative protein kinase. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKY.

[42814] The function of PRKY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Prion protein 2 (dublet) (PRND, Accession NP_036541.1) is another GAM2071 target gene, herein designated TARGET GENE. PRND BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRND, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRND BINDING SITE, designated SEQ ID:7084, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42815] Another function of GAM2071 is therefore inhibition of Prion protein 2 (dublet) (PRND, Accession NP_036541.1), a gene which is similar to prion protein PRNP. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRND.

[42816] The function of PRND and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.PRO0159 (Accession NP_054837.1) is another GAM2071 target gene, herein designated TARGET GENE. PRO0159 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0159, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0159 BINDING SITE, designated SEQ ID:4857, to the nucleotide sequence of GAM2071

RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42817] Another function of GAM2071 is therefore inhibition of PRO0159 (Accession NP_054837.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0159.

[42818] PRO0297 (Accession NP_054800.1) is another GAM2071 target gene, herein designated TARGET GENE. PRO0297 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0297, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0297 BINDING SITE, designated SEQ ID:1504, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42819] Another function of GAM2071 is therefore inhibition of PRO0297 (Accession NP_054800.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0297.

[42820] PRO0365 (Accession NP_054845.1) is another GAM2071 target gene, herein designated TARGET GENE. PRO0365 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0365, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0365 BINDING SITE, designated SEQ ID:7958, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42821] Another function of GAM2071 is therefore inhibition of PRO0365 (Accession NP_054845.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0365.

[42822] PROM2 (Accession NP_653308.1) is another GAM2071 target gene, herein designated TARGET GENE. PROM2 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by PROM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PROM2 BINDING SITE, designated SEQ ID:19427, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42823] Another function of GAM2071 is therefore inhibition of PROM2 (Accession NP_653308.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROM2.

[42824] Proteasome (prosome, macropain) 26s subunit, non-atpase, 9 (PSMD9, Accession NP_002804.2) is another GAM2071 target gene, herein designated TARGET GENE. PSMD9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSMD9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSMD9 BINDING SITE, designated SEQ ID:11654, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42825] Another function of GAM2071 is therefore inhibition of

Proteasome (prosome, macropain) 26s subunit, non-atpase, 9 (PSMD9, Accession NP_002804.2), a gene which acts as a regulatory subunit of the 26 proteasome. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSMD9.

[42826] The function of PSMD9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.PSME4 (Accession XP_040158.1) is another GAM2071 target gene, herein designated TARGET GENE. PSME4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSME4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSME4 BINDING SITE, designated SEQ ID:14216, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42827] Another function of GAM2071 is therefore inhibition of PSME4 (Accession XP_040158.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSME4.

[42828] Phosphoserine phosphatase (PSPH, Accession NP_004568.1) is another GAM2071 target gene, herein designated TARGET GENE. PSPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSPH BINDING SITE, designated SEQ ID:9102, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42829] Another function of GAM2071 is therefore inhibition of Phosphoserine phosphatase (PSPH, Accession NP_004568.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSPH.

[42830] Phosphatidylserine synthase 2 (PTDSS2, Accession NP_110410.1) is another GAM2071 target gene, herein designated TARGET GENE. PTDSS2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTDSS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of PTDSS2 BINDING SITE, designated SEQ ID:12204, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42831] Another function of GAM2071 is therefore inhibition of Phosphatidylserine synthase 2 (PTDSS2, Accession NP_110410.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTDSS2.

[42832] Prostaglandin e synthase (PTGES, Accession NP_004869.1) is another GAM2071 target gene, herein designated TARGET GENE. PTGES BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGES BINDING SITE, designated SEQ ID:11575, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42833] Another function of GAM2071 is therefore inhibition of Prostaglandin e synthase (PTGES, Accession NP_004869.1) . Accordingly, utilities of GAM2071 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with PTGES.

[42834] Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1) is another GAM2071 target gene, herein designated TARGET GENE. PTGIS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGIS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGIS BINDING SITE, designated SEQ ID:11917, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42835] Another function of GAM2071 is therefore inhibition of Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1), a gene which catalyzes the isomerization of prostaglandin h2 to prostacyclin (= prostaglandin i2). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGIS.

[42836] The function of PTGIS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM30.1.RAB11-FIP4 (Accession NP_116321.2) is another GAM2071 target gene, herein designated TARGET GENE. RAB11-FIP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB11-FIP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB11-FIP4 BINDING SITE, designated SEQ ID:5406, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42837] Another function of GAM2071 is therefore inhibition of RAB11-FIP4 (Accession NP_116321.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB11-FIP4.

[42838] Rab21, member ras oncogene family (RAB21, Accession NP_055814.1) is another GAM2071 target gene, herein designated TARGET GENE. RAB21 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of RAB21 BINDING SITE, designated SEQ ID:17172, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42839] Another function of GAM2071 is therefore inhibition of Rab21, member ras oncogene family (RAB21, Accession NP_055814.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB21.

[42840] Rab33b, member ras oncogene family (RAB33B, Accession NP_112586.1) is another GAM2071 target gene, herein designated TARGET GENE. RAB33B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB33B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB33B BINDING SITE, designated SEQ ID:15333, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42841] Another function of GAM2071 is therefore inhibition of Rab33b, member ras oncogene family (RAB33B, Accession NP_112586.1) . Accordingly, utilities of GAM2071 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB33B.

[42842] Rab36, member ras oncogene family (RAB36, Accession NP_004905.1) is another GAM2071 target gene, herein designated TARGET GENE. RAB36 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB36, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB36 BINDING SITE, designated SEQ ID:12750, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42843] Another function of GAM2071 is therefore inhibition of Rab36, member ras oncogene family (RAB36, Accession NP_004905.1), a gene which is involved in protein transport. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB36.

[42844] The function of RAB36 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Rab39, member ras oncogene family

(RAB39, Accession XP_084662.1) is another GAM2071 target gene, herein designated TARGET GENE. RAB39 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB39, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB39 BINDING SITE, designated SEQ ID:2158, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42845] Another function of GAM2071 is therefore inhibition of Rab39, member ras oncogene family (RAB39, Accession XP_084662.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB39.

[42846] Rab40c, member ras oncogene family (RAB40C, Accession NP_066991.1) is another GAM2071 target gene, herein designated TARGET GENE. RAB40C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB40C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB40C BINDING

SITE, designated SEQ ID:8129, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42847] Another function of GAM2071 is therefore inhibition of Rab40c, member ras oncogene family (RAB40C, Accession NP_066991.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB40C.

[42848] Rab, member of ras oncogene family-like 2a (RABL2A, Accession NP_038198.1) is another GAM2071 target gene, herein designated TARGET GENE. RABL2A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RABL2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RABL2A BINDING SITE, designated SEQ ID:14847, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42849] Another function of GAM2071 is therefore inhibition of Rab, member of ras oncogene family-like 2a (RABL2A, Accession NP_038198.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with RABL2A.

[42850] Rab, member of ras oncogene family-like 2b (RABL2B, Accession NP_009012.1) is another GAM2071 target gene, herein designated TARGET GENE. RABL2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RABL2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RABL2B BINDING SITE, designated SEQ ID:14847, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42851] Another function of GAM2071 is therefore inhibition of Rab, member of ras oncogene family-like 2b (RABL2B, Accession NP_009012.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABL2B.

[42852] Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602295.1) is another GAM2071 target gene, herein designated TARGET GENE. RAD52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAD52, corresponding to a target binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE, designated SEQ ID:4266, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42853] Another function of GAM2071 is therefore inhibition of Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602295.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52.

[42854] Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_002870.2) is another GAM2071 target gene, herein designated TARGET GENE. RAD52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAD52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE, designated SEQ ID:4266, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42855] Another function of GAM2071 is therefore inhibition of Rad52 homolog (s. cerevisiae) (RAD52, Accession

NP_002870.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52.

[42856] Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602296.1) is another GAM2071 target gene, herein designated TARGET GENE. RAD52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAD52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE, designated SEQ ID:4266, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42857] Another function of GAM2071 is therefore inhibition of Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602296.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52.

[42858] Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602294.1) is another GAM2071 target gene, herein designated TARGET GENE. RAD52 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by RAD52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE, designated SEQ ID:4266, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42859] Another function of GAM2071 is therefore inhibition of Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602294.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52.

[42860] RAI (Accession NP_006654.1) is another GAM2071 target gene, herein designated TARGET GENE. RAI BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI BINDING SITE, designated SEQ ID:17223, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42861] Another function of GAM2071 is therefore inhibition of

RAI (Accession NP_006654.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI.

[42862] Retinoic acid induced 3 (RAI3, Accession NP_003970.1) is another GAM2071 target gene, herein designated TARGET GENE. RAI3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAI3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI3 BINDING SITE, designated SEQ ID:16116, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42863] Another function of GAM2071 is therefore inhibition of Retinoic acid induced 3 (RAI3, Accession NP_003970.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI3.

[42864] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_055552.1) is another GAM2071 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:7664, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42865] Another function of GAM2071 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_055552.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[42866] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739580.1) is another GAM2071 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:7664, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42867] Another function of GAM2071 is therefore inhibition of

Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739580.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[42868] Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739579.1) is another GAM2071 target gene, herein designated TARGET GENE. RASSF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:7664, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42869] Another function of GAM2071 is therefore inhibition of Ras association (ralgds/af-6) domain family 2 (RASSF2, Accession NP_739579.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2.

[42870] RCBTB1 (Accession NP_060661.2) is another GAM2071 target gene, herein designated TARGET GENE. RCBTB1 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by RCBTB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RCBTB1 BINDING SITE, designated SEQ ID:3049, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42871] Another function of GAM2071 is therefore inhibition of RCBTB1 (Accession NP_060661.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RCBTB1.

[42872] Regulator of g-protein signalling 11 (RGS11, Accession NP_003825.1) is another GAM2071 target gene, herein designated TARGET GENE. RGS11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RGS11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RGS11 BINDING SITE, designated SEQ ID:7393, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42873] Another function of GAM2071 is therefore inhibition of Regulator of g-protein signalling 11 (RGS11, Accession NP_003825.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS11.

[42874] Rhesus blood group, d antigen (RHD, Accession NP_057208.2) is another GAM2071 target gene, herein designated TARGET GENE. RHD BINDING SITE1 and RHD BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by RHD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE1 and RHD BINDING SITE2, designated SEQ ID:442 and SEQ ID:8756 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42875] Another function of GAM2071 is therefore inhibition of Rhesus blood group, d antigen (RHD, Accession NP_057208.2), a gene which Major antigen of the RH system. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[42876] The function of RHD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Rhesus blood group, d antigen (RHD, Accession NP_057309.2) is another GAM2071 target gene, herein designated TARGET GENE. RHD BINDING SITE1 and RHD BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by RHD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE1 and RHD BINDING SITE2, designated SEQ ID:8756 and SEQ ID:442 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42877] Another function of GAM2071 is therefore inhibition of Rhesus blood group, d antigen (RHD, Accession NP_057309.2), a gene which Major antigen of the RH system. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[42878] The function of RHD and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM161.1.RHPN2 (Accession NP_149094.2) is another GAM2071 target gene, herein designated TARGET GENE. RHPN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RHPN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHPN2 BINDING SITE, designated SEQ ID:5481, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42879] Another function of GAM2071 is therefore inhibition of RHPN2 (Accession NP_149094.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHPN2.

[42880] RNF137 (Accession NP_060543.4) is another GAM2071 target gene, herein designated TARGET GENE. RNF137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF137 BINDING SITE, designated SEQ ID:8861, to the nu-

cleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42881] Another function of GAM2071 is therefore inhibition of RNF137 (Accession NP_060543.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF137.

[42882] Ring finger protein 19 (RNF19, Accession NP_056250.2) is another GAM2071 target gene, herein designated TARGET GENE. RNF19 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RNF19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF19 BINDING SITE, designated SEQ ID:14309, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42883] Another function of GAM2071 is therefore inhibition of Ring finger protein 19 (RNF19, Accession NP_056250.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF19.

[42884] RPP30 (Accession NP_006404.1) is another GAM2071 tar-

get gene, herein designated TARGET GENE. RPP30 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RPP30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RPP30 BINDING SITE, designated SEQ ID:3259, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42885] Another function of GAM2071 is therefore inhibition of RPP30 (Accession NP_006404.1), a gene which is a component of ribonuclease p that processes 5' ends of precursor tRNAs. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPP30.

[42886] The function of RPP30 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.S100A15 (Accession NP_789793.1) is another GAM2071 target gene, herein designated TARGET GENE. S100A15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100A15, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of S100A15 BINDING SITE, designated SEQ ID:18561, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42887] Another function of GAM2071 is therefore inhibition of S100A15 (Accession NP_789793.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with S100A15.

[42888] SBLF (Accession NP_006864.2) is another GAM2071 target gene, herein designated TARGET GENE. SBLF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SBLF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SBLF BINDING SITE, designated SEQ ID:14250, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42889] Another function of GAM2071 is therefore inhibition of SBLF (Accession NP_006864.2) . Accordingly, utilities of

GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SBLF.

[42890] SCAMP-4 (Accession NP_524558.1) is another GAM2071 target gene, herein designated TARGET GENE. SCAMP-4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCAMP-4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAMP-4 BINDING SITE, designated SEQ ID:19434, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42891] Another function of GAM2071 is therefore inhibition of SCAMP-4 (Accession NP_524558.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP-4.

[42892] Scan domain containing 2 (SCAND2, Accession NP_071333.2) is another GAM2071 target gene, herein designated TARGET GENE. SCAND2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SCAND2, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAND2 BINDING SITE, designated SEQ ID:16790, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42893] Another function of GAM2071 is therefore inhibition of Scan domain containing 2 (SCAND2, Accession NP_071333.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAND2.

[42894] Scavenger receptor class f, member 1 (SCARF1, Accession NP_003684.1) is another GAM2071 target gene, herein designated TARGET GENE. SCARF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCARF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCARF1 BINDING SITE, designated SEQ ID:12384, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42895] Another function of GAM2071 is therefore inhibition of Scavenger receptor class f, member 1 (SCARF1, Accession

NP_003684.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCARF1.

[42896] SCN3B (Accession NP_060870.1) is another GAM2071 target gene, herein designated TARGET GENE. SCN3B BINDING SITE1 and SCN3B BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SCN3B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCN3B BINDING SITE1 and SCN3B BINDING SITE2, designated SEQ ID:1471 and SEQ ID:9932 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42897] Another function of GAM2071 is therefore inhibition of SCN3B (Accession NP_060870.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN3B.

[42898] Stromal cell-derived factor 2 (SDF2, Accession NP_008854.2) is another GAM2071 target gene, herein designated TARGET GENE. SDF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by SDF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SDF2 BINDING SITE, designated SEQ ID:4852, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42899] Another function of GAM2071 is therefore inhibition of Stromal cell-derived factor 2 (SDF2, Accession NP_008854.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDF2.

[42900] SDS-RS1 (Accession NP_612441.1) is another GAM2071 target gene, herein designated TARGET GENE. SDS-RS1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SDS-RS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SDS-RS1 BINDING SITE, designated SEQ ID:2100, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42901] Another function of GAM2071 is therefore inhibition of

SDS-RS1 (Accession NP_612441.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDS-RS1.

[42902] Secreted and transmembrane 1 (SECTM1, Accession NP_002995.1) is another GAM2071 target gene, herein designated TARGET GENE. SECTM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SECTM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SECTM1 BINDING SITE, designated SEQ ID:14404, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42903] Another function of GAM2071 is therefore inhibition of Secreted and transmembrane 1 (SECTM1, Accession NP_002995.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SECTM1.

[42904] Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1) is another GAM2071 target gene, herein designated TARGET GENE. SEDL BINDING SITE1 through

SEDL BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by SEDL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEDL BINDING SITE1 through SEDL BINDING SITE3, designated SEQ ID:7261, SEQ ID:13400 and SEQ ID:16842 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42905] Another function of GAM2071 is therefore inhibition of Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1), a gene which may play role in vesicular transport from endoplasmic reticulum to golgi. and therefore may be associated with Spondyloepiphyseal dysplasia. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Spondyloepiphyseal dysplasia, and of other diseases and clinical conditions associated with SEDL.

[42906] The function of SEDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Sel-1 suppressor of lin-12-like (c. elegans) (SEL1L, Accession NP_005056.3) is another GAM2071 tar-

get gene, herein designated TARGET GENE. SEL1L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEL1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEL1L BINDING SITE, designated SEQ ID:16250, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42907] Another function of GAM2071 is therefore inhibition of Sel-1 suppressor of lin-12-like (c. elegans) (SEL1L, Accession NP_005056.3), a gene which may play a role in notch signaling (by similarity). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEL1L.

[42908] The function of SEL1L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM193.1.Selenoprotein n, 1 (SEPN1, Accession NP_065184.1) is another GAM2071 target gene, herein designated TARGET GENE. SEPN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEPN1, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEPN1 BINDING SITE, designated SEQ ID:1799, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42909] Another function of GAM2071 is therefore inhibition of Selenoprotein n, 1 (SEPN1, Accession NP_065184.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEPN1.

[42910] Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) is another GAM2071 target gene, herein designated TARGET GENE. SERF1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERF1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1A BINDING SITE, designated SEQ ID:11123, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42911] Another function of GAM2071 is therefore inhibition of

Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1A.

[42912] Small edrk-rich factor 1b (centromeric) (SERF1B, Accession NP_075267.1) is another GAM2071 target gene, herein designated TARGET GENE. SERF1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERF1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1B BINDING SITE, designated SEQ ID:11123, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42913] Another function of GAM2071 is therefore inhibition of Small edrk-rich factor 1b (centromeric) (SERF1B, Accession NP_075267.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1B.

[42914] Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 9 (SERPINB9, Accession NP_004146.1) is another GAM2071 target gene, herein

designated TARGET GENE. SERPINB9 BINDING SITE1 and SERPINB9 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERPINB9, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERPINB9 BINDING SITE1 and SERPINB9 BINDING SITE2, designated SEQ ID:437 and SEQ ID:4057 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42915] Another function of GAM2071 is therefore inhibition of Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 9 (SERPINB9, Accession NP_004146.1), a gene which may be a serpin serine protease inhibitor that interacts with granzyme B (GZMB). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB9.

[42916] The function of SERPINB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM88.2.Sh3-domain binding protein 2 (SH3BP2, Accession NP_003014.2) is another GAM2071 target gene,

herein designated TARGET GENE. SH3BP2 BINDING SITE1 and SH3BP2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SH3BP2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SH3BP2 BINDING SITE1 and SH3BP2 BINDING SITE2, designated SEQ ID:18716 and SEQ ID:12957 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42917] Another function of GAM2071 is therefore inhibition of Sh3-domain binding protein 2 (SH3BP2, Accession NP_003014.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BP2.

[42918] Sialic acid binding ig-like lectin 8 (SIGLEC8, Accession NP_055257.1) is another GAM2071 target gene, herein designated TARGET GENE. SIGLEC8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIGLEC8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIGLEC8 BIND-

ING SITE, designated SEQ ID:3441, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42919] Another function of GAM2071 is therefore inhibition of Sialic acid binding ig-like lectin 8 (SIGLEC8, Accession NP_055257.1), a gene which is a cell adhesion molecule for postnatal neural development. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIGLEC8.

[42920] The function of SIGLEC8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8, Accession NP_078904.1) is another GAM2071 target gene, herein designated TARGET GENE. SLC12A8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC12A8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC12A8 BINDING SITE, designated SEQ ID:18425, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA,

also designated SEQ ID:371.

[42921] Another function of GAM2071 is therefore inhibition of Solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8, Accession NP_078904.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC12A8.

[42922] Solute carrier family 13 (sodium/sulfate symporters), member 1 (SLC13A1, Accession NP_071889.2) is another GAM2071 target gene, herein designated TARGET GENE. SLC13A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC13A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC13A1 BINDING SITE, designated SEQ ID:15679, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42923] Another function of GAM2071 is therefore inhibition of Solute carrier family 13 (sodium/sulfate symporters), member 1 (SLC13A1, Accession NP_071889.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with SLC13A1.

[42924] Solute carrier family 14 (urea transporter), member 2 (SLC14A2, Accession NP_009094.2) is another GAM2071 target gene, herein designated TARGET GENE. SLC14A2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC14A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC14A2 BINDING SITE, designated SEQ ID:18700, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42925] Another function of GAM2071 is therefore inhibition of Solute carrier family 14 (urea transporter), member 2 (SLC14A2, Accession NP_009094.2), a gene which is a renal urea transporter 2. and therefore may be associated with Orthostatic hypotension. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Orthostatic hypotension, and of other diseases and clinical conditions associated with SLC14A2.

[42926] The function of SLC14A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM97.1.Solute carrier family 16 (monocarboxylic acid transporters), member 4 (SLC16A4, Accession NP_004687.1) is another GAM2071 target gene, herein designated TARGET GENE. SLC16A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC16A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A4 BINDING SITE, designated SEQ ID:20157, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42927] Another function of GAM2071 is therefore inhibition of Solute carrier family 16 (monocarboxylic acid transporters), member 4 (SLC16A4, Accession NP_004687.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A4.

[42928] Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) is another GAM2071 target gene, herein designated TARGET GENE. SLC16A6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

SLC16A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A6 BINDING SITE, designated SEQ ID:517, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42929] Another function of GAM2071 is therefore inhibition of Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A6.

[42930] Solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 (SLC25A1, Accession NP_005975.1) is another GAM2071 target gene, herein designated TARGET GENE. SLC25A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC25A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC25A1 BINDING SITE, designated SEQ ID:18982, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA,

also designated SEQ ID:371.

[42931] Another function of GAM2071 is therefore inhibition of Solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 (SLC25A1, Accession NP_005975.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC25A1.

[42932] SLC30A5 (Accession NP_076960.1) is another GAM2071 target gene, herein designated TARGET GENE. SLC30A5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLC30A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC30A5 BINDING SITE, designated SEQ ID:1341, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42933] Another function of GAM2071 is therefore inhibition of SLC30A5 (Accession NP_076960.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC30A5.

[42934] SLC35B2 (Accession NP_835361.1) is another GAM2071 target gene, herein designated TARGET GENE. SLC35B2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLC35B2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC35B2 BINDING SITE, designated SEQ ID:17255, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42935] Another function of GAM2071 is therefore inhibition of SLC35B2 (Accession NP_835361.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35B2.

[42936] SLC35B2 (Accession XP_300918.1) is another GAM2071 target gene, herein designated TARGET GENE. SLC35B2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLC35B2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of SLC35B2 BINDING SITE, designated SEQ ID:17255, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42937] Another function of GAM2071 is therefore inhibition of SLC35B2 (Accession XP_300918.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35B2.

[42938] SLC35E2 (Accession XP_049733.6) is another GAM2071 target gene, herein designated TARGET GENE. SLC35E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC35E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC35E2 BINDING SITE, designated SEQ ID:12300, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42939] Another function of GAM2071 is therefore inhibition of SLC35E2 (Accession XP_049733.6) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

SLC35E2.

[42940] Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2) is another GAM2071 target gene, herein designated TARGET GENE. SLC39A1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC39A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC39A1 BINDING SITE, designated SEQ ID:19430, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42941] Another function of GAM2071 is therefore inhibition of Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2), a gene which is a divalent (zinc/iron) metal ion transporter. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC39A1.

[42942] The function of SLC39A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM175.1.Solute carrier family 4, sodium bicarbonate

cotransporter, member 4 (SLC4A4, Accession NP_003750.1) is another GAM2071 target gene, herein designated TARGET GENE. SLC4A4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC4A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC4A4 BINDING SITE, designated SEQ ID:13075, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42943] Another function of GAM2071 is therefore inhibition of Solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4, Accession NP_003750.1), a gene which is a sodium bicarbonate cotransporter and therefore may be associated with Proximal renal tubular acidosis, mental retardation, and bilateral glaucoma, cataracts, and band keratopathy. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Proximal renal tubular acidosis, mental retardation, and bilateral glaucoma, cataracts, and band keratopathy, and of other diseases and clinical conditions associated with SLC4A4.

[42944] The function of SLC4A4 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14, Accession NP_009162.1) is another GAM2071 target gene, herein designated TARGET GENE. SLC6A14 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC6A14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC6A14 BINDING SITE, designated SEQ ID:16741, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42945] Another function of GAM2071 is therefore inhibition of Solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14, Accession NP_009162.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A14.

[42946] SMAC (Accession NP_620308.1) is another GAM2071 target gene, herein designated TARGET GENE. SMAC BINDING SITE1 and SMAC BINDING SITE2 are target binding sites

found in untranslated regions of multiple transcripts of mRNA encoded by SMAC, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMAC BINDING SITE1 and SMAC BINDING SITE2, designated SEQ ID:1245 and SEQ ID:15275 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42947] Another function of GAM2071 is therefore inhibition of SMAC (Accession NP_620308.1), a gene which promotes apoptosis via caspase activation. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMAC.

[42948] The function of SMAC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Synaptosomal-associated protein, 25kda (SNAP25, Accession NP_570824.1) is another GAM2071 target gene, herein designated TARGET GENE. SNAP25 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNAP25, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP25 BINDING SITE, designated SEQ ID:8525, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42949] Another function of GAM2071 is therefore inhibition of Synaptosomal-associated protein, 25kda (SNAP25, Accession NP_570824.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP25.

[42950] Synaptosomal-associated protein, 25kda (SNAP25, Accession NP_003072.2) is another GAM2071 target gene, herein designated TARGET GENE. SNAP25 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNAP25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP25 BINDING SITE, designated SEQ ID:8525, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42951] Another function of GAM2071 is therefore inhibition of

Synaptosomal-associated protein, 25kda (SNAP25, Accession NP_003072.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP25.

[42952] Syntaphilin (SNPH, Accession NP_055538.1) is another GAM2071 target gene, herein designated TARGET GENE. SNPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNPH BINDING SITE, designated SEQ ID:1354, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42953] Another function of GAM2071 is therefore inhibition of Syntaphilin (SNPH, Accession NP_055538.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNPH.

[42954] Sorting nexin 15 (SNX15, Accession NP_680086.1) is another GAM2071 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of

mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:2728, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42955] Another function of GAM2071 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NP_680086.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15.

[42956] Sorting nexin 15 (SNX15, Accession NP_037438.2) is another GAM2071 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:2728, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42957] Another function of GAM2071 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NP_037438.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15.

[42958] SNX27 (Accession NP_112180.4) is another GAM2071 target gene, herein designated TARGET GENE. SNX27 BINDING SITE1 and SNX27 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SNX27, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX27 BINDING SITE1 and SNX27 BINDING SITE2, designated SEQ ID:8857 and SEQ ID:1972 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42959] Another function of GAM2071 is therefore inhibition of SNX27 (Accession NP_112180.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX27.

[42960] Sry (sex determining region y)-box 8 (SOX8, Accession NP_055402.2) is another GAM2071 target gene, herein

designated TARGET GENE. SOX8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SOX8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SOX8 BINDING SITE, designated SEQ ID:12214, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42961] Another function of GAM2071 is therefore inhibition of Sry (sex determining region y)-box 8 (SOX8, Accession NP_055402.2), a gene which binds the consensus motif 5'- [at][at]caa[at]g- 3'. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX8.

[42962] The function of SOX8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM842.1.Sialophorin (gpl115, leukosialin, cd43) (SPN, Accession NP_003114.1) is another GAM2071 target gene, herein designated TARGET GENE. SPN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SPN, corresponding to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPN BINDING SITE, designated SEQ ID:19300, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42963] Another function of GAM2071 is therefore inhibition of Sialophorin (gpl115, leukosialin, cd43) (SPN, Accession NP_003114.1), a gene which plays a role in the physico-chemical properties of the t- cell surface and in lectin binding. presents carbohydrate ligands to selectins. . and therefore may be associated with Wiskott- aldrich syndrome. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Wiskott- aldrich syndrome, and of other diseases and clinical conditions associated with SPN.

[42964] The function of SPN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Speckle-type poz protein (SPOP, Accession NP_003554.1) is another GAM2071 target gene, herein designated TARGET GENE. SPOP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA

encoded by SPOP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPOP BINDING SITE, designated SEQ ID:7212, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42965] Another function of GAM2071 is therefore inhibition of Speckle-type poz protein (SPOP, Accession NP_003554.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPOP.

[42966] Scavenger receptor cysteine rich domain containing, group b (4 domains) (SRCRB4D, Accession NP_542782.1) is another GAM2071 target gene, herein designated TARGET GENE. SRCRB4D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SRCRB4D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRCRB4D BINDING SITE, designated SEQ ID:19630, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ

ID:371.

[42967] Another function of GAM2071 is therefore inhibition of Scavenger receptor cysteine rich domain containing, group b (4 domains) (SRCRB4D, Accession NP_542782.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRCRB4D.

[42968] Sarcalumenin (SRL, Accession XP_064152.3) is another GAM2071 target gene, herein designated TARGET GENE. SRL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SRL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRL BINDING SITE, designated SEQ ID:9910, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42969] Another function of GAM2071 is therefore inhibition of Sarcalumenin (SRL, Accession XP_064152.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRL.

[42970] Synovial sarcoma translocation, chromosome 18 (SS18,

Accession NP_005628.1) is another GAM2071 target gene, herein designated TARGET GENE. SS18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SS18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SS18 BINDING SITE, designated SEQ ID:10975, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42971] Another function of GAM2071 is therefore inhibition of Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1), a gene which is a putative transcriptional activator. and therefore is associated with Human synovial sarcomas. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Human synovial sarcomas., and of other diseases and clinical conditions associated with SS18.

[42972] The function of SS18 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.STAF65(gamma) (Accession NP_055675.1) is another GAM2071 target gene, herein designated TARGET

GENE. STAF65(gamma) BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STAF65(gamma), corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAF65(gamma) BINDING SITE, designated SEQ ID:6743, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42973] Another function of GAM2071 is therefore inhibition of STAF65(gamma) (Accession NP_055675.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAF65(gamma).

[42974] Signal transducing adaptor molecule (sh3 domain and itam motif) 2 (STAM2, Accession NP_005834.3) is another GAM2071 target gene, herein designated TARGET GENE. STAM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STAM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAM2 BINDING SITE, designated SEQ ID:5920, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42975] Another function of GAM2071 is therefore inhibition of Signal transducing adaptor molecule (sh3 domain and itam motif) 2 (STAM2, Accession NP_005834.3) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAM2.

[42976] Staufen, rna binding protein (drosophila) (STAU, Accession NP_004593.1) is another GAM2071 target gene, herein designated TARGET GENE. STAU BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by STAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAU BINDING SITE, designated SEQ ID:9365, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42977] Another function of GAM2071 is therefore inhibition of Staufen, rna binding protein (drosophila) (STAU, Accession NP_004593.1), a gene which may play a role in specific positioning of mrnas at given sites in the cell and in stim-

ulating their translation at the site. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAU.

[42978] The function of STAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM37.1.Six transmembrane epithelial antigen of prostate 2 (STEAP2, Accession NP_694544.1) is another GAM2071 target gene, herein designated TARGET GENE. STEAP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STEAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STEAP2 BINDING SITE, designated SEQ ID:1413, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42979] Another function of GAM2071 is therefore inhibition of Six transmembrane epithelial antigen of prostate 2 (STEAP2, Accession NP_694544.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STEAP2.

[42980] Syntaxin binding protein 6 (amisyn) (STXBP6, Accession NP_054897.4) is another GAM2071 target gene, herein designated TARGET GENE. STXBP6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by STXBP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STXBP6 BINDING SITE, designated SEQ ID:11916, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42981] Another function of GAM2071 is therefore inhibition of Syntaxin binding protein 6 (amisyn) (STXBP6, Accession NP_054897.4) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STXBP6.

[42982] Synaptotagmin xii (SYT12, Accession NP_808878.1) is another GAM2071 target gene, herein designated TARGET GENE. SYT12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYT12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of SYT12 BINDING SITE, designated SEQ ID:3730, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42983] Another function of GAM2071 is therefore inhibition of Synaptotagmin xii (SYT12, Accession NP_808878.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT12.

[42984] Synaptotagmin xiii (SYT13, Accession NP_065877.1) is another GAM2071 target gene, herein designated TARGET GENE. SYT13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYT13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYT13 BINDING SITE, designated SEQ ID:19065, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42985] Another function of GAM2071 is therefore inhibition of Synaptotagmin xiii (SYT13, Accession NP_065877.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT13.

[42986] TADA3L (Accession NP_597814.1) is another GAM2071 target gene, herein designated TARGET GENE. TADA3L BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TADA3L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TADA3L BINDING SITE, designated SEQ ID:10415, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42987] Another function of GAM2071 is therefore inhibition of TADA3L (Accession NP_597814.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TADA3L.

[42988] Taf11 rna polymerase ii, tata box binding protein (tbp)-associated factor, 28kda (TAF11, Accession NP_005634.1) is another GAM2071 target gene, herein designated TARGET GENE. TAF11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TAF11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAF11 BINDING SITE, designated SEQ ID:17432, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42989] Another function of GAM2071 is therefore inhibition of Taf11 rna polymerase ii, tata box binding protein (tbp)-associated factor, 28kda (TAF11, Accession NP_005634.1), a gene which plays a central role in mediating promoter responses to various activators and repressors. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAF11.

[42990] The function of TAF11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Tap binding protein (tapasin) (TAPBP, Accession NP_003181.3) is another GAM2071 target gene, herein designated TARGET GENE. TAPBP BINDING SITE1 through TAPBP BINDING SITE3 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TAPBP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAPBP BINDING SITE1 through TAPBP BINDING SITE3, designated SEQ ID:8861, SEQ ID:6086 and SEQ ID:3109 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42991] Another function of GAM2071 is therefore inhibition of Tap binding protein (tapasin) (TAPBP, Accession NP_003181.3), a gene which is involved in MHC class I-restricted antigen processing. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAPBP.

[42992] The function of TAPBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Tyrosine aminotransferase (TAT, Accession NP_000344.1) is another GAM2071 target gene, herein designated TARGET GENE. TAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAT BINDING SITE, designated

SEQ ID:20161, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42993] Another function of GAM2071 is therefore inhibition of Tyrosine aminotransferase (TAT, Accession NP_000344.1), a gene which is tyrosine aminotransferase and strongly similar to rat Rn.9947, which plays a role in gluconeogenesis. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAT.

[42994] The function of TAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Tbc1 domain family, member 5 (TBC1D5, Accession NP_055559.1) is another GAM2071 target gene, herein designated TARGET GENE. TBC1D5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TBC1D5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TBC1D5 BINDING SITE, designated SEQ ID:12382, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA,

also designated SEQ ID:371.

[42995] Another function of GAM2071 is therefore inhibition of Tbc1 domain family, member 5 (TBC1D5, Accession NP_055559.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBC1D5.

[42996] Transcription factor 2, hepatic; lf-b3; variant hepatic nuclear factor (TCF2, Accession NP_006472.1) is another GAM2071 target gene, herein designated TARGET GENE. TCF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TCF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCF2 BINDING SITE, designated SEQ ID:401, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42997] Another function of GAM2071 is therefore inhibition of Transcription factor 2, hepatic; lf-b3; variant hepatic nuclear factor (TCF2, Accession NP_006472.1), a gene which probably binds to the inverted palindrome 5'- gttaatnattaac- 3'. and therefore is associated with Maturity- onset diabetes of the young type 5 (mody5), familial hypoplastic

glomerulocystic kidney disease (gckd). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Maturity- onset diabetes of the young type 5 (mody5), familial hypoplastic glomerulocystic kidney disease (gckd), and of other diseases and clinical conditions associated with TCF2.

[42998] The function of TCF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.Teratocarcinoma-derived growth factor 1 (TDGF1, Accession NP_003203.1) is another GAM2071 target gene, herein designated TARGET GENE. TDGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TDGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TDGF1 BINDING SITE, designated SEQ ID:10005, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[42999] Another function of GAM2071 is therefore inhibition of Teratocarcinoma-derived growth factor 1 (TDGF1, Accession NP_003203.1), a gene which can play a role in the

determination of the epiblastic cells that subsequently give rise to the mesoderm. and therefore may be associated with Forebrain defects. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Forebrain defects, and of other diseases and clinical conditions associated with TDGF1.

[43000] The function of TDGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.TERA (Accession NP_067061.1) is another GAM2071 target gene, herein designated TARGET GENE. TERA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TERA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERA BINDING SITE, designated SEQ ID:971, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43001] Another function of GAM2071 is therefore inhibition of TERA (Accession NP_067061.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERA.

[43002] Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_059523.1) is another GAM2071 target gene, herein designated TARGET GENE. TERF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TERF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF1 BINDING SITE, designated SEQ ID:13870, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43003] Another function of GAM2071 is therefore inhibition of Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_059523.1), a gene which negatively regulates telomere length, involves in regulation of the mitotic spindle. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF1.

[43004] The function of TERF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Telomeric repeat binding factor

(nima-interacting) 1 (TERF1, Accession NP_003209.1) is another GAM2071 target gene, herein designated TARGET GENE. TERF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TERF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF1 BINDING SITE, designated SEQ ID:13870, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43005] Another function of GAM2071 is therefore inhibition of Telomeric repeat binding factor (nima-interacting) 1 (TERF1, Accession NP_003209.1), a gene which negatively regulates telomere length, involves in regulation of the mitotic spindle. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF1.

[43006] The function of TERF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Telomeric repeat binding factor 2 (TERF2, Accession NP_005643.1) is another GAM2071 target gene,

herein designated TARGET GENE. TERF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TERF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF2 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43007] Another function of GAM2071 is therefore inhibition of Telomeric repeat binding factor 2 (TERF2, Accession NP_005643.1), a gene which plays a key role in the protective activity of telomeres. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF2.

[43008] The function of TERF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM133.2.Transforming growth factor, beta receptor iii (betaglycan, 300kda) (TGFBR3, Accession NP_003234.1) is another GAM2071 target gene, herein designated TARGET GENE. TGFBR3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

TGFBR3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGFBR3 BINDING SITE, designated SEQ ID:4831, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43009] Another function of GAM2071 is therefore inhibition of Transforming growth factor, beta receptor iii (betaglycan, 300kda) (TGFBR3, Accession NP_003234.1), a gene which involves in capturing and retaining TGF- beta for presentation to the signaling receptors. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFBR3.

[43010] The function of TGFBR3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) is another GAM2071 target gene, herein designated TARGET GENE. TGIF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGIF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGIF2 BINDING SITE, designated SEQ ID:7274, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43011] Another function of GAM2071 is therefore inhibition of Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGIF2.

[43012] Transmembrane, cochlear expressed, 1 (TMC1, Accession NP_619636.2) is another GAM2071 target gene, herein designated TARGET GENE. TMC1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TMC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMC1 BINDING SITE, designated SEQ ID:19429, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43013] Another function of GAM2071 is therefore inhibition of Transmembrane, cochlear expressed, 1 (TMC1, Accession

NP_619636.2), a gene which is required for normal function of cochlear hair cells and therefore may be associated with Autosomal recessive nonsyndromic neurosensory deafness and autosomal dominant nonsyndromic sensorineural hearing loss . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Autosomal recessive nonsyndromic neurosensory deafness and autosomal dominant nonsyndromic sensorineural hearing loss ., and of other diseases and clinical conditions associated with TMC1.

[43014] The function of TMC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.TMEM14A (Accession NP_054770.1) is another GAM2071 target gene, herein designated TARGET GENE. TMEM14A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TMEM14A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMEM14A BINDING SITE, designated SEQ ID:7622, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ

ID:371.

[43015] Another function of GAM2071 is therefore inhibition of TMEM14A (Accession NP_054770.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEM14A.

[43016] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_076927.1) is another GAM2071 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE, designated SEQ ID:15133, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43017] Another function of GAM2071 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_076927.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[43018] Transmembrane protease, serine 3 (TMPRSS3, Accession

NP_115777.1) is another GAM2071 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE, designated SEQ ID:15133, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43019] Another function of GAM2071 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115777.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[43020] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115780.1) is another GAM2071 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

TMPRSS3 BINDING SITE, designated SEQ ID:15133, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43021] Another function of GAM2071 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115780.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[43022] Tumor necrosis factor, alpha-induced protein 2 (TNFAIP2, Accession NP_006282.2) is another GAM2071 target gene, herein designated TARGET GENE. TNFAIP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFAIP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFAIP2 BINDING SITE, designated SEQ ID:14228, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43023] Another function of GAM2071 is therefore inhibition of Tumor necrosis factor, alpha-induced protein 2 (TNFAIP2, Accession NP_006282.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with TNFAIP2.

[43024] Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_671716.1) is another GAM2071 target gene, herein designated TARGET GENE. TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF10B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2, designated SEQ ID:9933 and SEQ ID:9933 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43025] Another function of GAM2071 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_671716.1), a gene which forms complex that induces apoptosis. and therefore may be associated with Squamous cell carcinoma . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Squamous cell carcinoma ., and of other diseases and clinical conditions associated with TNFRSF10B.

[43026] The function of TNFRSF10B and its association with vari-

ous diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_003833.3) is another GAM2071 target gene, herein designated TARGET GENE. TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF10B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2, designated SEQ ID:14554 and SEQ ID:14554 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43027] Another function of GAM2071 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_003833.3), a gene which forms complex that induces apoptosis. and therefore may be associated with Squamous cell carcinoma . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Squamous cell carcinoma ., and of other diseases

and clinical conditions associated with TNFRSF10B.

[43028] The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tumor necrosis factor receptor superfamily, member 11a, activator of nfkb (TNFRSF11A, Accession NP_003830.1) is another GAM2071 target gene, herein designated TARGET GENE. TNFRSF11A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF11A BINDING SITE, designated SEQ ID:11190, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43029] Another function of GAM2071 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 11a, activator of nfkb (TNFRSF11A, Accession NP_003830.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF11A.

[43030] Tumor necrosis factor receptor superfamily, member 9

(TNFRSF9, Accession NP_001552.2) is another GAM2071 target gene, herein designated TARGET GENE. TNFRSF9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF9 BINDING SITE, designated SEQ ID:438, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43031] Another function of GAM2071 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 9 (TNFRSF9, Accession NP_001552.2), a gene which inhibits proliferation of activated T lymphocytes. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF9.

[43032] The function of TNFRSF9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.TOMM20-PENDING (Accession NP_055580.1) is another GAM2071 target gene, herein designated TARGET GENE. TOMM20-PENDING BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TOMM20-PENDING, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOMM20-PENDING BINDING SITE, designated SEQ ID:11702, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43033] Another function of GAM2071 is therefore inhibition of TOMM20-PENDING (Accession NP_055580.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOMM20-PENDING.

[43034] Torsin family 1, member b (torsin b) (TOR1B, Accession NP_055321.1) is another GAM2071 target gene, herein designated TARGET GENE. TOR1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TOR1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOR1B BINDING SITE, designated SEQ ID:2429, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ

ID:371.

[43035] Another function of GAM2071 is therefore inhibition of Torsin family 1, member b (torsin b) (TOR1B, Accession NP_055321.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOR1B.

[43036] Tumor protein p53 (li-fraumeni syndrome) (TP53, Accession NP_000537.2) is another GAM2071 target gene, herein designated TARGET GENE. TP53 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TP53, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TP53 BINDING SITE, designated SEQ ID:2118, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43037] Another function of GAM2071 is therefore inhibition of Tumor protein p53 (li-fraumeni syndrome) (TP53, Accession NP_000537.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53.

[43038] Thiopurine s-methyltransferase (TPMT, Accession

NP_000358.1) is another GAM2071 target gene, herein designated TARGET GENE. TPMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TPMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPMT BINDING SITE, designated SEQ ID:10218, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43039] Another function of GAM2071 is therefore inhibition of Thiopurine s-methyltransferase (TPMT, Accession NP_000358.1), a gene which catalyzes the s- methylation of thiopurine drugs such as 6- mercaptopurine. and therefore may be associated with Thiopurine s- methyl-transferase polymorphism. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Thiopurine s- methyltransferase polymorphism, and of other diseases and clinical conditions associated with TPMT.

[43040] The function of TPMT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM130.1.Tnf receptor-associated factor 5 (TRAF5, Accession NP_665702.1) is another GAM2071 target gene, herein designated TARGET GENE. TRAF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRAF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:10175, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43041] Another function of GAM2071 is therefore inhibition of Tnf receptor-associated factor 5 (TRAF5, Accession NP_665702.1), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5.

[43042] The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Tnf receptor-associated factor 5 (TRAF5, Accession NP_004610.1) is another GAM2071 target gene,

herein designated TARGET GENE. TRAF5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRAF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:10175, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43043] Another function of GAM2071 is therefore inhibition of Tnf receptor-associated factor 5 (TRAF5, Accession NP_004610.1), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5.

[43044] The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Tripartite motif-containing 6 (TRIM6, Accession NP_477514.1) is another GAM2071 target gene, herein designated TARGET GENE. TRIM6 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by TRIM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM6 BINDING SITE, designated SEQ ID:13974, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43045] Another function of GAM2071 is therefore inhibition of Tripartite motif-containing 6 (TRIM6, Accession NP_477514.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM6.

[43046] Transient receptor potential cation channel, subfamily m, member 6 (TRPM6, Accession NP_060132.3) is another GAM2071 target gene, herein designated TARGET GENE. TRPM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPM6 BINDING SITE, designated SEQ ID:1713, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43047] Another function of GAM2071 is therefore inhibition of Transient receptor potential cation channel, subfamily m, member 6 (TRPM6, Accession NP_060132.3), a gene which contains a predicted ion channel domain and a protein kinase domain. and therefore is associated with Hypomagnesemia with secondary hypocalcemia. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Hypomagnesemia with secondary hypocalcemia, and of other diseases and clinical conditions associated with TRPM6.

[43048] The function of TRPM6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_061197.3) is another GAM2071 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING

SITE2, designated SEQ ID:15897 and SEQ ID:1587 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43049] Another function of GAM2071 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_061197.3), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[43050] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542437.1) is another GAM2071 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:1587 and SEQ ID:15897 respec-

tively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43051] Another function of GAM2071 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542437.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[43052] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542435.1) is another GAM2071 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:1587 and SEQ ID:15897 respectively, to the nucleotide sequence of GAM2071 RNA,

herein designated GAM RNA, also designated SEQ ID:371.

[43053] Another function of GAM2071 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542435.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[43054] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542435.1) is another GAM2071 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:15897 and SEQ ID:1587 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43055] Another function of GAM2071 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542435.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[43056] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.TSARG1 (Accession NP_620712.2) is another GAM2071 target gene, herein designated TARGET GENE. TSARG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSARG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TSARG1 BINDING SITE, designated SEQ ID:15069, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43057] Another function of GAM2071 is therefore inhibition of TSARG1 (Accession NP_620712.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

TSARG1.

[43058] Tspy-like (TSPYL, Accession XP_166325.1) is another GAM2071 target gene, herein designated TARGET GENE. TSPYL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSPYL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TSPYL BINDING SITE, designated SEQ ID:9101, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43059] Another function of GAM2071 is therefore inhibition of Tspy-like (TSPYL, Accession XP_166325.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSPYL.

[43060] TU12B1-TY (Accession NP_057659.1) is another GAM2071 target gene, herein designated TARGET GENE. TU12B1-TY BINDING SITE1 and TU12B1-TY BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TU12B1-TY, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of TU12B1-TY BINDING SITE1 and TU12B1-TY BINDING SITE2, designated SEQ ID:17849 and SEQ ID:12270 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43061] Another function of GAM2071 is therefore inhibition of TU12B1-TY (Accession NP_057659.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TU12B1-TY.

[43062] TUCAN (Accession NP_055774.1) is another GAM2071 target gene, herein designated TARGET GENE. TUCAN BINDING SITE1 and TUCAN BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by TUCAN, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUCAN BINDING SITE1 and TUCAN BINDING SITE2, designated SEQ ID:2265 and SEQ ID:10630 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43063] Another function of GAM2071 is therefore inhibition of

TUCAN (Accession NP_055774.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUCAN.

[43064] Tuftelin 1 (TUFT1, Accession NP_064512.1) is another GAM2071 target gene, herein designated TARGET GENE. TUFT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TUFT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUFT1 BINDING SITE, designated SEQ ID:19342, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43065] Another function of GAM2071 is therefore inhibition of Tuftelin 1 (TUFT1, Accession NP_064512.1), a gene which appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and capping. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUFT1.

[43066] The function of TUFT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM136.1.Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) is another GAM2071 target gene, herein designated TARGET GENE. TXNL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TXNL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TXNL2 BINDING SITE, designated SEQ ID:1413, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43067] Another function of GAM2071 is therefore inhibition of Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TXNL2.

[43068] Ubiquitin associated protein 2 (UBAP2, Accession NP_680476.1) is another GAM2071 target gene, herein designated TARGET GENE. UBAP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UBAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates

the complementarity of the nucleotide sequences of UBAP2 BINDING SITE, designated SEQ ID:5122, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43069] Another function of GAM2071 is therefore inhibition of Ubiquitin associated protein 2 (UBAP2, Accession NP_680476.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBAP2.

[43070] Ubiquitin associated protein 2 (UBAP2, Accession NP_060919.2) is another GAM2071 target gene, herein designated TARGET GENE. UBAP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UBAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBAP2 BINDING SITE, designated SEQ ID:5122, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43071] Another function of GAM2071 is therefore inhibition of Ubiquitin associated protein 2 (UBAP2, Accession NP_060919.2) . Accordingly, utilities of GAM2071 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with UBAP2.

[43072] Ubiquitin associated protein 2 (UBAP2, Accession NP_065918.1) is another GAM2071 target gene, herein designated TARGET GENE. UBAP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UBAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBAP2 BINDING SITE, designated SEQ ID:5122, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43073] Another function of GAM2071 is therefore inhibition of Ubiquitin associated protein 2 (UBAP2, Accession NP_065918.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBAP2.

[43074] UBF-fl (Accession NP_116217.1) is another GAM2071 target gene, herein designated TARGET GENE. UBF-fl BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBF-fl, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBF-fl BINDING SITE, designated SEQ ID:17229, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43075] Another function of GAM2071 is therefore inhibition of UBF-fl (Accession NP_116217.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBF-fl.

[43076] Udp-glucose dehydrogenase (UGDH, Accession NP_003350.1) is another GAM2071 target gene, herein designated TARGET GENE. UGDH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UGDH BINDING SITE, designated SEQ ID:12092, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43077] Another function of GAM2071 is therefore inhibition of Udp-glucose dehydrogenase (UGDH, Accession NP_003350.1), a gene which is an UDP- glucose dehydro-

genase. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGDH.

[43078] The function of UGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS, Accession NP_000364.1) is another GAM2071 target gene, herein designated TARGET GENE. UMPS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UMPS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UMPS BINDING SITE, designated SEQ ID:19428, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43079] Another function of GAM2071 is therefore inhibition of Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS, Accession NP_000364.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with UMPS.

[43080] Uracil-dna glycosylase 2 (UNG2, Accession NP_066970.1) is another GAM2071 target gene, herein designated TARGET GENE. UNG2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UNG2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UNG2 BINDING SITE, designated SEQ ID:10716, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43081] Another function of GAM2071 is therefore inhibition of Uracil-dna glycosylase 2 (UNG2, Accession NP_066970.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNG2.

[43082] Ubiquitin specific protease 22 (USP22, Accession XP_042698.2) is another GAM2071 target gene, herein designated TARGET GENE. USP22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by USP22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of USP22 BINDING SITE, designated SEQ ID:20055, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43083] Another function of GAM2071 is therefore inhibition of Ubiquitin specific protease 22 (USP22, Accession XP_042698.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP22.

[43084] VDU1 (Accession NP_055832.2) is another GAM2071 target gene, herein designated TARGET GENE. VDU1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VDU1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VDU1 BINDING SITE, designated SEQ ID:794, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43085] Another function of GAM2071 is therefore inhibition of VDU1 (Accession NP_055832.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VDU1.

[43086] Vent-like homeobox 2 (VENTX2, Accession NP_055283.1) is another GAM2071 target gene, herein designated TARGET GENE. VENTX2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VENTX2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VENTX2 BINDING SITE, designated SEQ ID:13003, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43087] Another function of GAM2071 is therefore inhibition of Vent-like homeobox 2 (VENTX2, Accession NP_055283.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VENTX2.

[43088] Von hippel-lindau syndrome (VHL, Accession NP_000542.1) is another GAM2071 target gene, herein designated TARGET GENE. VHL BINDING SITE1 and VHL BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by VHL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of VHL BINDING SITE1 and VHL BINDING SITE2, designated SEQ ID:19946 and SEQ ID:969 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43089] Another function of GAM2071 is therefore inhibition of Von hippel-lindau syndrome (VHL, Accession NP_000542.1), a gene which may control rna stability through the selective degradation of rna- bound proteins. and therefore is associated with Von hippel- lindau disease. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Von hippel- lindau disease, and of other diseases and clinical conditions associated with VHL.

[43090] The function of VHL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Vasoactive intestinal peptide receptor 2 (VIPR2, Accession NP_003373.2) is another GAM2071 target gene, herein designated TARGET GENE. VIPR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VIPR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VIPR2 BINDING SITE, designated SEQ ID:861, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43091] Another function of GAM2071 is therefore inhibition of Vasoactive intestinal peptide receptor 2 (VIPR2, Accession NP_003373.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIPR2.

[43092] Vacuolar protein sorting 33a (yeast) (VPS33A, Accession NP_075067.2) is another GAM2071 target gene, herein designated TARGET GENE. VPS33A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VPS33A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VPS33A BINDING SITE, designated SEQ ID:4137, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43093] Another function of GAM2071 is therefore inhibition of Vacuolar protein sorting 33a (yeast) (VPS33A, Accession

NP_075067.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS33A.

[43094] Vesicle transport through interaction with t-snares homolog 1a (yeast) (VTI1A, Accession NP_660207.1) is another GAM2071 target gene, herein designated TARGET GENE. VTI1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VTI1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VTI1A BINDING SITE, designated SEQ ID:1472, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43095] Another function of GAM2071 is therefore inhibition of Vesicle transport through interaction with t-snares homolog 1a (yeast) (VTI1A, Accession NP_660207.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VTI1A.

[43096] Williams beuren syndrome chromosome region 18 (WBSCR18, Accession NP_115693.2) is another GAM2071 target gene, herein designated TARGET GENE. WBSCR18

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WBSCR18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR18 BINDING SITE, designated SEQ ID:10631, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43097] Another function of GAM2071 is therefore inhibition of Williams beuren syndrome chromosome region 18 (WBSCR18, Accession NP_115693.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR18.

[43098] Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_579889.1) is another GAM2071 target gene, herein designated TARGET GENE. WHSC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WHSC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE, designated SEQ ID:12602, to the

nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43099] Another function of GAM2071 is therefore inhibition of Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_579889.1), a gene which binds covalently to and repairs g/t mismatches. and therefore may be associated with Wolf- hirschhorn syndrome. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of Wolf- hirschhorn syndrome, and of other diseases and clinical conditions associated with WHSC1.

[43100] The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Wnt1 inducible signaling pathway protein 1 (WISP1, Accession NP_003873.1) is another GAM2071 target gene, herein designated TARGET GENE. WISP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WISP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WISP1 BINDING SITE, designated SEQ ID:6051, to the nucleotide sequence of GAM2071 RNA, herein des-

ignated GAM RNA, also designated SEQ ID:371.

[43101] Another function of GAM2071 is therefore inhibition of Wnt1 inducible signaling pathway protein 1 (WISP1, Accession NP_003873.1), a gene which is a member of connective tissue growth factor family. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WISP1.

[43102] The function of WISP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM629.1.X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1) is another GAM2071 target gene, herein designated TARGET GENE. XRCC2 BINDING SITE1 and XRCC2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by XRCC2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of XRCC2 BINDING SITE1 and XRCC2 BINDING SITE2, designated SEQ ID:19967 and SEQ ID:6034 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43103] Another function of GAM2071 is therefore inhibition of X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1), a gene which involves in the homologous recombination repair (hrr) pathway of double- stranded dna. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XRCC2.

[43104] The function of XRCC2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.V-yes-1 yamaguchi sarcoma viral oncogene homolog 1 (YES1, Accession NP_005424.1) is another GAM2071 target gene, herein designated TARGET GENE. YES1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by YES1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of YES1 BINDING SITE, designated SEQ ID:18699, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43105] Another function of GAM2071 is therefore inhibition of V-

yes-1 yamaguchi sarcoma viral oncogene homolog 1 (YES1, Accession NP_005424.1), a gene which is a putative protein- tyrosine kinase. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YES1.

[43106] The function of YES1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.ZAP (Accession NP_064504.2) is another GAM2071 target gene, herein designated TARGET GENE. ZAP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAP BINDING SITE, designated SEQ ID:19083, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43107] Another function of GAM2071 is therefore inhibition of ZAP (Accession NP_064504.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAP.

[43108] ZFP42 (Accession NP_777560.1) is another GAM2071 tar-

get gene, herein designated TARGET GENE. ZFP42 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZFP42, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP42 BINDING SITE, designated SEQ ID:6576, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43109] Another function of GAM2071 is therefore inhibition of ZFP42 (Accession NP_777560.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP42.

[43110] Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_060667.1) is another GAM2071 target gene, herein designated TARGET GENE. ZFP64 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP64, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP64 BINDING SITE, designated SEQ ID:13869, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA,

also designated SEQ ID:371.

[43111] Another function of GAM2071 is therefore inhibition of Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_060667.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP64.

[43112] Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_071371.2) is another GAM2071 target gene, herein designated TARGET GENE. ZFP64 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP64, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP64 BINDING SITE, designated SEQ ID:13869, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43113] Another function of GAM2071 is therefore inhibition of Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_071371.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP64.

[43114] ZMYND17 (Accession NP_848546.1) is another GAM2071

target gene, herein designated TARGET GENE. ZMYND17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZMYND17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZMYND17 BINDING SITE, designated SEQ ID:11022, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43115] Another function of GAM2071 is therefore inhibition of ZMYND17 (Accession NP_848546.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZMYND17.

[43116] Zinc finger protein 253 (ZNF253, Accession NP_066385.1) is another GAM2071 target gene, herein designated TARGET GENE. ZNF253 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF253, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF253 BINDING SITE, designated SEQ ID:12223, to the nucleotide sequence of GAM2071

RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43117] Another function of GAM2071 is therefore inhibition of Zinc finger protein 253 (ZNF253, Accession NP_066385.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF253.

[43118] Zinc finger protein 264 (ZNF264, Accession NP_003408.1) is another GAM2071 target gene, herein designated TARGET GENE. ZNF264 BINDING SITE1 and ZNF264 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ZNF264, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF264 BINDING SITE1 and ZNF264 BINDING SITE2, designated SEQ ID:438 and SEQ ID:15406 respectively, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43119] Another function of GAM2071 is therefore inhibition of Zinc finger protein 264 (ZNF264, Accession NP_003408.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with ZNF264.

[43120] Zinc finger protein 302 (ZNF302, Accession NP_061145.1) is another GAM2071 target gene, herein designated TARGET GENE. ZNF302 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZNF302, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF302 BINDING SITE, designated SEQ ID:19157, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43121] Another function of GAM2071 is therefore inhibition of Zinc finger protein 302 (ZNF302, Accession NP_061145.1). Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF302.

[43122] Zinc finger protein 302 (ZNF302, Accession NP_060913.1) is another GAM2071 target gene, herein designated TARGET GENE. ZNF302 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZNF302, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF302 BINDING SITE, designated SEQ ID:19157, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43123] Another function of GAM2071 is therefore inhibition of Zinc finger protein 302 (ZNF302, Accession NP_060913.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF302.

[43124] Zinc finger protein 305 (ZNF305, Accession NP_055539.1) is another GAM2071 target gene, herein designated TARGET GENE. ZNF305 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF305, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF305 BINDING SITE, designated SEQ ID:10363, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43125] Another function of GAM2071 is therefore inhibition of Zinc finger protein 305 (ZNF305, Accession NP_055539.1)

. Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF305.

[43126] Zinc finger protein 334 (ZNF334, Accession NP_060572.2) is another GAM2071 target gene, herein designated TARGET GENE. ZNF334 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZNF334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF334 BINDING SITE, designated SEQ ID:7143, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43127] Another function of GAM2071 is therefore inhibition of Zinc finger protein 334 (ZNF334, Accession NP_060572.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF334.

[43128] Zinc finger protein 339 (ZNF339, Accession NP_067043.1) is another GAM2071 target gene, herein designated TARGET GENE. ZNF339 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

ZNF339, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF339 BINDING SITE, designated SEQ ID:9097, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43129] Another function of GAM2071 is therefore inhibition of Zinc finger protein 339 (ZNF339, Accession NP_067043.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF339.

[43130] Zinc finger protein 345 (ZNF345, Accession NP_003410.1) is another GAM2071 target gene, herein designated TARGET GENE. ZNF345 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF345, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF345 BINDING SITE, designated SEQ ID:11758, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43131] Another function of GAM2071 is therefore inhibition of Zinc finger protein 345 (ZNF345, Accession NP_003410.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF345.

[43132] ZNF431 (Accession XP_086098.2) is another GAM2071 target gene, herein designated TARGET GENE. ZNF431 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF431, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF431 BINDING SITE, designated SEQ ID:9382, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43133] Another function of GAM2071 is therefore inhibition of ZNF431 (Accession XP_086098.2) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF431.

[43134] ZNF440 (Accession NP_689570.1) is another GAM2071 target gene, herein designated TARGET GENE. ZNF440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF440, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF440 BINDING SITE, designated SEQ ID:11659, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43135] Another function of GAM2071 is therefore inhibition of ZNF440 (Accession NP_689570.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF440.

[43136] ZNF450 (Accession NP_055612.1) is another GAM2071 target gene, herein designated TARGET GENE. ZNF450 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF450, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF450 BINDING SITE, designated SEQ ID:13289, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43137] Another function of GAM2071 is therefore inhibition of ZNF450 (Accession NP_055612.1) . Accordingly, utilities

of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF450.

[43138] Zinc finger protein 74 (cos52) (ZNF74, Accession NP_003417.1) is another GAM2071 target gene, herein designated TARGET GENE. ZNF74 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZNF74, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF74 BINDING SITE, designated SEQ ID:2276, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43139] Another function of GAM2071 is therefore inhibition of Zinc finger protein 74 (cos52) (ZNF74, Accession NP_003417.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF74.

[43140] ZSIG11 (Accession NP_057010.1) is another GAM2071 target gene, herein designated TARGET GENE. ZSIG11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZSIG11, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZSIG11 BINDING SITE, designated SEQ ID:13057, to the nucleotide sequence of GAM2071 RNA, herein designated GAM RNA, also designated SEQ ID:371.

[43141] Another function of GAM2071 is therefore inhibition of ZSIG11 (Accession NP_057010.1) . Accordingly, utilities of GAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZSIG11.

[43142]

[43143] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 2608 (GAM2608), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[43144] GAM2608 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM2608 was detected is described hereinabove with reference to Figs. 8-15.

[43145] GAM2608 gene, herein designated GAM GENE, and GAM2608 target gene, herein designated TARGET GENE,

are human genes contained in the human genome.

[43146] GAM2608 gene encodes a GAM2608 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM2608 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM2608 precursor RNA is designated SEQ ID:153, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:153 is located at position 131249166 relative to chromosome X.

[43147] GAM2608 precursor RNA folds onto itself, forming GAM2608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[43148] GAM2608 precursor RNA folds onto itself, forming GAM2608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this

`hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[43149] Nucleotide sequence of GAM2608 precursor RNA, designated SEQ-ID: 153, and a schematic representation of a predicted secondary folding of GAM2608 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[43150] An enzyme complex designated DICER COMPLEX, `dices` the GAM2608 folded precursor RNA into GAM2608 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM2608 RNA is designated SEQ ID:245, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[43151] GAM2608 target gene, herein designated TARGET GENE,

encodes a corresponding messenger RNA, GAM2608 target RNA, herein designated GAM TARGET RNA. GAM2608 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[43152] GAM2608 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM2608 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM2608 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM2608 RNA may have a different number of target binding sites in untranslated regions of a GAM2608 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[43153] The complementary binding of GAM2608 RNA, herein designated GAM RNA, to target binding sites on GAM2608 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM2608 target RNA into GAM2608 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[43154] It is appreciated that GAM2608 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM2608 target genes. The mRNA of each one of this plurality of GAM2608 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM2608 RNA, herein designated GAM RNA, and which when bound by GAM2608 RNA causes inhibition of translation of respective one or more GAM2608 target proteins.

[43155] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM2608 gene, herein designated GAM GENE, on one or more GAM2608 target genes, herein collectively desig-

nated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[43156] It is appreciated that specific functions and accordingly utilities of GAM2608 correlate with, and may be deduced from, the identity of the target genes which GAM2608 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[43157]

[43158]

[43159] Atp-binding cassette, sub-family c (cftr/mrp), member 3 (ABCC3, Accession NP_064422.1) is a GAM2608 target gene, herein designated TARGET GENE. ABCC3 BINDING SITE is a target binding site found in the 3` untranslated

region of multiple transcripts of mRNA encoded by ABCC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCC3 BINDING SITE, designated SEQ ID:19582, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43160] A function of GAM2608 is therefore inhibition of Atp-binding cassette, sub-family c (cftr/mrp), member 3 (ABCC3, Accession NP_064422.1), a gene which may act as an inducible transporter in the biliary and intestinal excretion of organic anions. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC3.

[43161] The function of ABCC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Atp-binding cassette, sub-family c (cftr/mrp), member 3 (ABCC3, Accession NP_064421.1) is another GAM2608 target gene, herein designated TARGET GENE. ABCC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA

encoded by ABCC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCC3 BINDING SITE, designated SEQ ID:19582, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43162] Another function of GAM2608 is therefore inhibition of Atp-binding cassette, sub-family c (cftr/mrp), member 3 (ABCC3, Accession NP_064421.1), a gene which may act as an inducible transporter in the biliary and intestinal excretion of organic anions. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC3.

[43163] The function of ABCC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Atp-binding cassette, sub-family c (cftr/mrp), member 3 (ABCC3, Accession NP_003777.2) is another GAM2608 target gene, herein designated TARGET GENE. ABCC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABCC3, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCC3 BINDING SITE, designated SEQ ID:19582, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43164] Another function of GAM2608 is therefore inhibition of Atp-binding cassette, sub-family c (cftr/mrp), member 3 (ABCC3, Accession NP_003777.2), a gene which may act as an inducible transporter in the biliary and intestinal excretion of organic anions. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC3.

[43165] The function of ABCC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) is another GAM2608 target gene, herein designated TARGET GENE. ATP7A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:10811, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43166] Another function of GAM2608 is therefore inhibition of Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A.

[43167] Beta-site app-cleaving enzyme (BACE, Accession NP_036236.1) is another GAM2608 target gene, herein designated TARGET GENE. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE BINDING SITE, designated SEQ ID:13378, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43168] Another function of GAM2608 is therefore inhibition of Beta-site app-cleaving enzyme (BACE, Accession

NP_036236.1), a gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore may be associated with Alzheimer disease. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of Alzheimer disease, and of other diseases and clinical conditions associated with BACE.

[43169] The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.Beta-site app-cleaving enzyme (BACE, Accession NP_620428.1) is another GAM2608 target gene, herein designated TARGET GENE. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE BINDING SITE, designated SEQ ID:13378, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43170] Another function of GAM2608 is therefore inhibition of Beta-site app-cleaving enzyme (BACE, Accession NP_620428.1), a gene which is responsible for the prote-

olytic processing of the amyloid precursor protein and therefore may be associated with Alzheimer disease. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of Alzheimer disease, and of other diseases and clinical conditions associated with BACE.

[43171] The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.Beta-site app-cleaving enzyme (BACE, Accession NP_620427.1) is another GAM2608 target gene, herein designated TARGET GENE. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE BINDING SITE, designated SEQ ID:13378, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43172] Another function of GAM2608 is therefore inhibition of Beta-site app-cleaving enzyme (BACE, Accession NP_620427.1), a gene which is responsible for the proteolytic processing of the amyloid precursor protein and

therefore may be associated with Alzheimer disease. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of Alzheimer disease, and of other diseases and clinical conditions associated with BACE.

[43173] The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.Beta-site app-cleaving enzyme (BACE, Accession NP_620429.1) is another GAM2608 target gene, herein designated TARGET GENE. BACE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BACE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACE BINDING SITE, designated SEQ ID:13378, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43174] Another function of GAM2608 is therefore inhibition of Beta-site app-cleaving enzyme (BACE, Accession NP_620429.1), a gene which is responsible for the proteolytic processing of the amyloid precursor protein and therefore may be associated with Alzheimer disease. Ac-

cordingly, utilities of GAM2608 include diagnosis, prevention and treatment of Alzheimer disease, and of other diseases and clinical conditions associated with BACE.

[43175] The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.BMF (Accession NP_277038.1) is another GAM2608 target gene, herein designated TARGET GENE. BMF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BMF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BMF BINDING SITE, designated SEQ ID:14471, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43176] Another function of GAM2608 is therefore inhibition of BMF (Accession NP_277038.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMF.

[43177] Camp responsive element binding protein-like 2 (CREBL2, Accession NP_001301.1) is another GAM2608 target gene, herein designated TARGET GENE. CREBL2 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by CREBL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CREBL2 BINDING SITE, designated SEQ ID:10963, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43178] Another function of GAM2608 is therefore inhibition of Camp responsive element binding protein-like 2 (CREBL2, Accession NP_001301.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CREBL2.

[43179] DJ465N24.2.1 (Accession NP_064713.2) is another GAM2608 target gene, herein designated TARGET GENE. DJ465N24.2.1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DJ465N24.2.1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DJ465N24.2.1 BINDING SITE, designated SEQ ID:7651, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:245.

[43180] Another function of GAM2608 is therefore inhibition of DJ465N24.2.1 (Accession NP_064713.2) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DJ465N24.2.1.

[43181] DKFZP586C1619 (Accession NP_665803.1) is another GAM2608 target gene, herein designated TARGET GENE. DKFZP586C1619 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586C1619, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586C1619 BINDING SITE, designated SEQ ID:1283, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43182] Another function of GAM2608 is therefore inhibition of DKFZP586C1619 (Accession NP_665803.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586C1619.

[43183] DMN (Accession NP_056101.4) is another GAM2608 target

gene, herein designated TARGET GENE. DMN BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DMN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DMN BINDING SITE, designated SEQ ID:5539, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43184] Another function of GAM2608 is therefore inhibition of DMN (Accession NP_056101.4), a gene which may participate in maintaining muscle cell integrity. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMN.

[43185] The function of DMN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.DMN (Accession NP_663780.1) is another GAM2608 target gene, herein designated TARGET GENE. DMN BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DMN, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DMN BINDING SITE, designated SEQ ID:5539, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43186] Another function of GAM2608 is therefore inhibition of DMN (Accession NP_663780.1), a gene which may participate in maintaining muscle cell integrity. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMN.

[43187] The function of DMN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Elongation of very long chain fatty acids (fen1/elo2, sur4/elo3, yeast)-like 1 (ELOVL1, Accession NP_073732.1) is another GAM2608 target gene, herein designated TARGET GENE. ELOVL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ELOVL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of ELOVL1 BINDING SITE, designated SEQ ID:11677, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43188] Another function of GAM2608 is therefore inhibition of Elongation of very long chain fatty acids (fen1/elo2, sur4/elo3, yeast)-like 1 (ELOVL1, Accession NP_073732.1). Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELOVL1.

[43189] Endothelial cell-specific molecule 1 (ESM1, Accession NP_008967.1) is another GAM2608 target gene, herein designated TARGET GENE. ESM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ESM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ESM1 BINDING SITE, designated SEQ ID:4688, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43190] Another function of GAM2608 is therefore inhibition of Endothelial cell-specific molecule 1 (ESM1, Accession

NP_008967.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESM1.

[43191] Family with sequence similarity 3, member c (FAM3C, Accession NP_055703.1) is another GAM2608 target gene, herein designated TARGET GENE. FAM3C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FAM3C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FAM3C BINDING SITE, designated SEQ ID:8964, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43192] Another function of GAM2608 is therefore inhibition of Family with sequence similarity 3, member c (FAM3C, Accession NP_055703.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAM3C.

[43193] F-box and leucine-rich repeat protein 3a (FBXL3A, Accession NP_036290.1) is another GAM2608 target gene, herein designated TARGET GENE. FBXL3A BINDING SITE is a target binding site found in the 3` untranslated region

of mRNA encoded by FBXL3A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXL3A BINDING SITE, designated SEQ ID:14877, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43194] Another function of GAM2608 is therefore inhibition of F-box and leucine-rich repeat protein 3a (FBXL3A, Accession NP_036290.1), a gene which is a putative SCF ubiquitin ligase subunit involved in protein degradation. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXL3A.

[43195] The function of FBXL3A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM670.1.FLJ10898 (Accession NP_060733.1) is another GAM2608 target gene, herein designated TARGET GENE. FLJ10898 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10898, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10898 BINDING SITE, designated SEQ ID:16988, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43196] Another function of GAM2608 is therefore inhibition of FLJ10898 (Accession NP_060733.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10898.

[43197] FLJ14810 (Accession NP_116232.2) is another GAM2608 target gene, herein designated TARGET GENE. FLJ14810 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14810, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14810 BINDING SITE, designated SEQ ID:4188, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43198] Another function of GAM2608 is therefore inhibition of FLJ14810 (Accession NP_116232.2) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ14810.

[43199] FLJ14906 (Accession NP_116248.1) is another GAM2608 target gene, herein designated TARGET GENE. FLJ14906 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14906, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14906 BINDING SITE, designated SEQ ID:9840, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43200] Another function of GAM2608 is therefore inhibition of FLJ14906 (Accession NP_116248.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14906.

[43201] FLJ33990 (Accession NP_694958.1) is another GAM2608 target gene, herein designated TARGET GENE. FLJ33990 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33990, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ33990 BINDING SITE, designated SEQ ID:13443, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43202] Another function of GAM2608 is therefore inhibition of FLJ33990 (Accession NP_694958.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33990.

[43203] FLJ39821 (Accession NP_775971.1) is another GAM2608 target gene, herein designated TARGET GENE. FLJ39821 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ39821, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39821 BINDING SITE, designated SEQ ID:12614, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43204] Another function of GAM2608 is therefore inhibition of FLJ39821 (Accession NP_775971.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ39821.

[43205] FLJ40288 (Accession NP_775953.1) is another GAM2608 target gene, herein designated TARGET GENE. FLJ40288 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ40288, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ40288 BINDING SITE, designated SEQ ID:4292, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43206] Another function of GAM2608 is therefore inhibition of FLJ40288 (Accession NP_775953.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ40288.

[43207] FLJ40584 (Accession XP_069189.2) is another GAM2608 target gene, herein designated TARGET GENE. FLJ40584 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ40584, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ40584 BINDING SITE, designated SEQ ID:17085, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43208] Another function of GAM2608 is therefore inhibition of FLJ40584 (Accession XP_069189.2) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ40584.

[43209] Glutaminase (GLS, Accession NP_055720.2) is another GAM2608 target gene, herein designated TARGET GENE. GLS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GLS BINDING SITE, designated SEQ ID:9171, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43210] Another function of GAM2608 is therefore inhibition of Glutaminase (GLS, Accession NP_055720.2) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLS.

[43211] Glutamate receptor, ionotropic, ampa 1 (GRIA1, Accession NP_000818.1) is another GAM2608 target gene, herein designated TARGET GENE. GRIA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRIA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRIA1 BINDING SITE, designated SEQ ID:16531, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43212] Another function of GAM2608 is therefore inhibition of Glutamate receptor, ionotropic, ampa 1 (GRIA1, Accession NP_000818.1), a gene which acts as an excitatory neurotransmitter at many synapses in the central nervous system. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIA1.

[43213] The function of GRIA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM412.1.Heparanase (HPSE, Accession NP_006656.1) is another GAM2608 target gene, herein designated TAR-

GET GENE. HPSE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HPSE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HPSE BINDING SITE, designated SEQ ID:6950, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43214] Another function of GAM2608 is therefore inhibition of Heparanase (HPSE, Accession NP_006656.1), a gene which is an endoglycosidase that cleaves heparan sulfate, and therefore may be associated with Breast cancer. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of Breast cancer, and of other diseases and clinical conditions associated with HPSE.

[43215] The function of HPSE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Inositol 1,4,5-trisphosphate 3-kinase b (ITPKB, Accession NP_002212.1) is another GAM2608 target gene, herein designated TARGET GENE. ITPKB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITPKB, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITPKB BINDING SITE, designated SEQ ID:3880, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43216] Another function of GAM2608 is therefore inhibition of Inositol 1,4,5-trisphosphate 3-kinase b (ITPKB, Accession NP_002212.1), a gene which is a type B inositol 1,4,5-triphosphate 3 kinase. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPKB.

[43217] The function of ITPKB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.KIAA0326 (Accession XP_034819.1) is another GAM2608 target gene, herein designated TARGET GENE. KIAA0326 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0326, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0326 BINDING SITE, designated

SEQ ID:16873, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43218] Another function of GAM2608 is therefore inhibition of KIAA0326 (Accession XP_034819.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0326.

[43219] KIAA1826 (Accession XP_040784.1) is another GAM2608 target gene, herein designated TARGET GENE. KIAA1826 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1826, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1826 BINDING SITE, designated SEQ ID:13511, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43220] Another function of GAM2608 is therefore inhibition of KIAA1826 (Accession XP_040784.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1826.

[43221] KIAA1853 (Accession XP_045184.1) is another GAM2608 target gene, herein designated TARGET GENE. KIAA1853 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1853, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1853 BINDING SITE, designated SEQ ID:2810, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43222] Another function of GAM2608 is therefore inhibition of KIAA1853 (Accession XP_045184.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1853.

[43223] Lysosomal-associated membrane protein 1 (LAMP1, Accession NP_005552.2) is another GAM2608 target gene, herein designated TARGET GENE. LAMP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAMP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMP1 BINDING

SITE, designated SEQ ID:6326, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43224] Another function of GAM2608 is therefore inhibition of Lysosomal-associated membrane protein 1 (LAMP1, Accession NP_005552.2), a gene which presents carbohydrate ligands to selectins. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP1.

[43225] The function of LAMP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM483.1.Lysosomal-associated protein transmembrane 4 alpha (LAPTM4A, Accession NP_055528.1) is another GAM2608 target gene, herein designated TARGET GENE. LAPTM4A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAPTM4A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAPTM4A BINDING SITE, designated SEQ ID:6126, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ

ID:245.

[43226] Another function of GAM2608 is therefore inhibition of Lysosomal-associated protein transmembrane 4 alpha (LAPTM4A, Accession NP_055528.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAPTM4A.

[43227] Luteinizing hormone/choriogonadotropin receptor (LHCGR, Accession NP_000224.1) is another GAM2608 target gene, herein designated TARGET GENE. LHCGR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LHCGR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LHCGR BINDING SITE, designated SEQ ID:15507, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43228] Another function of GAM2608 is therefore inhibition of Luteinizing hormone/choriogonadotropin receptor (LHCGR, Accession NP_000224.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHCGR.

[43229] LOC114971 (Accession XP_054936.4) is another GAM2608 target gene, herein designated TARGET GENE. LOC114971 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC114971, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC114971 BINDING SITE, designated SEQ ID:14175, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43230] Another function of GAM2608 is therefore inhibition of LOC114971 (Accession XP_054936.4) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC114971.

[43231] LOC147136 (Accession XP_300674.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC147136 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC147136 BINDING SITE, designated SEQ ID:18650, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43232] Another function of GAM2608 is therefore inhibition of LOC147136 (Accession XP_300674.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147136.

[43233] LOC150279 (Accession XP_086820.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC150279 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150279, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150279 BINDING SITE, designated SEQ ID:8823, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43234] Another function of GAM2608 is therefore inhibition of LOC150279 (Accession XP_086820.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC150279.

[43235] LOC158863 (Accession XP_098999.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC158863 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158863, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158863 BINDING SITE, designated SEQ ID:5453, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43236] Another function of GAM2608 is therefore inhibition of LOC158863 (Accession XP_098999.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158863.

[43237] LOC201287 (Accession XP_113947.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC201287 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC201287, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201287 BINDING SITE, designated SEQ ID:15360, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43238] Another function of GAM2608 is therefore inhibition of LOC201287 (Accession XP_113947.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201287.

[43239] LOC220486 (Accession XP_165391.2) is another GAM2608 target gene, herein designated TARGET GENE. LOC220486 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC220486, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220486 BINDING SITE, designated SEQ ID:5591, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43240] Another function of GAM2608 is therefore inhibition of

LOC220486 (Accession XP_165391.2) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220486.

[43241] LOC253609 (Accession XP_172986.2) is another GAM2608 target gene, herein designated TARGET GENE. LOC253609 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253609, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253609 BINDING SITE, designated SEQ ID:17912, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43242] Another function of GAM2608 is therefore inhibition of LOC253609 (Accession XP_172986.2) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253609.

[43243] LOC253805 (Accession XP_172854.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC253805 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC253805, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253805 BINDING SITE, designated SEQ ID:7852, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43244] Another function of GAM2608 is therefore inhibition of LOC253805 (Accession XP_172854.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253805.

[43245] LOC283116 (Accession XP_208043.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC283116 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283116, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283116 BINDING SITE, designated SEQ ID:8224, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:245.

[43246] Another function of GAM2608 is therefore inhibition of LOC283116 (Accession XP_208043.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283116.

[43247] LOC283830 (Accession XP_211223.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC283830 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283830, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283830 BINDING SITE, designated SEQ ID:16975, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43248] Another function of GAM2608 is therefore inhibition of LOC283830 (Accession XP_211223.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283830.

[43249] LOC284996 (Accession NP_775918.1) is another

GAM2608 target gene, herein designated TARGET GENE. LOC284996 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284996, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284996 BINDING SITE, designated SEQ ID:13549, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43250] Another function of GAM2608 is therefore inhibition of LOC284996 (Accession NP_775918.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284996.

[43251] LOC285595 (Accession XP_211948.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC285595 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285595, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285595 BINDING SITE, desig-

nated SEQ ID:13348, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43252] Another function of GAM2608 is therefore inhibition of LOC285595 (Accession XP_211948.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285595.

[43253] LOC285656 (Accession XP_211976.2) is another GAM2608 target gene, herein designated TARGET GENE. LOC285656 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285656, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285656 BINDING SITE, designated SEQ ID:13348, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43254] Another function of GAM2608 is therefore inhibition of LOC285656 (Accession XP_211976.2) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285656.

[43255] LOC286460 (Accession XP_208425.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC286460 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286460, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286460 BINDING SITE, designated SEQ ID:8964, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43256] Another function of GAM2608 is therefore inhibition of LOC286460 (Accession XP_208425.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286460.

[43257] LOC339005 (Accession XP_290661.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC339005 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339005, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339005 BINDING SITE, designated SEQ ID:3940, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43258] Another function of GAM2608 is therefore inhibition of LOC339005 (Accession XP_290661.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339005.

[43259] LOC339263 (Accession XP_294889.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC339263 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339263, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339263 BINDING SITE, designated SEQ ID:2561, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43260] Another function of GAM2608 is therefore inhibition of LOC339263 (Accession XP_294889.1) . Accordingly, utili-

ties of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339263.

[43261] LOC348989 (Accession XP_302935.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC348989 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348989, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348989 BINDING SITE, designated SEQ ID:13348, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43262] Another function of GAM2608 is therefore inhibition of LOC348989 (Accession XP_302935.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348989.

[43263] LOC349440 (Accession XP_300513.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC349440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC349440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349440 BINDING SITE, designated SEQ ID:10811, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43264] Another function of GAM2608 is therefore inhibition of LOC349440 (Accession XP_300513.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349440.

[43265] LOC55974 (Accession NP_061333.1) is another GAM2608 target gene, herein designated TARGET GENE. LOC55974 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC55974, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC55974 BINDING SITE, designated SEQ ID:17137, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43266] Another function of GAM2608 is therefore inhibition of

LOC55974 (Accession NP_061333.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC55974.

[43267] Mastermind-like 2 (drosophila) (MAML2, Accession XP_045716.1) is another GAM2608 target gene, herein designated TARGET GENE. MAML2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAML2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAML2 BINDING SITE, designated SEQ ID:11423, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43268] Another function of GAM2608 is therefore inhibition of Mastermind-like 2 (drosophila) (MAML2, Accession XP_045716.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAML2.

[43269] Mitogen-activated protein kinase kinase kinase 8 (MAP3K8, Accession NP_005195.2) is another GAM2608 target gene, herein designated TARGET GENE. MAP3K8

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MAP3K8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAP3K8 BINDING SITE, designated SEQ ID:17674, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43270] Another function of GAM2608 is therefore inhibition of Mitogen-activated protein kinase kinase kinase 8 (MAP3K8, Accession NP_005195.2), a gene which is able to activate nf- kappa- b 1 by stimulating proteasome-mediated p. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K8.

[43271] The function of MAP3K8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Mitogen-activated protein kinase kinase kinase kinase 5 (MAP4K5, Accession NP_006566.2) is another GAM2608 target gene, herein designated TARGET GENE. MAP4K5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

MAP4K5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAP4K5 BINDING SITE, designated SEQ ID:14765, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43272] Another function of GAM2608 is therefore inhibition of Mitogen-activated protein kinase kinase kinase kinase 5 (MAP4K5, Accession NP_006566.2) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP4K5.

[43273] Mannan-binding lectin serine protease 1 (c4/c2 activating component of ra-reactive factor) (MASP1, Accession NP_001870.3) is another GAM2608 target gene, herein designated TARGET GENE. MASP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MASP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MASP1 BINDING SITE, designated SEQ ID:16184, to the

nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43274] Another function of GAM2608 is therefore inhibition of Mannan-binding lectin serine protease 1 (c4/c2 activating component of ra-reactive factor) (MASP1, Accession NP_001870.3), a gene which a complement- dependent bactericidal factor . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MASP1.

[43275] The function of MASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.MGC10561 (Accession NP_116036.1) is another GAM2608 target gene, herein designated TARGET GENE. MGC10561 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10561, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10561 BINDING SITE, designated SEQ ID:2731, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43276] Another function of GAM2608 is therefore inhibition of MGC10561 (Accession NP_116036.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10561.

[43277] MGC13024 (Accession NP_689501.1) is another GAM2608 target gene, herein designated TARGET GENE. MGC13024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13024 BINDING SITE, designated SEQ ID:9146, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43278] Another function of GAM2608 is therefore inhibition of MGC13024 (Accession NP_689501.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13024.

[43279] Monocyte to macrophage differentiation-associated (MMD, Accession NP_036461.1) is another GAM2608 target gene, herein designated TARGET GENE. MMD BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MMD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MMD BINDING SITE, designated SEQ ID:14690, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43280] Another function of GAM2608 is therefore inhibition of Monocyte to macrophage differentiation-associated (MMD, Accession NP_036461.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMD.

[43281] Matrix metalloproteinase 26 (MMP26, Accession NP_068573.1) is another GAM2608 target gene, herein designated TARGET GENE. MMP26 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MMP26, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MMP26 BINDING SITE, designated SEQ ID:3864, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:245.

[43282] Another function of GAM2608 is therefore inhibition of Matrix metalloproteinase 26 (MMP26, Accession NP_068573.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMP26.

[43283] Matrix metalloproteinase 3 (stromelysin 1, progelatinase) (MMP3, Accession NP_002413.1) is another GAM2608 target gene, herein designated TARGET GENE. MMP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MMP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MMP3 BINDING SITE, designated SEQ ID:13663, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43284] Another function of GAM2608 is therefore inhibition of Matrix metalloproteinase 3 (stromelysin 1, progelatinase) (MMP3, Accession NP_002413.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMP3.

[43285] Neural precursor cell expressed, developmentally down-

regulated 4 (NEDD4, Accession XP_046129.4) is another GAM2608 target gene, herein designated TARGET GENE. NEDD4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NEDD4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEDD4 BINDING SITE, designated SEQ ID:15072, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43286] Another function of GAM2608 is therefore inhibition of Neural precursor cell expressed, developmentally down-regulated 4 (NEDD4, Accession XP_046129.4), a gene which ubiquitinates regulatory proteins involved in transcription. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEDD4.

[43287] The function of NEDD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM48.2.Nuclear receptor subfamily 1, group i, member 2 (NR1I2, Accession NP_148934.1) is another GAM2608 target gene, herein designated TARGET GENE.

NR1I2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NR1I2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NR1I2 BINDING SITE, designated SEQ ID:11884, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43288] Another function of GAM2608 is therefore inhibition of Nuclear receptor subfamily 1, group i, member 2 (NR1I2, Accession NP_148934.1), a gene which binds to a response element in the cyp3a4 gene promoter and activates its expression in response to a wide variety of endobiotics and xenobiotics. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR1I2.

[43289] The function of NR1I2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Nuclear receptor subfamily 1, group i, member 2 (NR1I2, Accession NP_003880.2) is another GAM2608 target gene, herein designated TARGET GENE.

NR1I2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NR1I2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NR1I2 BINDING SITE, designated SEQ ID:11884, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43290] Another function of GAM2608 is therefore inhibition of Nuclear receptor subfamily 1, group i, member 2 (NR1I2, Accession NP_003880.2), a gene which binds to a response element in the cyp3a4 gene promoter and activates its expression in response to a wide variety of endobiotics and xenobiotics. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR1I2.

[43291] The function of NR1I2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Nuclear receptor subfamily 1, group i, member 2 (NR1I2, Accession NP_071285.1) is another GAM2608 target gene, herein designated TARGET GENE.

NR1I2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NR1I2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NR1I2 BINDING SITE, designated SEQ ID:11884, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43292] Another function of GAM2608 is therefore inhibition of Nuclear receptor subfamily 1, group i, member 2 (NR1I2, Accession NP_071285.1), a gene which binds to a response element in the cyp3a4 gene promoter and activates its expression in response to a wide variety of endobiotics and xenobiotics. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR1I2.

[43293] The function of NR1I2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Nudix (nucleoside diphosphate linked moiety x)-type motif 4 (NUDT4, Accession NP_061967.2) is another GAM2608 target gene, herein designated TARGET

GENE. NUDT4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NUDT4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUDT4 BINDING SITE, designated SEQ ID:18737, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43294] Another function of GAM2608 is therefore inhibition of Nudix (nucleoside diphosphate linked moiety x)-type motif 4 (NUDT4, Accession NP_061967.2) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUDT4.

[43295] Protein kinase c and casein kinase substrate in neurons 1 (PACSIN1, Accession NP_065855.1) is another GAM2608 target gene, herein designated TARGET GENE. PACSIN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PACSIN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

PACSIN1 BINDING SITE, designated SEQ ID:4408, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43296] Another function of GAM2608 is therefore inhibition of Protein kinase c and casein kinase substrate in neurons 1 (PACSIN1, Accession NP_065855.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAC-SIN1.

[43297] Phosphodiesterase 4d, camp-specific (phosphodiesterase e3 dunce homolog, drosophila) (PDE4D, Accession NP_006194.1) is another GAM2608 target gene, herein designated TARGET GENE. PDE4D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDE4D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDE4D BINDING SITE, designated SEQ ID:15887, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43298] Another function of GAM2608 is therefore inhibition of Phosphodiesterase 4d, camp-specific (phosphodiesterase

e3 dunce homolog, drosophila) (PDE4D, Accession NP_006194.1), a gene which has similarity to Drosophila dnc, which is the affected protein in learning and memory mutant dunce. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4D.

[43299] The function of PDE4D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM217.1.Perq amino acid rich, with gyf domain 1 (PERQ1, Accession NP_072096.1) is another GAM2608 target gene, herein designated TARGET GENE. PERQ1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PERQ1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PERQ1 BINDING SITE, designated SEQ ID:13107, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43300] Another function of GAM2608 is therefore inhibition of Perq amino acid rich, with gyf domain 1 (PERQ1, Accession NP_072096.1) . Accordingly, utilities of GAM2608 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with PERQ1.

[43301] Progesterone receptor membrane component 1 (PGRMC1, Accession NP_006658.1) is another GAM2608 target gene, herein designated TARGET GENE. PGRMC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PGRMC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PGRMC1 BINDING SITE, designated SEQ ID:12615, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43302] Another function of GAM2608 is therefore inhibition of Progesterone receptor membrane component 1 (PGRMC1, Accession NP_006658.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGRMC1.

[43303] Rab5a, member ras oncogene family (RAB5A, Accession NP_004153.2) is another GAM2608 target gene, herein designated TARGET GENE. RAB5A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB5A, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB5A BINDING SITE, designated SEQ ID:5501, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43304] Another function of GAM2608 is therefore inhibition of Rab5a, member ras oncogene family (RAB5A, Accession NP_004153.2), a gene which is a rate- limiting component of the machinery regulating the kinetics of membrane traffic. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB5A.

[43305] The function of RAB5A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Ring finger protein 18 (RNF18, Accession NP_065091.1) is another GAM2608 target gene, herein designated TARGET GENE. RNF18 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RNF18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of RNF18 BINDING SITE, designated SEQ ID:8224, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43306] Another function of GAM2608 is therefore inhibition of Ring finger protein 18 (RNF18, Accession NP_065091.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF18.

[43307] Rho-associated, coiled-coil containing protein kinase 2 (ROCK2, Accession NP_004841.1) is another GAM2608 target gene, herein designated TARGET GENE. ROCK2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ROCK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ROCK2 BINDING SITE, designated SEQ ID:19439, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43308] Another function of GAM2608 is therefore inhibition of Rho-associated, coiled-coil containing protein kinase 2 (ROCK2, Accession NP_004841.1), a gene which regulates

cytokinesis, smooth muscle contraction, the formation of actin stress fibers and focal adhesions. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ROCK2.

[43309] The function of ROCK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM90.1.Sh3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2, Accession NP_113657.1) is another GAM2608 target gene, herein designated TARGET GENE. SH3BGRL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SH3BGRL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SH3BGRL2 BINDING SITE, designated SEQ ID:18614, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43310] Another function of GAM2608 is therefore inhibition of Sh3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2, Accession NP_113657.1) . Accordingly, utili-

ties of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BGRL2.

[43311] Single-minded homolog 2 (drosophila) (SIM2, Accession NP_005060.1) is another GAM2608 target gene, herein designated TARGET GENE. SIM2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SIM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIM2 BINDING SITE, designated SEQ ID:4214, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43312] Another function of GAM2608 is therefore inhibition of Single-minded homolog 2 (drosophila) (SIM2, Accession NP_005060.1), a gene which may be a master gene of cns development. and therefore may be associated with Dysmorphic features, abnormalities of brain development, down syndrome. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of Dysmorphic features, abnormalities of brain development, down syndrome., and of other diseases and clinical conditions as-

sociated with SIM2.

[43313] The function of SIM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.1.Serine/threonine kinase 38 like (STK38L, Accession NP_055815.1) is another GAM2608 target gene, herein designated TARGET GENE. STK38L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STK38L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STK38L BINDING SITE, designated SEQ ID:8158, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43314] Another function of GAM2608 is therefore inhibition of Serine/threonine kinase 38 like (STK38L, Accession NP_055815.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK38L.

[43315] Transcription factor b2, mitochondrial (TFB2M, Accession NP_071761.1) is another GAM2608 target gene, herein designated TARGET GENE. TFB2M BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by TFB2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TFB2M BINDING SITE, designated SEQ ID:2805, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43316] Another function of GAM2608 is therefore inhibition of Transcription factor b2, mitochondrial (TFB2M, Accession NP_071761.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TFB2M.

[43317] Titin immunoglobulin domain protein (myotilin) (TTID, Accession NP_006781.1) is another GAM2608 target gene, herein designated TARGET GENE. TTID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TTID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TTID BINDING SITE, designated SEQ ID:10202, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:245.

[43318] Another function of GAM2608 is therefore inhibition of Titin immunoglobulin domain protein (myotilin) (TTID, Accession NP_006781.1), a gene which is a sarcomeric structural protein and therefore may be associated with Limb- girdle muscular dystrophy. Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of Limb- girdle muscular dystrophy, and of other diseases and clinical conditions associated with TTID.

[43319] The function of TTID and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1631.1.Usher syndrome 2a (autosomal recessive, mild) (USH2A, Accession NP_009054.3) is another GAM2608 target gene, herein designated TARGET GENE. USH2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by USH2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of USH2A BINDING SITE, designated SEQ ID:4007, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43320] Another function of GAM2608 is therefore inhibition of Usher syndrome 2a (autosomal recessive, mild) (USH2A, Accession NP_009054.3) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USH2A.

[43321] ZID (Accession NP_006617.1) is another GAM2608 target gene, herein designated TARGET GENE. ZID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZID BINDING SITE, designated SEQ ID:5650, to the nucleotide sequence of GAM2608 RNA, herein designated GAM RNA, also designated SEQ ID:245.

[43322] Another function of GAM2608 is therefore inhibition of ZID (Accession NP_006617.1) . Accordingly, utilities of GAM2608 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZID.

[43323]

[43324] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 3027

(GAM3027), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[43325] GAM3027 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM3027 was detected is described hereinabove with reference to Figs. 8-15.

[43326] GAM3027 gene, herein designated GAM GENE, and GAM3027 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[43327] GAM3027 gene encodes a GAM3027 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM3027 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3027 precursor RNA is designated SEQ ID:8, and is provided hereinbelow with reference to the sequence listing part.

[43328] GAM3027 precursor RNA folds onto itself, forming GAM3027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA

genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[43329] GAM3027 precursor RNA folds onto itself, forming GAM3027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[43330] Nucleotide sequence of GAM3027 precursor RNA, designated SEQ-ID: 8, and a schematic representation of a predicted secondary folding of GAM3027 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[43331] An enzyme complex designated DICER COMPLEX, `dices` the GAM3027 folded precursor RNA into GAM3027 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM3027 RNA is designated SEQ ID:242, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[43332] GAM3027 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM3027 target RNA, herein designated GAM TARGET RNA. GAM3027 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[43333] GAM3027 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3027 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3027 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING

SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM3027 RNA may have a different number of target binding sites in untranslated regions of a GAM3027 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[43334] The complementary binding of GAM3027 RNA, herein designated GAM RNA, to target binding sites on GAM3027 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3027 target RNA into GAM3027 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[43335] It is appreciated that GAM3027 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM3027 target genes. The mRNA of each one of this plurality of GAM3027 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3027 RNA,

herein designated GAM RNA, and which when bound by GAM3027 RNA causes inhibition of translation of respective one or more GAM3027 target proteins.

[43336] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM3027 gene, herein designated GAM GENE, on one or more GAM3027 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[43337] It is appreciated that specific functions and accordingly utilities of GAM3027 correlate with, and may be deduced from, the identity of the target genes which GAM3027 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[43338]

[43339]

[43340] (Accession NP_444285.1) is a GAM3027 target gene, herein designated TARGET GENE. BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BINDING SITE, designated SEQ ID:16500, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43341] A function of GAM3027 is therefore inhibition of (Accession NP_444285.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with .

[43342] Absent in melanoma 1-like (AIM1L, Accession NP_060447.1) is another GAM3027 target gene, herein designated TARGET GENE. AIM1L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AIM1L, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AIM1L BINDING SITE, designated SEQ ID:7873, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43343] Another function of GAM3027 is therefore inhibition of Absent in melanoma 1-like (AIM1L, Accession NP_060447.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AIM1L.

[43344] Btb and cnc homology 1, basic leucine zipper transcription factor 2 (BACH2, Accession NP_068585.1) is another GAM3027 target gene, herein designated TARGET GENE. BACH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BACH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BACH2 BINDING SITE, designated SEQ ID:1058, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43345] Another function of GAM3027 is therefore inhibition of

Btb and cnc homology 1, basic leucine zipper transcription factor 2 (BACH2, Accession NP_068585.1), a gene which acts as repressor or activator, binds to maf recognition elements and therefore may be associated with Non-hodgkin lymphoma. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of Non-hodgkin lymphoma, and of other diseases and clinical conditions associated with BACH2.

[43346] The function of BACH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.C14orf116 (Accession NP_061059.1) is another GAM3027 target gene, herein designated TARGET GENE. C14orf116 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf116, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf116 BINDING SITE, designated SEQ ID:9141, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43347] Another function of GAM3027 is therefore inhibition of

C14orf116 (Accession NP_061059.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf116.

[43348] C5orf13 (Accession NP_004763.1) is another GAM3027 target gene, herein designated TARGET GENE. C5orf13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C5orf13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C5orf13 BINDING SITE, designated SEQ ID:11415, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43349] Another function of GAM3027 is therefore inhibition of C5orf13 (Accession NP_004763.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf13.

[43350] Chromosome 5 open reading frame 5 (C5orf5, Accession NP_057687.1) is another GAM3027 target gene, herein designated TARGET GENE. C5orf5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by C5orf5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C5orf5 BINDING SITE, designated SEQ ID:11857, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43351] Another function of GAM3027 is therefore inhibition of Chromosome 5 open reading frame 5 (C5orf5, Accession NP_057687.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf5.

[43352] Chemokine (c-c motif) receptor-like 1 (CCRL1, Accession NP_848540.1) is another GAM3027 target gene, herein designated TARGET GENE. CCRL1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CCRL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCRL1 BINDING SITE, designated SEQ ID:11537, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43353] Another function of GAM3027 is therefore inhibition of Chemokine (c-c motif) receptor-like 1 (CCRL1, Accession NP_848540.1), a gene which is a G protein- coupled receptor that binds chemokines of the CC subfamily, especially MCP- 4, ELC (SCYA19) and TECK (SCYA25). Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCRL1.

[43354] The function of CCRL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Collagen, type iv, alpha 5 (alport syndrome) (COL4A5, Accession NP_203700.1) is another GAM3027 target gene, herein designated TARGET GENE. COL4A5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COL4A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL4A5 BINDING SITE, designated SEQ ID:18409, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43355] Another function of GAM3027 is therefore inhibition of Collagen, type iv, alpha 5 (alport syndrome) (COL4A5, Accession NP_203700.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A5.

[43356] Collagen, type iv, alpha 5 (alport syndrome) (COL4A5, Accession NP_000486.1) is another GAM3027 target gene, herein designated TARGET GENE. COL4A5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COL4A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL4A5 BINDING SITE, designated SEQ ID:18409, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43357] Another function of GAM3027 is therefore inhibition of Collagen, type iv, alpha 5 (alport syndrome) (COL4A5, Accession NP_000486.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A5.

[43358] Collagen, type iv, alpha 5 (alport syndrome) (COL4A5, Accession NP_203699.1) is another GAM3027 target gene,

herein designated TARGET GENE. COL4A5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COL4A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL4A5 BINDING SITE, designated SEQ ID:18409, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43359] Another function of GAM3027 is therefore inhibition of Collagen, type iv, alpha 5 (alport syndrome) (COL4A5, Accession NP_203699.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A5.

[43360] Collagen, type v, alpha 2 (COL5A2, Accession NP_000384.1) is another GAM3027 target gene, herein designated TARGET GENE. COL5A2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by COL5A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL5A2 BINDING SITE, designated SEQ ID:17367, to the nucleotide se-

quence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43361] Another function of GAM3027 is therefore inhibition of Collagen, type v, alpha 2 (COL5A2, Accession NP_000384.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL5A2.

[43362] Collagen, type vi, alpha 3 (COL6A3, Accession NP_476507.1) is another GAM3027 target gene, herein designated TARGET GENE. COL6A3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COL6A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL6A3 BINDING SITE, designated SEQ ID:16712, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43363] Another function of GAM3027 is therefore inhibition of Collagen, type vi, alpha 3 (COL6A3, Accession NP_476507.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A3.

[43364] Collagen, type vi, alpha 3 (COL6A3, Accession NP_476505.1) is another GAM3027 target gene, herein designated TARGET GENE. COL6A3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COL6A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL6A3 BINDING SITE, designated SEQ ID:16712, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43365] Another function of GAM3027 is therefore inhibition of Collagen, type vi, alpha 3 (COL6A3, Accession NP_476505.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A3.

[43366] Collagen, type vi, alpha 3 (COL6A3, Accession NP_004360.1) is another GAM3027 target gene, herein designated TARGET GENE. COL6A3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COL6A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of COL6A3 BINDING SITE, designated SEQ ID:16712, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43367] Another function of GAM3027 is therefore inhibition of Collagen, type vi, alpha 3 (COL6A3, Accession NP_004360.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A3.

[43368] Collagen, type vi, alpha 3 (COL6A3, Accession NP_476506.1) is another GAM3027 target gene, herein designated TARGET GENE. COL6A3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COL6A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL6A3 BINDING SITE, designated SEQ ID:16712, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43369] Another function of GAM3027 is therefore inhibition of Collagen, type vi, alpha 3 (COL6A3, Accession NP_476506.1) . Accordingly, utilities of GAM3027 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A3.

[43370] Collagen, type vi, alpha 3 (COL6A3, Accession NP_476508.1) is another GAM3027 target gene, herein designated TARGET GENE. COL6A3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COL6A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL6A3 BINDING SITE, designated SEQ ID:16712, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43371] Another function of GAM3027 is therefore inhibition of Collagen, type vi, alpha 3 (COL6A3, Accession NP_476508.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A3.

[43372] Chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4, Accession NP_001888.1) is another GAM3027 target gene, herein designated TARGET GENE. CSPG4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

CSPG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSPG4 BINDING SITE, designated SEQ ID:1254, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43373] Another function of GAM3027 is therefore inhibition of Chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4, Accession NP_001888.1), a gene which plays a role in stabilizing cell- substratum interactions. and therefore may be associated with Childhood acute lymphoblastic leukemias. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of Childhood acute lymphoblastic leukemias, and of other diseases and clinical conditions associated with CSPG4.

[43374] The function of CSPG4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM579.1.CYCS (Accession NP_061820.1) is another GAM3027 target gene, herein designated TARGET GENE. CYCS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYCS, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYCS BINDING SITE, designated SEQ ID:1967, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43375] Another function of GAM3027 is therefore inhibition of CYCS (Accession NP_061820.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYCS.

[43376] Dead/h (asp-glu-ala-asp/his) box polypeptide 4 (DDX4, Accession NP_077726.1) is another GAM3027 target gene, herein designated TARGET GENE. DDX4 BINDING SITE1 and DDX4 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by DDX4, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX4 BINDING SITE1 and DDX4 BINDING SITE2, designated SEQ ID:4569 and SEQ ID:14219 respectively, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43377] Another function of GAM3027 is therefore inhibition of Dead/h (asp-glu-ala-asp/his) box polypeptide 4 (DDX4, Accession NP_077726.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX4.

[43378] DKFZp434O0515 (Accession NP_835224.1) is another GAM3027 target gene, herein designated TARGET GENE. DKFZp434O0515 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434O0515, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434O0515 BINDING SITE, designated SEQ ID:2186, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43379] Another function of GAM3027 is therefore inhibition of DKFZp434O0515 (Accession NP_835224.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434O0515.

[43380] EBRP (Accession NP_115954.1) is another GAM3027 target gene, herein designated TARGET GENE. EBRP BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by EBRP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EBRP BINDING SITE, designated SEQ ID:13938, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43381] Another function of GAM3027 is therefore inhibition of EBRP (Accession NP_115954.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EBRP.

[43382] ESDN (Accession NP_563615.2) is another GAM3027 target gene, herein designated TARGET GENE. ESDN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ESDN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ESDN BINDING SITE, designated SEQ ID:700, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43383] Another function of GAM3027 is therefore inhibition of

ESDN (Accession NP_563615.2) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESDN.

[43384] Endothelial cell-specific molecule 1 (ESM1, Accession NP_008967.1) is another GAM3027 target gene, herein designated TARGET GENE. ESM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ESM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ESM1 BINDING SITE, designated SEQ ID:11981, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43385] Another function of GAM3027 is therefore inhibition of Endothelial cell-specific molecule 1 (ESM1, Accession NP_008967.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESM1.

[43386] Fgd1 family, member 2 (FGD2, Accession NP_775829.1) is another GAM3027 target gene, herein designated TARGET GENE. FGD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FGD2,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGD2 BINDING SITE, designated SEQ ID:8607, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43387] Another function of GAM3027 is therefore inhibition of Fgd1 family, member 2 (FGD2, Accession NP_775829.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGD2.

[43388] FLJ10251 (Accession NP_060509.1) is another GAM3027 target gene, herein designated TARGET GENE. FLJ10251 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10251, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10251 BINDING SITE, designated SEQ ID:11858, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43389] Another function of GAM3027 is therefore inhibition of FLJ10251 (Accession NP_060509.1) . Accordingly, utilities

of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10251.

[43390] FLJ10292 (Accession NP_060518.1) is another GAM3027 target gene, herein designated TARGET GENE. FLJ10292 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10292, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10292 BINDING SITE, designated SEQ ID:3351, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43391] Another function of GAM3027 is therefore inhibition of FLJ10292 (Accession NP_060518.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10292.

[43392] FLJ10404 (Accession NP_061930.1) is another GAM3027 target gene, herein designated TARGET GENE. FLJ10404 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10404, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10404 BINDING SITE, designated SEQ ID:2867, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43393] Another function of GAM3027 is therefore inhibition of FLJ10404 (Accession NP_061930.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10404.

[43394] FLJ25555 (Accession NP_689558.2) is another GAM3027 target gene, herein designated TARGET GENE. FLJ25555 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25555, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25555 BINDING SITE, designated SEQ ID:14472, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43395] Another function of GAM3027 is therefore inhibition of FLJ25555 (Accession NP_689558.2) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ25555.

[43396] FLJ32468 (Accession NP_660090.1) is another GAM3027 target gene, herein designated TARGET GENE. FLJ32468 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32468, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32468 BINDING SITE, designated SEQ ID:5290, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43397] Another function of GAM3027 is therefore inhibition of FLJ32468 (Accession NP_660090.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32468.

[43398] FLJ34922 (Accession NP_689483.1) is another GAM3027 target gene, herein designated TARGET GENE. FLJ34922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ34922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ34922 BINDING SITE, designated SEQ ID:13523, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43399] Another function of GAM3027 is therefore inhibition of FLJ34922 (Accession NP_689483.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34922.

[43400] FLJ36000 (Accession NP_787101.1) is another GAM3027 target gene, herein designated TARGET GENE. FLJ36000 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36000, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36000 BINDING SITE, designated SEQ ID:11041, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43401] Another function of GAM3027 is therefore inhibition of FLJ36000 (Accession NP_787101.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ36000.

[43402] FLJ36331 (Accession XP_211925.1) is another GAM3027 target gene, herein designated TARGET GENE. FLJ36331 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36331, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36331 BINDING SITE, designated SEQ ID:13204, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43403] Another function of GAM3027 is therefore inhibition of FLJ36331 (Accession XP_211925.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36331.

[43404] Udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 8 (galnac-t8) (GALNT8, Accession NP_059113.1) is another GAM3027 target gene, herein designated TARGET GENE. GALNT8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GALNT8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GALNT8 BINDING SITE, designated SEQ ID:10446, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43405] Another function of GAM3027 is therefore inhibition of Udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 8 (galnac-t8) (GALNT8, Accession NP_059113.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNT8.

[43406] HBP1 (Accession NP_036389.2) is another GAM3027 target gene, herein designated TARGET GENE. HBP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HBP1 BINDING SITE, designated SEQ ID:16151, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43407] Another function of GAM3027 is therefore inhibition of HBP1 (Accession NP_036389.2) . Accordingly, utilities of

GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HBP1.

[43408] Hepatic leukemia factor (HLF, Accession NP_002117.1) is another GAM3027 target gene, herein designated TARGET GENE. HLF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HLF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HLF BINDING SITE, designated SEQ ID:18455, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43409] Another function of GAM3027 is therefore inhibition of Hepatic leukemia factor (HLF, Accession NP_002117.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLF.

[43410] Integrin, alpha d (ITGAD, Accession XP_113880.1) is another GAM3027 target gene, herein designated TARGET GENE. ITGAD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITGAD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of ITGAD BINDING SITE, designated SEQ ID:7734, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43411] Another function of GAM3027 is therefore inhibition of Integrin, alpha d (ITGAD, Accession XP_113880.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAD.

[43412] Inositol 1,4,5-triphosphate receptor, type 1 (ITPR1, Accession NP_002213.1) is another GAM3027 target gene, herein designated TARGET GENE. ITPR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITPR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITPR1 BINDING SITE, designated SEQ ID:623, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43413] Another function of GAM3027 is therefore inhibition of Inositol 1,4,5-triphosphate receptor, type 1 (ITPR1, Accession NP_002213.1), a gene which couples cell mem-

brane receptors to Ca2+ signal transduction pathways. and therefore may be associated with Ataxia and epileptic seizures. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of Ataxia and epileptic seizures, and of other diseases and clinical conditions associated with ITPR1.

[43414] The function of ITPR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM404.2.Potassium voltage-gated channel, subfamily h (eag-related), member 7 (KCNH7, Accession NP_775185.1) is another GAM3027 target gene, herein designated TARGET GENE. KCNH7 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by KCNH7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNH7 BINDING SITE, designated SEQ ID:11768, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43415] Another function of GAM3027 is therefore inhibition of Potassium voltage-gated channel, subfamily h

(eag-related), member 7 (KCNH7, Accession NP_775185.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNH7.

[43416] Potassium voltage-gated channel, subfamily h (eag-related), member 7 (KCNH7, Accession NP_150375.2) is another GAM3027 target gene, herein designated TARGET GENE. KCNH7 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by KCNH7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNH7 BINDING SITE, designated SEQ ID:11768, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43417] Another function of GAM3027 is therefore inhibition of Potassium voltage-gated channel, subfamily h (eag-related), member 7 (KCNH7, Accession NP_150375.2) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNH7.

[43418] KIAA0125 (Accession NP_055607.1) is another GAM3027

target gene, herein designated TARGET GENE. KIAA0125 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0125, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0125 BINDING SITE, designated SEQ ID:16707, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43419] Another function of GAM3027 is therefore inhibition of KIAA0125 (Accession NP_055607.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0125.

[43420] KIAA0256 (Accession XP_034905.1) is another GAM3027 target gene, herein designated TARGET GENE. KIAA0256 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0256, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0256 BINDING SITE, designated SEQ ID:16077, to the nucleotide sequence of GAM3027 RNA, herein designated

GAM RNA, also designated SEQ ID:242.

[43421] Another function of GAM3027 is therefore inhibition of KIAA0256 (Accession XP_034905.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0256.

[43422] KIAA1399 (Accession XP_046685.4) is another GAM3027 target gene, herein designated TARGET GENE. KIAA1399 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1399, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1399 BINDING SITE, designated SEQ ID:18563, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43423] Another function of GAM3027 is therefore inhibition of KIAA1399 (Accession XP_046685.4) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1399.

[43424] KIAA1666 (Accession XP_036936.1) is another GAM3027 target gene, herein designated TARGET GENE. KIAA1666

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1666, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1666 BINDING SITE, designated SEQ ID:2583, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43425] Another function of GAM3027 is therefore inhibition of KIAA1666 (Accession XP_036936.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1666.

[43426] KIAA2022 (Accession XP_291326.1) is another GAM3027 target gene, herein designated TARGET GENE. KIAA2022 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA2022, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA2022 BINDING SITE, designated SEQ ID:14473, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43427] Another function of GAM3027 is therefore inhibition of KIAA2022 (Accession XP_291326.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2022.

[43428] Kruppel-like factor 12 (KLF12, Accession NP_009180.3) is another GAM3027 target gene, herein designated TARGET GENE. KLF12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLF12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLF12 BINDING SITE, designated SEQ ID:19711, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43429] Another function of GAM3027 is therefore inhibition of Kruppel-like factor 12 (KLF12, Accession NP_009180.3) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF12.

[43430] Leucine proline-enriched proteoglycan (leprecan) 1 (LEPRE1, Accession NP_071751.2) is another GAM3027

target gene, herein designated TARGET GENE. LEPRE1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LEPRE1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LEPRE1 BINDING SITE, designated SEQ ID:12458, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43431] Another function of GAM3027 is therefore inhibition of Leucine proline-enriched proteoglycan (leprecan) 1 (LEPRE1, Accession NP_071751.2) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LEPRE1.

[43432] LOC150221 (Accession XP_036942.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC150221 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150221, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150221 BINDING SITE, designated SEQ ID:2583, to the nucleotide sequence of

GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43433] Another function of GAM3027 is therefore inhibition of LOC150221 (Accession XP_036942.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150221.

[43434] LOC151720 (Accession XP_087279.6) is another GAM3027 target gene, herein designated TARGET GENE. LOC151720 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151720, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151720 BINDING SITE, designated SEQ ID:12738, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43435] Another function of GAM3027 is therefore inhibition of LOC151720 (Accession XP_087279.6) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151720.

[43436] LOC159053 (Accession XP_099021.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC159053 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC159053, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC159053 BINDING SITE, designated SEQ ID:16816, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43437] Another function of GAM3027 is therefore inhibition of LOC159053 (Accession XP_099021.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159053.

[43438] LOC222001 (Accession XP_167489.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC222001 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC222001 BINDING SITE, designated SEQ ID:17330, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43439] Another function of GAM3027 is therefore inhibition of LOC222001 (Accession XP_167489.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222001.

[43440] LOC283120 (Accession XP_208516.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC283120 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283120, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283120 BINDING SITE, designated SEQ ID:5389, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43441] Another function of GAM3027 is therefore inhibition of LOC283120 (Accession XP_208516.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283120.

[43442] LOC283368 (Accession XP_208080.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC283368 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283368, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283368 BINDING SITE, designated SEQ ID:8708, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43443] Another function of GAM3027 is therefore inhibition of LOC283368 (Accession XP_208080.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283368.

[43444] LOC283528 (Accession XP_208708.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC283528 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283528, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283528 BINDING SITE, designated SEQ ID:6585, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43445] Another function of GAM3027 is therefore inhibition of LOC283528 (Accession XP_208708.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283528.

[43446] LOC283570 (Accession XP_211118.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC283570 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283570, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283570 BINDING SITE, designated SEQ ID:4895, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43447] Another function of GAM3027 is therefore inhibition of

LOC283570 (Accession XP_211118.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283570.

[43448] LOC284124 (Accession XP_294862.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC284124 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284124, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284124 BINDING SITE, designated SEQ ID:11041, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43449] Another function of GAM3027 is therefore inhibition of LOC284124 (Accession XP_294862.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284124.

[43450] LOC284375 (Accession XP_209154.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC284375 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC284375, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284375 BINDING SITE, designated SEQ ID:19882, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43451] Another function of GAM3027 is therefore inhibition of LOC284375 (Accession XP_209154.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284375.

[43452] LOC284463 (Accession XP_210788.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC284463 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284463, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284463 BINDING SITE, designated SEQ ID:8159, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:242.

[43453] Another function of GAM3027 is therefore inhibition of LOC284463 (Accession XP_210788.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284463.

[43454] LOC284709 (Accession XP_209331.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC284709 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284709, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284709 BINDING SITE, designated SEQ ID:10590, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43455] Another function of GAM3027 is therefore inhibition of LOC284709 (Accession XP_209331.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284709.

[43456] LOC285167 (Accession XP_211790.1) is another

GAM3027 target gene, herein designated TARGET GENE. LOC285167 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285167 BINDING SITE, designated SEQ ID:8965, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43457] Another function of GAM3027 is therefore inhibition of LOC285167 (Accession XP_211790.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285167.

[43458] LOC285695 (Accession XP_209722.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC285695 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285695, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285695 BINDING SITE, desig-

nated SEQ ID:9924, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43459] Another function of GAM3027 is therefore inhibition of LOC285695 (Accession XP_209722.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285695.

[43460] LOC285827 (Accession XP_212604.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC285827 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC285827, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285827 BINDING SITE, designated SEQ ID:1968, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43461] Another function of GAM3027 is therefore inhibition of LOC285827 (Accession XP_212604.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285827.

[43462] LOC285827 (Accession XP_212038.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC285827 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC285827, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285827 BINDING SITE, designated SEQ ID:1968, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43463] Another function of GAM3027 is therefore inhibition of LOC285827 (Accession XP_212038.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285827.

[43464] LOC285827 (Accession XP_212645.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC285827 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC285827, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285827 BINDING SITE, designated SEQ ID:1968, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43465] Another function of GAM3027 is therefore inhibition of LOC285827 (Accession XP_212645.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285827.

[43466] LOC285939 (Accession XP_208364.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC285939 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285939, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285939 BINDING SITE, designated SEQ ID:11415, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43467] Another function of GAM3027 is therefore inhibition of LOC285939 (Accession XP_208364.1) . Accordingly, utili-

ties of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285939.

[43468] LOC286173 (Accession XP_209928.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC286173 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286173, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286173 BINDING SITE, designated SEQ ID:11415, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43469] Another function of GAM3027 is therefore inhibition of LOC286173 (Accession XP_209928.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286173.

[43470] LOC338921 (Accession XP_290624.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC338921 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC338921, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338921 BINDING SITE, designated SEQ ID:19734, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43471] Another function of GAM3027 is therefore inhibition of LOC338921 (Accession XP_290624.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338921.

[43472] LOC339856 (Accession XP_295087.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC339856 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339856 BINDING SITE, designated SEQ ID:15901, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43473] Another function of GAM3027 is therefore inhibition of LOC339856 (Accession XP_295087.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339856.

[43474] LOC340362 (Accession XP_295225.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC340362 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340362, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340362 BINDING SITE, designated SEQ ID:1433, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43475] Another function of GAM3027 is therefore inhibition of LOC340362 (Accession XP_295225.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340362.

[43476] LOC340428 (Accession XP_290420.1) is another GAM3027 target gene, herein designated TARGET GENE.

LOC340428 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340428, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340428 BINDING SITE, designated SEQ ID:7731, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43477] Another function of GAM3027 is therefore inhibition of LOC340428 (Accession XP_290420.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340428.

[43478] LOC340542 (Accession XP_291335.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC340542 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340542, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340542 BINDING SITE, designated SEQ ID:16315, to the nucleotide sequence of

GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43479] Another function of GAM3027 is therefore inhibition of LOC340542 (Accession XP_291335.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340542.

[43480] LOC348393 (Accession XP_302741.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC348393 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348393 BINDING SITE, designated SEQ ID:1132, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43481] Another function of GAM3027 is therefore inhibition of LOC348393 (Accession XP_302741.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348393.

[43482] LOC348532 (Accession XP_302818.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC348532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348532 BINDING SITE, designated SEQ ID:1132, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43483] Another function of GAM3027 is therefore inhibition of LOC348532 (Accession XP_302818.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348532.

[43484] LOC348572 (Accession XP_290964.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC348572 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348572, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC348572 BINDING SITE, designated SEQ ID:17835, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43485] Another function of GAM3027 is therefore inhibition of LOC348572 (Accession XP_290964.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348572.

[43486] LOC348601 (Accession XP_300791.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC348601 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348601, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348601 BINDING SITE, designated SEQ ID:2583, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43487] Another function of GAM3027 is therefore inhibition of LOC348601 (Accession XP_300791.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348601.

[43488] LOC349667 (Accession XP_303448.1) is another GAM3027 target gene, herein designated TARGET GENE. LOC349667 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349667, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349667 BINDING SITE, designated SEQ ID:9490, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43489] Another function of GAM3027 is therefore inhibition of LOC349667 (Accession XP_303448.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349667.

[43490] Mesoderm specific transcript homolog (mouse) (MEST, Accession NP_803491.1) is another GAM3027 target gene, herein designated TARGET GENE. MEST BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MEST, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MEST BINDING SITE, designated SEQ ID:8219, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43491] Another function of GAM3027 is therefore inhibition of Mesoderm specific transcript homolog (mouse) (MEST, Accession NP_803491.1), a gene which appears to be required for the appropriate immediate response of females to their pups. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEST.

[43492] The function of MEST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM291.1.Mesoderm specific transcript homolog (mouse) (MEST, Accession NP_002393.2) is another GAM3027 target gene, herein designated TARGET GENE. MEST BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MEST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MEST BINDING SITE, designated SEQ ID:8219, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43493] Another function of GAM3027 is therefore inhibition of Mesoderm specific transcript homolog (mouse) (MEST, Accession NP_002393.2), a gene which appears to be required for the appropriate immediate response of females to their pups. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEST.

[43494] The function of MEST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM291.1.Mesoderm specific transcript homolog (mouse) (MEST, Accession NP_803490.1) is another GAM3027 target gene, herein designated TARGET GENE. MEST BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MEST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of MEST BINDING SITE, designated SEQ ID:8219, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43495] Another function of GAM3027 is therefore inhibition of Mesoderm specific transcript homolog (mouse) (MEST, Accession NP_803490.1), a gene which appears to be required for the appropriate immediate response of females to their pups. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEST.

[43496] The function of MEST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM291.1.Methyltransferase-like 1 (METTL1, Accession NP_075421.1) is another GAM3027 target gene, herein designated TARGET GENE. METTL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by METTL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of METTL1 BINDING SITE, designated SEQ ID:12414, to the

nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43497] Another function of GAM3027 is therefore inhibition of Methyltransferase-like 1 (METTL1, Accession NP_075421.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with METTL1.

[43498] MGC22014 (Accession XP_035307.1) is another GAM3027 target gene, herein designated TARGET GENE. MGC22014 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC22014, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC22014 BINDING SITE, designated SEQ ID:4508, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43499] Another function of GAM3027 is therefore inhibition of MGC22014 (Accession XP_035307.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC22014.

[43500] MGC2705 (Accession NP_116090.2) is another GAM3027

target gene, herein designated TARGET GENE. MGC2705 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2705, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2705 BINDING SITE, designated SEQ ID:1363, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43501] Another function of GAM3027 is therefore inhibition of MGC2705 (Accession NP_116090.2) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2705.

[43502] MORF4 (Accession XP_165470.1) is another GAM3027 target gene, herein designated TARGET GENE. MORF4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MORF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MORF4 BINDING SITE, designated SEQ ID:7924, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA,

also designated SEQ ID:242.

[43503] Another function of GAM3027 is therefore inhibition of MORF4 (Accession XP_165470.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MORF4.

[43504] Nuclear autoantigenic sperm protein (histone-binding) (NASP, Accession NP_751896.1) is another GAM3027 target gene, herein designated TARGET GENE. NASP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NASP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NASP BINDING SITE, designated SEQ ID:16483, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43505] Another function of GAM3027 is therefore inhibition of Nuclear autoantigenic sperm protein (histone-binding) (NASP, Accession NP_751896.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NASP.

[43506] Nuclear autoantigenic sperm protein (histone-binding) (NASP, Accession NP_002473.2) is another GAM3027 tar-

get gene, herein designated TARGET GENE. NASP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NASP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NASP BINDING SITE, designated SEQ ID:16483, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43507] Another function of GAM3027 is therefore inhibition of Nuclear autoantigenic sperm protein (histone-binding) (NASP, Accession NP_002473.2) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NASP.

[43508] Nuclear autoantigenic sperm protein (histone-binding) (NASP, Accession NP_689511.2) is another GAM3027 target gene, herein designated TARGET GENE. NASP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NASP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NASP BINDING SITE, designated SEQ ID:16483,

to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43509] Another function of GAM3027 is therefore inhibition of Nuclear autoantigenic sperm protein (histone-binding) (NASP, Accession NP_689511.2) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NASP.

[43510] Neuron navigator 3 (NAV3, Accession NP_055718.2) is another GAM3027 target gene, herein designated TARGET GENE. NAV3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NAV3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NAV3 BINDING SITE, designated SEQ ID:9220, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43511] Another function of GAM3027 is therefore inhibition of Neuron navigator 3 (NAV3, Accession NP_055718.2) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAV3.

[43512] Nuclear receptor coactivator 2 (NCOA2, Accession

NP_006531.1) is another GAM3027 target gene, herein designated TARGET GENE. NCOA2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCOA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA2 BINDING SITE, designated SEQ ID:4666, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43513] Another function of GAM3027 is therefore inhibition of Nuclear receptor coactivator 2 (NCOA2, Accession NP_006531.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA2.

[43514] Nima (never in mitosis gene a)-related kinase 2 (NEK2, Accession NP_002488.1) is another GAM3027 target gene, herein designated TARGET GENE. NEK2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NEK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEK2 BINDING SITE,

designated SEQ ID:18583, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43515] Another function of GAM3027 is therefore inhibition of Nima (never in mitosis gene a)-related kinase 2 (NEK2, Accession NP_002488.1), a gene which is involved in mitotic regulation. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEK2.

[43516] The function of NEK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM473.1.Polyhomeotic-like 1 (drosophila) (PHC1, Accession NP_004417.1) is another GAM3027 target gene, herein designated TARGET GENE. PHC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PHC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PHC1 BINDING SITE, designated SEQ ID:8708, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43517] Another function of GAM3027 is therefore inhibition of Polyhomeotic-like 1 (drosophila) (PHC1, Accession NP_004417.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHC1.

[43518] Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) is another GAM3027 target gene, herein designated TARGET GENE. PNMA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PNMA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PNMA2 BINDING SITE, designated SEQ ID:16185, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43519] Another function of GAM3027 is therefore inhibition of Paraneoplastic antigen ma2 (PNMA2, Accession NP_009188.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNMA2.

[43520] Protein phosphatase 2, regulatory subunit b (b56), gamma isoform (PPP2R5C, Accession NP_848701.1) is another

GAM3027 target gene, herein designated TARGET GENE. PPP2R5C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP2R5C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP2R5C BINDING SITE, designated SEQ ID:14122, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43521] Another function of GAM3027 is therefore inhibition of Protein phosphatase 2, regulatory subunit b (b56), gamma isoform (PPP2R5C, Accession NP_848701.1), a gene which is a regulatory subunit of protein phosphatase 2A. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R5C.

[43522] The function of PPP2R5C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.1.Protein phosphatase 2, regulatory subunit b (b56), gamma isoform (PPP2R5C, Accession NP_002710.2) is another GAM3027 target gene, herein designated TAR-

GET GENE. PPP2R5C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP2R5C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP2R5C BINDING SITE, designated SEQ ID:14122, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43523] Another function of GAM3027 is therefore inhibition of Protein phosphatase 2, regulatory subunit b (b56), gamma isoform (PPP2R5C, Accession NP_002710.2), a gene which is a regulatory subunit of protein phosphatase 2A. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R5C.

[43524] The function of PPP2R5C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.1.PRO0132 (Accession NP_054835.1) is another GAM3027 target gene, herein designated TARGET GENE. PRO0132 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

PRO0132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0132 BINDING SITE, designated SEQ ID:18429, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43525] Another function of GAM3027 is therefore inhibition of PRO0132 (Accession NP_054835.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0132.

[43526] PRO2964 (Accession NP_061017.1) is another GAM3027 target gene, herein designated TARGET GENE. PRO2964 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO2964, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO2964 BINDING SITE, designated SEQ ID:7172, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43527] Another function of GAM3027 is therefore inhibition of

PRO2964 (Accession NP_061017.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2964.

[43528] Rab30, member ras oncogene family (RAB30, Accession NP_055303.2) is another GAM3027 target gene, herein designated TARGET GENE. RAB30 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB30 BINDING SITE, designated SEQ ID:1946, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43529] Another function of GAM3027 is therefore inhibition of Rab30, member ras oncogene family (RAB30, Accession NP_055303.2), a gene which is a GTP- binding protein. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB30.

[43530] The function of RAB30 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM129.1.Regulatory factor x-associated protein (RFXAP, Accession NP_000529.1) is another GAM3027 target gene, herein designated TARGET GENE. RFXAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RFXAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RFXAP BINDING SITE, designated SEQ ID:11150, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43531] Another function of GAM3027 is therefore inhibition of Regulatory factor x-associated protein (RFXAP, Accession NP_000529.1), a gene which binds to the x- box of mhc ii promoters and is a transcriptional regulator. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFXAP.

[43532] The function of RFXAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.2.Ribonuclease, rnase a family, k6 (RNASE6,

Accession NP_005606.1) is another GAM3027 target gene, herein designated TARGET GENE. RNASE6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RNASE6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNASE6 BINDING SITE, designated SEQ ID:3045, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43533] Another function of GAM3027 is therefore inhibition of Ribonuclease, rnase a family, k6 (RNASE6, Accession NP_005606.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNASE6.

[43534] Ribonuclease l (2',5'-oligoisoadenylate synthetase-dependent) (RNASEL, Accession NP_066956.1) is another GAM3027 target gene, herein designated TARGET GENE. RNASEL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNASEL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of RNASEL BINDING SITE, designated SEQ ID:12262, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43535] Another function of GAM3027 is therefore inhibition of Ribonuclease l (2',5'-oligoisoadenylate synthetase-dependent) (RNASEL, Accession NP_066956.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNASEL.

[43536] Rna guanylyltransferase and 5'-phosphatase (RNGTT, Accession NP_003791.1) is another GAM3027 target gene, herein designated TARGET GENE. RNGTT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNGTT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNGTT BINDING SITE, designated SEQ ID:16779, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43537] Another function of GAM3027 is therefore inhibition of Rna guanylyltransferase and 5'-phosphatase (RNGTT, Accession NP_003791.1), a gene which is an MRNA capping

enzyme; bifunctional enzyme containing both 5'- triphosphatase and mRNA guanylyltransferase activity. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNGTT.

[43538] The function of RNGTT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM475.2.Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (SLC11A2, Accession NP_000608.1) is another GAM3027 target gene, herein designated TARGET GENE. SLC11A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC11A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC11A2 BINDING SITE, designated SEQ ID:10424, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43539] Another function of GAM3027 is therefore inhibition of Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (SLC11A2, Accession

NP_000608.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC11A2.

[43540] Solute carrier family 26, member 7 (SLC26A7, Accession NP_439897.1) is another GAM3027 target gene, herein designated TARGET GENE. SLC26A7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLC26A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC26A7 BINDING SITE, designated SEQ ID:19030, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43541] Another function of GAM3027 is therefore inhibition of Solute carrier family 26, member 7 (SLC26A7, Accession NP_439897.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC26A7.

[43542] Solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6, Accession NP_003974.1) is another GAM3027 target gene, herein designated TARGET GENE. SLC7A6 BINDING SITE is a target binding site found

in the 3` untranslated region of mRNA encoded by SLC7A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC7A6 BINDING SITE, designated SEQ ID:17897, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43543] Another function of GAM3027 is therefore inhibition of Solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6, Accession NP_003974.1), a gene which is involved in mediating amino acid transport. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC7A6.

[43544] The function of SLC7A6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM74.1.SNURF-SNRPN (Accession XP_085186.4) is another GAM3027 target gene, herein designated TARGET GENE. SNURF-SNRPN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNURF-SNRPN, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNURF-SNRPN BINDING SITE, designated SEQ ID:3268, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43545] Another function of GAM3027 is therefore inhibition of SNURF-SNRPN (Accession XP_085186.4) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNURF-SNRPN.

[43546] Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1) is another GAM3027 target gene, herein designated TARGET GENE. SS18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SS18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SS18 BINDING SITE, designated SEQ ID:9679, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43547] Another function of GAM3027 is therefore inhibition of

Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1), a gene which is a putative transcriptional activator. and therefore is associated with Human synovial sarcomas. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of Human synovial sarcomas., and of other diseases and clinical conditions associated with SS18.

[43548] The function of SS18 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.T-cell leukemia/lymphoma 1a (TCL1A, Accession NP_068801.1) is another GAM3027 target gene, herein designated TARGET GENE. TCL1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TCL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL1A BINDING SITE, designated SEQ ID:14577, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43549] Another function of GAM3027 is therefore inhibition of T-cell leukemia/lymphoma 1a (TCL1A, Accession

NP_068801.1) . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL1A.

[43550] Thiamin pyrophosphokinase 1 (TPK1, Accession NP_071890.2) is another GAM3027 target gene, herein designated TARGET GENE. TPK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TPK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPK1 BINDING SITE, designated SEQ ID:3731, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43551] Another function of GAM3027 is therefore inhibition of Thiamin pyrophosphokinase 1 (TPK1, Accession NP_071890.2), a gene which catalyzes the conversion of thiamine, a form of vitamin B1, to thiamine pyrophosphate . Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TPK1.

[43552] The function of TPK1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM1435.2.Tripartite motif-containing 9 (TRIM9, Accession NP_443210.1) is another GAM3027 target gene, herein designated TARGET GENE. TRIM9 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRIM9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM9 BINDING SITE, designated SEQ ID:17715, to the nucleotide sequence of GAM3027 RNA, herein designated GAM RNA, also designated SEQ ID:242.

[43553] Another function of GAM3027 is therefore inhibition of Tripartite motif-containing 9 (TRIM9, Accession NP_443210.1), a gene which may function as a positive regulator for mannosylphosphate transferase and is required to mediate mannosylphosphate transfer in both the core and outer chain portions of n- linked. oligosaccharides. Accordingly, utilities of GAM3027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM9.

[43554] The function of TRIM9 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM72.1.

[43555] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 3229 (GAM3229), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[43556] GAM3229 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM3229 was detected is described hereinabove with reference to Figs. 8-15.

[43557] GAM3229 gene, herein designated GAM GENE, and GAM3229 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[43558] GAM3229 gene encodes a GAM3229 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM3229 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3229 precursor RNA is designated SEQ ID:46, and is provided hereinbelow with reference to the sequence listing part.

[43559] GAM3229 precursor RNA folds onto itself, forming GAM3229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[43560] GAM3229 precursor RNA folds onto itself, forming GAM3229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[43561] Nucleotide sequence of GAM3229 precursor RNA, designated SEQ-ID: 46, and a schematic representation of a predicted secondary folding of GAM3229 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[43562] An enzyme complex designated DICER COMPLEX, `dices` the GAM3229 folded precursor RNA into GAM3229 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM3229 RNA is designated SEQ ID:221, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[43563] GAM3229 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM3229 target RNA, herein designated GAM TARGET RNA. GAM3229 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[43564] GAM3229 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3229 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM3229 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM3229 RNA may have a different number of target binding sites in untranslated regions of a GAM3229 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[43565] The complementary binding of GAM3229 RNA, herein designated GAM RNA, to target binding sites on GAM3229 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3229 target RNA into GAM3229 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[43566] It is appreciated that GAM3229 target gene, herein desig-

nated TARGET GENE, in fact represents a plurality of GAM3229 target genes. The mRNA of each one of this plurality of GAM3229 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3229 RNA, herein designated GAM RNA, and which when bound by GAM3229 RNA causes inhibition of translation of respective one or more GAM3229 target proteins.

[43567] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM3229 gene, herein designated GAM GENE, on one or more GAM3229 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[43568] It is appreciated that specific functions and accordingly utilities of GAM3229 correlate with, and may be deduced from, the identity of the target genes which GAM3229 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[43569]

[43570]

[43571] 15E1.2 (Accession XP_290596.1) is a GAM3229 target gene, herein designated TARGET GENE. 15E1.2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by 15E1.2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of 15E1.2 BINDING SITE, designated SEQ ID:7550, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43572] A function of GAM3229 is therefore inhibition of 15E1.2 (Accession XP_290596.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 15E1.2.

[43573] Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2) is another GAM3229 target gene, herein designated TARGET GENE. A1BG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by A1BG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A1BG BINDING SITE, designated SEQ ID:4606, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43574] Another function of GAM3229 is therefore inhibition of Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2), a gene which a plasma protein of unknown function. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A1BG.

[43575] The function of A1BG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Atp-binding cassette, sub-family b (mdr/tap), member 5 (ABCB5, Accession XP_291215.1) is another GAM3229 target gene, herein designated TARGET GENE. ABCB5 BINDING SITE is a target binding site found

in the 3` untranslated region of mRNA encoded by ABCB5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCB5 BINDING SITE, designated SEQ ID:14539, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43576] Another function of GAM3229 is therefore inhibition of Atp-binding cassette, sub-family b (mdr/tap), member 5 (ABCB5, Accession XP_291215.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCB5.

[43577] Amiloride-sensitive cation channel 2, neuronal (ACCN2, Accession NP_001086.2) is another GAM3229 target gene, herein designated TARGET GENE. ACCN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACCN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACCN2 BINDING SITE, designated SEQ ID:11565, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43578] Another function of GAM3229 is therefore inhibition of Amiloride-sensitive cation channel 2, neuronal (ACCN2, Accession NP_001086.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACCN2.

[43579] Amiloride-sensitive cation channel 2, neuronal (ACCN2, Accession NP_064423.2) is another GAM3229 target gene, herein designated TARGET GENE. ACCN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACCN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACCN2 BINDING SITE, designated SEQ ID:11565, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43580] Another function of GAM3229 is therefore inhibition of Amiloride-sensitive cation channel 2, neuronal (ACCN2, Accession NP_064423.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACCN2.

[43581] A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4 (ADAMTS4, Acces-

sion NP_005090.1) is another GAM3229 target gene, herein designated TARGET GENE. ADAMTS4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAMTS4 BINDING SITE, designated SEQ ID:4409, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43582] Another function of GAM3229 is therefore inhibition of A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4 (ADAMTS4, Accession NP_005090.1), a gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAMTS4.

[43583] The function of ADAMTS4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Adenylate cyclase 6 (ADCY6, Accession NP_056085.1) is another GAM3229 target gene, herein

designated TARGET GENE. ADCY6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ADCY6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY6 BINDING SITE, designated SEQ ID:16258, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43584] Another function of GAM3229 is therefore inhibition of Adenylate cyclase 6 (ADCY6, Accession NP_056085.1), a gene which this a membrane- bound, ca(2+)- inhibitable adenylyl cyclase (by similarity). Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY6.

[43585] The function of ADCY6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.2.Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type iii) (AGL, Accession NP_000637.1) is another GAM3229 target gene, herein designated TARGET GENE. AGL BINDING SITE is a target

binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by AGL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGL BINDING SITE, designated SEQ ID:14206, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43586] Another function of GAM3229 is therefore inhibition of Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type iii) (AGL, Accession NP_000637.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGL.

[43587] Absent in melanoma 1 (AIM1, Accession XP_166300.1) is another GAM3229 target gene, herein designated TARGET GENE. AIM1 BINDING SITE1 through AIM1 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by AIM1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AIM1 BINDING SITE1 through

AIM1 BINDING SITE3, designated SEQ ID:15456, SEQ ID:4262 and SEQ ID:3982 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43588] Another function of GAM3229 is therefore inhibition of Absent in melanoma 1 (AIM1, Accession XP_166300.1), a gene which is altered in association with tumor suppression in a model of human melanoma and therefore may be associated with Malignant melanoma. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Malignant melanoma, and of other diseases and clinical conditions associated with AIM1.

[43589] The function of AIM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1) is another GAM3229 target gene, herein designated TARGET GENE. ALOX15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALOX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALOX15 BINDING

SITE, designated SEQ ID:13880, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43590] Another function of GAM3229 is therefore inhibition of Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1), a gene which converts arachidonic acid to 15s- hydroperoxyeicosatetraenoic acid. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALOX15.

[43591] The function of ALOX15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.AP1S3 (Accession XP_291023.1) is another GAM3229 target gene, herein designated TARGET GENE. AP1S3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1S3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1S3 BINDING SITE, designated SEQ ID:7058, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ

ID:221.

[43592] Another function of GAM3229 is therefore inhibition of AP1S3 (Accession XP_291023.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1S3.

[43593] Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) is another GAM3229 target gene, herein designated TARGET GENE. AP3S2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AP3S2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP3S2 BINDING SITE, designated SEQ ID:4992, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43594] Another function of GAM3229 is therefore inhibition of Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3S2.

[43595] Apoptotic protease activating factor (APAF1, Accession NP_037361.1) is another GAM3229 target gene, herein

designated TARGET GENE. APAF1 BINDING SITE1 and APAF1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APAF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE1 and APAF1 BINDING SITE2, designated SEQ ID:15973 and SEQ ID:15973 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43596] Another function of GAM3229 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_037361.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[43597] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apoptotic protease activating factor (APAF1,

Accession NP_001151.1) is another GAM3229 target gene, herein designated TARGET GENE. APAF1 BINDING SITE1 and APAF1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by APAF1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE1 and APAF1 BINDING SITE2, designated SEQ ID:2783 and SEQ ID:2783 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43598] Another function of GAM3229 is therefore inhibition of Apoptotic protease activating factor (APAF1, Accession NP_001151.1), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent activation of caspase 3 and therefore may be associated with Cancer. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with APAF1.

[43599] The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM30.1.APM1 (Accession NP_004788.1) is another GAM3229 target gene, herein designated TARGET GENE. APM1 BINDING SITE1 and APM1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by APM1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APM1 BINDING SITE1 and APM1 BINDING SITE2, designated SEQ ID:12655 and SEQ ID:9383 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43600] Another function of GAM3229 is therefore inhibition of APM1 (Accession NP_004788.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1.

[43601] Apolipoprotein c-iii (APOC3, Accession NP_000031.1) is another GAM3229 target gene, herein designated TARGET GENE. APOC3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APOC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of APOC3 BINDING SITE, designated SEQ ID:20001, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43602] Another function of GAM3229 is therefore inhibition of Apolipoprotein c-iii (APOC3, Accession NP_000031.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOC3.

[43603] Aprataxin (APTX, Accession NP_778243.1) is another GAM3229 target gene, herein designated TARGET GENE. APTX BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by APTX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated SEQ ID:404, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43604] Another function of GAM3229 is therefore inhibition of Aprataxin (APTX, Accession NP_778243.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with APTX.

[43605] Aprataxin (APTX, Accession NP_778242.1) is another GAM3229 target gene, herein designated TARGET GENE. APTX BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by APTX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated SEQ ID:404, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43606] Another function of GAM3229 is therefore inhibition of Aprataxin (APTX, Accession NP_778242.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APTX.

[43607] Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1) is another GAM3229 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:3122, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43608] Another function of GAM3229 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[43609] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1) is another GAM3229 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

AQP6 BINDING SITE, designated SEQ ID:3122, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43610] Another function of GAM3229 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[43611] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Archain 1 (ARCN1, Accession NP_001646.2) is another GAM3229 target gene, herein designated TARGET GENE. ARCN1 BINDING SITE1 and ARCN1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ARCN1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARCN1 BINDING SITE1 and ARCN1 BINDING SITE2, designated SEQ ID:2072 and

SEQ ID:17074 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43612] Another function of GAM3229 is therefore inhibition of Archain 1 (ARCN1, Accession NP_001646.2), a gene which plays a fundamental role in eukaryotic cell biology. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARCN1.

[43613] The function of ARCN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) is another GAM3229 target gene, herein designated TARGET GENE. ARHGAP1 BINDING SITE1 and ARHGAP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ARHGAP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP1 BINDING SITE1 and ARHGAP1 BINDING SITE2, designated SEQ ID:2783 and SEQ ID:7041 respectively, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43614] Another function of GAM3229 is therefore inhibition of Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP1.

[43615] Rho guanine nucleotide exchange factor (gef) 7 (ARHGEF7, Accession NP_663788.1) is another GAM3229 target gene, herein designated TARGET GENE. ARHGEF7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ARHGEF7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGEF7 BINDING SITE, designated SEQ ID:13696, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43616] Another function of GAM3229 is therefore inhibition of Rho guanine nucleotide exchange factor (gef) 7 (ARHGEF7, Accession NP_663788.1), a gene which acts as a rac1 guanine nucleotide exchange factor (gef) and can induce

membrane ruffling. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF7.

[43617] The function of ARHGEF7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.2.ARPP-19 (Accession NP_006619.1) is another GAM3229 target gene, herein designated TARGET GENE. ARPP-19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARPP-19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARPP-19 BINDING SITE, designated SEQ ID:9396, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43618] Another function of GAM3229 is therefore inhibition of ARPP-19 (Accession NP_006619.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARPP-19.

[43619] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) is another GAM3229 target gene,

herein designated TARGET GENE. ASB6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ASB6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE, designated SEQ ID:10286, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43620] Another function of GAM3229 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[43621] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) is another GAM3229 target gene, herein designated TARGET GENE. ASB6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ASB6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE, designated SEQ ID:10286, to the nu-

cleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43622] Another function of GAM3229 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[43623] ATF7IP2 (Accession NP_079273.1) is another GAM3229 target gene, herein designated TARGET GENE. ATF7IP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATF7IP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATF7IP2 BINDING SITE, designated SEQ ID:9615, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43624] Another function of GAM3229 is therefore inhibition of ATF7IP2 (Accession NP_079273.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATF7IP2.

[43625] Atpase, na+/k+ transporting, beta 2 polypeptide

(ATP1B2, Accession NP_001669.1) is another GAM3229 target gene, herein designated TARGET GENE. ATP1B2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP1B2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP1B2 BINDING SITE, designated SEQ ID:4784, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43626] Another function of GAM3229 is therefore inhibition of Atpase, na+/k+ transporting, beta 2 polypeptide (ATP1B2, Accession NP_001669.1), a gene which catalyzes the hydrolysis of ATP coupled with the exchange of Na +/K+ ions across the plasma membrane. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B2.

[43627] The function of ATP1B2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Atpase, h+ transporting, lysosomal 38kda, v0 subunit d isoform 2 (ATP6V0D2, Accession

NP_689778.1) is another GAM3229 target gene, herein designated TARGET GENE. ATP6V0D2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP6V0D2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP6V0D2 BINDING SITE, designated SEQ ID:19565, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43628] Another function of GAM3229 is therefore inhibition of Atpase, h+ transporting, lysosomal 38kda, v0 subunit d isoform 2 (ATP6V0D2, Accession NP_689778.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V0D2.

[43629] ATP6V1A (Accession NP_001681.2) is another GAM3229 target gene, herein designated TARGET GENE. ATP6V1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP6V1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

ATP6V1A BINDING SITE, designated SEQ ID:9671, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43630] Another function of GAM3229 is therefore inhibition of ATP6V1A (Accession NP_001681.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V1A.

[43631] Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) is another GAM3229 target gene, herein designated TARGET GENE. ATP7A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:9876, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43632] Another function of GAM3229 is therefore inhibition of Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with ATP7A.

[43633] Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) is another GAM3229 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:3840, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43634] Another function of GAM3229 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[43635] Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) is another GAM3229 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AXL, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:3840, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43636] Another function of GAM3229 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[43637] Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5, Accession NP_004767.1) is another GAM3229 target gene, herein designated TARGET GENE. B4GALT5 BINDING SITE1 and B4GALT5 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by B4GALT5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B4GALT5 BINDING SITE1 and B4GALT5 BINDING SITE2, designated SEQ ID:10951 and SEQ ID:4737 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[43638] Another function of GAM3229 is therefore inhibition of Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5, Accession NP_004767.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT5.

[43639] BCAP31 (Accession NP_005736.2) is another GAM3229 target gene, herein designated TARGET GENE. BCAP31 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCAP31, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCAP31 BINDING SITE, designated SEQ ID:3188, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43640] Another function of GAM3229 is therefore inhibition of BCAP31 (Accession NP_005736.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCAP31.

[43641] B-cell cll/lymphoma 10 (BCL10, Accession NP_003912.1)

is another GAM3229 target gene, herein designated TARGET GENE. BCL10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCL10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCL10 BINDING SITE, designated SEQ ID:7414, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43642] Another function of GAM3229 is therefore inhibition of B-cell cll/lymphoma 10 (BCL10, Accession NP_003912.1), a gene which is a positive regulator of lymphocyte proliferation, NF- kappaB activator. and therefore may be associated with Malt lymphoma, follicular lymphoma. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Malt lymphoma, follicular lymphoma, and of other diseases and clinical conditions associated with BCL10.

[43643] The function of BCL10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Bradykinin receptor b1 (BDKRB1, Accession

NP_000701.2) is another GAM3229 target gene, herein designated TARGET GENE. BDKRB1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BDKRB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BDKRB1 BINDING SITE, designated SEQ ID:15600, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43644] Another function of GAM3229 is therefore inhibition of Bradykinin receptor b1 (BDKRB1, Accession NP_000701.2), a gene which mediates intracellular calcium flux. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDKRB1.

[43645] The function of BDKRB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.BHD (Accession NP_659434.2) is another GAM3229 target gene, herein designated TARGET GENE. BHD BINDING SITE1 and BHD BINDING SITE2 are target binding sites found in untranslated regions of multiple

transcripts of mRNA encoded by BHD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BHD BINDING SITE1 and BHD BINDING SITE2, designated SEQ ID:2783 and SEQ ID:15210 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43646] Another function of GAM3229 is therefore inhibition of BHD (Accession NP_659434.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BHD.

[43647] Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession NP_008979.2) is another GAM3229 target gene, herein designated TARGET GENE. BTN3A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTN3A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTN3A1 BINDING SITE, designated SEQ ID:12851, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43648] Another function of GAM3229 is therefore inhibition of Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession NP_008979.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN3A1.

[43649] BXDC1 (Accession XP_166303.1) is another GAM3229 target gene, herein designated TARGET GENE. BXDC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BXDC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BXDC1 BINDING SITE, designated SEQ ID:9229, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43650] Another function of GAM3229 is therefore inhibition of BXDC1 (Accession XP_166303.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BXDC1.

[43651] Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) is another GAM3229 target gene, herein designated TARGET GENE. C1orf24 BINDING SITE is a target binding site found in the 3` untranslated region

of multiple transcripts of mRNA encoded by C1orf24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:3152, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43652] Another function of GAM3229 is therefore inhibition of Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24.

[43653] C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) is another GAM3229 target gene, herein designated TARGET GENE. C1QTNF6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1QTNF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1QTNF6 BINDING SITE, designated SEQ ID:19016, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43654] Another function of GAM3229 is therefore inhibition of C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QTNF6.

[43655] Chromosome 20 open reading frame 110 (C20orf110, Accession XP_086728.2) is another GAM3229 target gene, herein designated TARGET GENE. C20orf110 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf110, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf110 BINDING SITE, designated SEQ ID:19165, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43656] Another function of GAM3229 is therefore inhibition of Chromosome 20 open reading frame 110 (C20orf110, Accession XP_086728.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf110.

[43657] Chromosome 20 open reading frame 147 (C20orf147, Ac-

cession NP_689880.1) is another GAM3229 target gene, herein designated TARGET GENE. C20orf147 BINDING SITE1 and C20orf147 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C20orf147, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf147 BINDING SITE1 and C20orf147 BINDING SITE2, designated SEQ ID:14837 and SEQ ID:4689 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43658] Another function of GAM3229 is therefore inhibition of Chromosome 20 open reading frame 147 (C20orf147, Accession NP_689880.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf147.

[43659] Chromosome 20 open reading frame 161 (C20orf161, Accession NP_690857.1) is another GAM3229 target gene, herein designated TARGET GENE. C20orf161 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C20orf161, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf161 BINDING SITE, designated SEQ ID:16804, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43660] Another function of GAM3229 is therefore inhibition of Chromosome 20 open reading frame 161 (C20orf161, Accession NP_690857.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf161.

[43661] Chromosome 20 open reading frame 161 (C20orf161, Accession NP_219489.1) is another GAM3229 target gene, herein designated TARGET GENE. C20orf161 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C20orf161, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf161 BINDING SITE, designated SEQ ID:16804, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43662] Another function of GAM3229 is therefore inhibition of Chromosome 20 open reading frame 161 (C20orf161, Accession NP_219489.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf161.

[43663] Chromosome 20 open reading frame 177 (C20orf177, Accession XP_290955.1) is another GAM3229 target gene, herein designated TARGET GENE. C20orf177 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf177 BINDING SITE, designated SEQ ID:18324, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43664] Another function of GAM3229 is therefore inhibition of Chromosome 20 open reading frame 177 (C20orf177, Accession XP_290955.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf177.

[43665] Chromosome 22 open reading frame 19 (C22orf19, Accession NP_003669.2) is another GAM3229 target gene,

herein designated TARGET GENE. C22orf19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C22orf19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C22orf19 BINDING SITE, designated SEQ ID:12716, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43666] Another function of GAM3229 is therefore inhibition of Chromosome 22 open reading frame 19 (C22orf19, Accession NP_003669.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C22orf19.

[43667] C6orf141 (Accession NP_699175.1) is another GAM3229 target gene, herein designated TARGET GENE. C6orf141 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf141, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf141 BINDING SITE, designated SEQ ID:3400, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[43668] Another function of GAM3229 is therefore inhibition of C6orf141 (Accession NP_699175.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf141.

[43669] Chromosome 6 open reading frame 33 (C6orf33, Accession NP_588608.1) is another GAM3229 target gene, herein designated TARGET GENE. C6orf33 BINDING SITE1 and C6orf33 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C6orf33, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf33 BINDING SITE1 and C6orf33 BINDING SITE2, designated SEQ ID:15159 and SEQ ID:19984 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43670] Another function of GAM3229 is therefore inhibition of Chromosome 6 open reading frame 33 (C6orf33, Accession NP_588608.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf33.

[43671] C6orf57 (Accession NP_660310.1) is another GAM3229 target gene, herein designated TARGET GENE. C6orf57 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf57, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf57 BINDING SITE, designated SEQ ID:16359, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43672] Another function of GAM3229 is therefore inhibition of C6orf57 (Accession NP_660310.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf57.

[43673] C6orf65 (Accession NP_689944.1) is another GAM3229 target gene, herein designated TARGET GENE. C6orf65 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf65, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf65 BINDING SITE, designated SEQ ID:12905, to the

nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43674] Another function of GAM3229 is therefore inhibition of C6orf65 (Accession NP_689944.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf65.

[43675] Chromosome 6 open reading frame 9 (C6orf9, Accession NP_071390.1) is another GAM3229 target gene, herein designated TARGET GENE. C6orf9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf9 BINDING SITE, designated SEQ ID:8509, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43676] Another function of GAM3229 is therefore inhibition of Chromosome 6 open reading frame 9 (C6orf9, Accession NP_071390.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf9.

[43677] Reserved (C8orf13, Accession XP_088377.1) is another GAM3229 target gene, herein designated TARGET GENE. C8orf13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C8orf13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C8orf13 BINDING SITE, designated SEQ ID:7963, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43678] Another function of GAM3229 is therefore inhibition of Reserved (C8orf13, Accession XP_088377.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf13.

[43679] Calcium modulating ligand (CAMLG, Accession NP_001736.1) is another GAM3229 target gene, herein designated TARGET GENE. CAMLG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAMLG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMLG BINDING SITE, designated

SEQ ID:19721, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43680] Another function of GAM3229 is therefore inhibition of Calcium modulating ligand (CAMLG, Accession NP_001736.1), a gene which is likely involved in the mobilization of calcium as a result of the tcr/cd3 complex interaction. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMLG.

[43681] The function of CAMLG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Calpain 5 (CAPN5, Accession NP_004046.1) is another GAM3229 target gene, herein designated TARGET GENE. CAPN5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAPN5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAPN5 BINDING SITE, designated SEQ ID:8293, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ

ID:221.

[43682] Another function of GAM3229 is therefore inhibition of Calpain 5 (CAPN5, Accession NP_004046.1), a gene which . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPN5.

[43683] The function of CAPN5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM307.1.CAPRI (Accession NP_008920.3) is another GAM3229 target gene, herein designated TARGET GENE. CAPRI BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAPRI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAPRI BINDING SITE, designated SEQ ID:16875, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43684] Another function of GAM3229 is therefore inhibition of CAPRI (Accession NP_008920.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPRI.

[43685] Caspase 10, apoptosis-related cysteine protease (CASP10, Accession NP_001221.1) is another GAM3229 target gene, herein designated TARGET GENE. CASP10 BINDING SITE1 and CASP10 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CASP10, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP10 BINDING SITE1 and CASP10 BINDING SITE2, designated SEQ ID:10169 and SEQ ID:9941 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43686] Another function of GAM3229 is therefore inhibition of Caspase 10, apoptosis-related cysteine protease (CASP10, Accession NP_001221.1), a gene which is one aspartate-specific cysteine protease and important in death receptor signaling or other cellular processes. and therefore may be associated with Gastric cancers . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Gastric cancers ., and of other diseases and clinical conditions associated with CASP10.

[43687] The function of CASP10 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.Caspase 10, apoptosis-related cysteine protease (CASP10, Accession NP_116758.1) is another GAM3229 target gene, herein designated TARGET GENE. CASP10 BINDING SITE1 and CASP10 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CASP10, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP10 BINDING SITE1 and CASP10 BINDING SITE2, designated SEQ ID:10169 and SEQ ID:10169 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43688] Another function of GAM3229 is therefore inhibition of Caspase 10, apoptosis-related cysteine protease (CASP10, Accession NP_116758.1), a gene which is one aspartate-specific cysteine protease and important in death receptor signaling or other cellular processes. and therefore may be associated with Gastric cancers . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Gastric cancers ., and of other diseases and clinical

conditions associated with CASP10.

[43689] The function of CASP10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.Caspase 10, apoptosis-related cysteine protease (CASP10, Accession NP_001221.1) is another GAM3229 target gene, herein designated TARGET GENE. CASP10 BINDING SITE1 and CASP10 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CASP10, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CASP10 BINDING SITE1 and CASP10 BINDING SITE2, designated SEQ ID:9941 and SEQ ID:9941 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43690] Another function of GAM3229 is therefore inhibition of Caspase 10, apoptosis-related cysteine protease (CASP10, Accession NP_001221.1), a gene which is one aspartate-specific cysteine protease and important in death receptor signaling or other cellular processes. and therefore may be associated with Gastric cancers . Accordingly, utilities

of GAM3229 include diagnosis, prevention and treatment of Gastric cancers ., and of other diseases and clinical conditions associated with CASP10.

[43691] The function of CASP10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.Chemokine (c-c motif) ligand 16 (CCL16, Accession NP_004581.1) is another GAM3229 target gene, herein designated TARGET GENE. CCL16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL16 BINDING SITE, designated SEQ ID:5788, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43692] Another function of GAM3229 is therefore inhibition of Chemokine (c-c motif) ligand 16 (CCL16, Accession NP_004581.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL16.

[43693] Chemokine (c-c motif) ligand 22 (CCL22, Accession

NP_002981.2) is another GAM3229 target gene, herein designated TARGET GENE. CCL22 BINDING SITE1 and CCL22 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CCL22, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL22 BINDING SITE1 and CCL22 BINDING SITE2, designated SEQ ID:3458 and SEQ ID:15508 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43694] Another function of GAM3229 is therefore inhibition of Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL22.

[43695] CDCP1 (Accession NP_073753.3) is another GAM3229 target gene, herein designated TARGET GENE. CDCP1 BINDING SITE1 and CDCP1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CDCP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of CDCP1 BINDING SITE1 and CDCP1 BINDING SITE2, designated SEQ ID:10837 and SEQ ID:15862 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43696] Another function of GAM3229 is therefore inhibition of CDCP1 (Accession NP_073753.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDCP1.

[43697] Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) is another GAM3229 target gene, herein designated TARGET GENE. CDH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH1 BINDING SITE, designated SEQ ID:15318, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43698] Another function of GAM3229 is therefore inhibition of Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) . Accordingly, utilities of GAM3229 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH1.

[43699] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) is another GAM3229 target gene, herein designated TARGET GENE. CECR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CECR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE, designated SEQ ID:4587, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43700] Another function of GAM3229 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[43701] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) is another GAM3229 target gene, herein designated TARGET GENE. CECR1 BINDING SITE is a target binding site found in the 3` un-

translated region of multiple transcripts of mRNA encoded by CECR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE, designated SEQ ID:4587, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43702] Another function of GAM3229 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[43703] Centromere protein h (CENPH, Accession NP_075060.1) is another GAM3229 target gene, herein designated TARGET GENE. CENPH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CENPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CENPH BINDING SITE, designated SEQ ID:14468, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ

ID:221.

[43704] Another function of GAM3229 is therefore inhibition of Centromere protein h (CENPH, Accession NP_075060.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENPH.

[43705] CGI-43 (Accession NP_056437.1) is another GAM3229 target gene, herein designated TARGET GENE. CGI-43 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CGI-43, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-43 BINDING SITE, designated SEQ ID:3459, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43706] Another function of GAM3229 is therefore inhibition of CGI-43 (Accession NP_056437.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-43.

[43707] Chk1 checkpoint homolog (s. pombe) (CHEK1, Accession NP_001265.1) is another GAM3229 target gene, herein designated TARGET GENE. CHEK1 BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by CHEK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHEK1 BINDING SITE, designated SEQ ID:1819, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43708] Another function of GAM3229 is therefore inhibition of Chk1 checkpoint homolog (s. pombe) (CHEK1, Accession NP_001265.1), a gene which a protein kinase that is required for the DNA damage checkpoint. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHEK1.

[43709] The function of CHEK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3154.1.Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2) is another GAM3229 target gene, herein designated TARGET GENE. CIAS1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CIAS1, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIAS1 BINDING SITE, designated SEQ ID:8694, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43710] Another function of GAM3229 is therefore inhibition of Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2), a gene which may mediate protein- protein interactions; contains a leucine rich repeat and therefore may be associated with Familial cold autoinflammatory syndrome, muckle- wells syndrome. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Familial cold autoinflammatory syndrome, muckle- wells syndrome, and of other diseases and clinical conditions associated with CIAS1.

[43711] The function of CIAS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM90.1.CIP29 (Accession NP_115740.3) is another GAM3229 target gene, herein designated TARGET GENE. CIP29 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CIP29, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIP29 BINDING SITE, designated SEQ ID:8546, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43712] Another function of GAM3229 is therefore inhibition of CIP29 (Accession NP_115740.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIP29.

[43713] C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 11 (CLECSF11, Accession NP_569708.1) is another GAM3229 target gene, herein designated TARGET GENE. CLECSF11 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CLECSF11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLECSF11 BINDING SITE, designated SEQ ID:17166, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43714] Another function of GAM3229 is therefore inhibition of C-

type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 11 (CLECSF11, Accession NP_569708.1), a gene which may play a role in ligand internalization and presentation. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLECSF11.

[43715] The function of CLECSF11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM571.1.C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2) is another GAM3229 target gene, herein designated TARGET GENE. CLECSF12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLECSF12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLECSF12 BINDING SITE, designated SEQ ID:2783, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43716] Another function of GAM3229 is therefore inhibition of C-type (calcium dependent, carbohydrate-recognition do-

main) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2), a gene which is a pattern- recognition receptor . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLECSF12.

[43717] The function of CLECSF12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9 (CLECSF9, Accession NP_055173.1) is another GAM3229 target gene, herein designated TARGET GENE. CLECSF9 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CLECSF9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLECSF9 BINDING SITE, designated SEQ ID:12935, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43718] Another function of GAM3229 is therefore inhibition of C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9 (CLECSF9, Accession

NP_055173.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLECSF9.

[43719] CMRF-35H (Accession XP_046925.1) is another GAM3229 target gene, herein designated TARGET GENE. CMRF-35H BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CMRF-35H, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CMRF-35H BINDING SITE, designated SEQ ID:3608, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43720] Another function of GAM3229 is therefore inhibition of CMRF-35H (Accession XP_046925.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CMRF-35H.

[43721] Contactin associated protein-like 2 (CNTNAP2, Accession NP_054860.1) is another GAM3229 target gene, herein designated TARGET GENE. CNTNAP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNTNAP2, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNTNAP2 BINDING SITE, designated SEQ ID:17240, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43722] Another function of GAM3229 is therefore inhibition of Contactin associated protein-like 2 (CNTNAP2, Accession NP_054860.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNTNAP2.

[43723] Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) is another GAM3229 target gene, herein designated TARGET GENE. COLEC12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COLEC12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COLEC12 BINDING SITE, designated SEQ ID:5286, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43724] Another function of GAM3229 is therefore inhibition of

Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC12.

[43725] Coenzyme q7 homolog, ubiquinone (yeast) (COQ7, Accession NP_057222.2) is another GAM3229 target gene, herein designated TARGET GENE. COQ7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by COQ7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COQ7 BINDING SITE, designated SEQ ID:5762, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43726] Another function of GAM3229 is therefore inhibition of Coenzyme q7 homolog, ubiquinone (yeast) (COQ7, Accession NP_057222.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COQ7.

[43727] Carboxypeptidase a4 (CPA4, Accession NP_057436.1) is another GAM3229 target gene, herein designated TARGET GENE. CPA4 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by CPA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPA4 BINDING SITE, designated SEQ ID:2783, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43728] Another function of GAM3229 is therefore inhibition of Carboxypeptidase a4 (CPA4, Accession NP_057436.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPA4.

[43729] cPLA2delta (Accession XP_208820.2) is another GAM3229 target gene, herein designated TARGET GENE. cPLA2delta BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by cPLA2delta, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of cPLA2delta BINDING SITE, designated SEQ ID:5366, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43730] Another function of GAM3229 is therefore inhibition of cPLA2delta (Accession XP_208820.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with cPLA2delta.

[43731] cPLA2delta (Accession NP_828848.1) is another GAM3229 target gene, herein designated TARGET GENE. cPLA2delta BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by cPLA2delta, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of cPLA2delta BINDING SITE, designated SEQ ID:5366, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43732] Another function of GAM3229 is therefore inhibition of cPLA2delta (Accession NP_828848.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with cPLA2delta.

[43733] Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) is another GAM3229 tar-

get gene, herein designated TARGET GENE. CPSF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPSF2 BINDING SITE, designated SEQ ID:17815, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43734] Another function of GAM3229 is therefore inhibition of Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPSF2.

[43735] CRB3 (Accession NP_777378.1) is another GAM3229 target gene, herein designated TARGET GENE. CRB3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CRB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRB3 BINDING SITE, designated SEQ ID:2333, to the nucleotide sequence of GAM3229 RNA, herein des-

ignated GAM RNA, also designated SEQ ID:221.

[43736] Another function of GAM3229 is therefore inhibition of CRB3 (Accession NP_777378.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRB3.

[43737] Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) is another GAM3229 target gene, herein designated TARGET GENE. CRLF3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRLF3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRLF3 BINDING SITE, designated SEQ ID:18242, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43738] Another function of GAM3229 is therefore inhibition of Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRLF3.

[43739] Cartilage associated protein (CRTAP, Accession NP_006362.1) is another GAM3229 target gene, herein

designated TARGET GENE. CRTAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRTAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRTAP BINDING SITE, designated SEQ ID:7898, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43740] Another function of GAM3229 is therefore inhibition of Cartilage associated protein (CRTAP, Accession NP_006362.1), a gene which is a novel developmentally regulated chick embryo protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRTAP.

[43741] The function of CRTAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.CST (Accession NP_004852.1) is another GAM3229 target gene, herein designated TARGET GENE. CST BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CST, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CST BINDING SITE, designated SEQ ID:19277, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43742] Another function of GAM3229 is therefore inhibition of CST (Accession NP_004852.1), a gene which nucleotide-sugar transporter. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CST.

[43743] The function of CST and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM221.1.CTEN (Accession NP_116254.3) is another GAM3229 target gene, herein designated TARGET GENE. CTEN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTEN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTEN BINDING SITE, designated SEQ ID:12312, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43744] Another function of GAM3229 is therefore inhibition of CTEN (Accession NP_116254.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTEN.

[43745] Cathepsin b (CTSB, Accession NP_680090.1) is another GAM3229 target gene, herein designated TARGET GENE. CTSB BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSB BINDING SITE, designated SEQ ID:1677, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43746] Another function of GAM3229 is therefore inhibition of Cathepsin b (CTSB, Accession NP_680090.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSB.

[43747] Cathepsin b (CTSB, Accession NP_680092.1) is another GAM3229 target gene, herein designated TARGET GENE. CTSB BINDING SITE is a target binding site found in the 5`

untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSB BINDING SITE, designated SEQ ID:1677, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43748] Another function of GAM3229 is therefore inhibition of Cathepsin b (CTSB, Accession NP_680092.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSB.

[43749] Cytochrome p450, subfamily i (aromatic compound-inducible), polypeptide 2 (CYP1A2, Accession NP_000752.1) is another GAM3229 target gene, herein designated TARGET GENE. CYP1A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP1A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP1A2 BINDING SITE, designated SEQ ID:4564, to the nucleotide sequence of GAM3229

RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43750] Another function of GAM3229 is therefore inhibition of Cytochrome p450, subfamily i (aromatic compound-inducible), polypeptide 2 (CYP1A2, Accession NP_000752.1), a gene which intervenes in an NADPH- dependent electron transport pathway. and therefore may be associated with Porphyria cutanea tarda. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Porphyria cutanea tarda, and of other diseases and clinical conditions associated with CYP1A2.

[43751] The function of CYP1A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1) is another GAM3229 target gene, herein designated TARGET GENE. CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CYP2B6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2, designated SEQ ID:5285 and SEQ ID:11371 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43752] Another function of GAM3229 is therefore inhibition of Cytochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1), a gene which oxidizes a variety of structurally unrelated compounds, including steroids, fatty acids, and xenobiotics. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP2B6.

[43753] The function of CYP2B6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily iic (mephenytoin 4-hydroxylase), polypeptide 18 (CYP2C18, Accession NP_000763.1) is another GAM3229 target gene, herein designated TARGET GENE. CYP2C18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP2C18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of CYP2C18 BINDING SITE, designated SEQ ID:7874, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43754] Another function of GAM3229 is therefore inhibition of Cytochrome p450, subfamily iic (mephenytoin 4-hydroxylase), polypeptide 18 (CYP2C18, Accession NP_000763.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP2C18.

[43755] CYP51A1 (Accession NP_000777.1) is another GAM3229 target gene, herein designated TARGET GENE. CYP51A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP51A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP51A1 BINDING SITE, designated SEQ ID:18360, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43756] Another function of GAM3229 is therefore inhibition of CYP51A1 (Accession NP_000777.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with CYP51A1.

[43757] Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1) is another GAM3229 target gene, herein designated TARGET GENE. CYP8B1 BINDING SITE1 and CYP8B1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CYP8B1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP8B1 BINDING SITE1 and CYP8B1 BINDING SITE2, designated SEQ ID:5673 and SEQ ID:15966 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43758] Another function of GAM3229 is therefore inhibition of Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1), a gene which functions in bile acid biosynthesis. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP8B1.

[43759] The function of CYP8B1 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Debranching enzyme homolog 1 (s. cerevisiae) (DBR1, Accession NP_057300.1) is another GAM3229 target gene, herein designated TARGET GENE. DBR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DBR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DBR1 BINDING SITE, designated SEQ ID:6398, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43760] Another function of GAM3229 is therefore inhibition of Debranching enzyme homolog 1 (s. cerevisiae) (DBR1, Accession NP_057300.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBR1.

[43761] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) is another GAM3229 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:8602, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43762] Another function of GAM3229 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[43763] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) is another GAM3229 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:8602, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43764] Another function of GAM3229 is therefore inhibition of

Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[43765] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) is another GAM3229 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:8602, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43766] Another function of GAM3229 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[43767] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835364.1) is another GAM3229 target gene, herein designated TARGET GENE. DCX BINDING SITE

is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:8602, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43768] Another function of GAM3229 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835364.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[43769] DEPP (Accession NP_008952.1) is another GAM3229 target gene, herein designated TARGET GENE. DEPP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DEPP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DEPP BINDING SITE, designated SEQ ID:10348, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43770] Another function of GAM3229 is therefore inhibition of DEPP (Accession NP_008952.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DEPP.

[43771] Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1) is another GAM3229 target gene, herein designated TARGET GENE. DFFB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DFFB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DFFB BINDING SITE, designated SEQ ID:8629, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43772] Another function of GAM3229 is therefore inhibition of Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1), a gene which induces DNA fragmentation and chromatin condensation during apoptosis. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DFFB.

[43773] The function of DFFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Dihydrofolate reductase (DHFR, Accession NP_000782.1) is another GAM3229 target gene, herein designated TARGET GENE. DHFR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DHFR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DHFR BINDING SITE, designated SEQ ID:19487, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43774] Another function of GAM3229 is therefore inhibition of Dihydrofolate reductase (DHFR, Accession NP_000782.1), a gene which converts dihydrofolate into tetrahydrofolate. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DHFR.

[43775] The function of DHFR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM64.1.DIRAS1 (Accession NP_660156.1) is another GAM3229 target gene, herein designated TARGET GENE. DIRAS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DIRAS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DIRAS1 BINDING SITE, designated SEQ ID:19599, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43776] Another function of GAM3229 is therefore inhibition of DIRAS1 (Accession NP_660156.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIRAS1.

[43777] Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1) is another GAM3229 target gene, herein designated TARGET GENE. DISC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DISC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DISC1 BINDING SITE, designated SEQ ID:14849, to the nucleotide sequence of GAM3229

RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43778] Another function of GAM3229 is therefore inhibition of Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1), a gene which has globular N- terminal domain(s) and a helical C- terminal domain. and therefore may be associated with Schizophrenia . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Schizophrenia ., and of other diseases and clinical conditions associated with DISC1.

[43779] The function of DISC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.DKFZP434B044 (Accession NP_113664.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZP434B044 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434B044, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434B044 BINDING SITE, designated SEQ ID:13291, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[43780] Another function of GAM3229 is therefore inhibition of DKFZP434B044 (Accession NP_113664.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434B044.

[43781] DKFZp434C0923 (Accession NP_060068.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZp434C0923 BINDING SITE1 and DKFZp434C0923 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DKFZp434C0923, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434C0923 BINDING SITE1 and DKFZp434C0923 BINDING SITE2, designated SEQ ID:12561 and SEQ ID:15862 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43782] Another function of GAM3229 is therefore inhibition of DKFZp434C0923 (Accession NP_060068.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZp434C0923.

[43783] DKFZP434F0318 (Accession NP_110444.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZP434F0318 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F0318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434F0318 BINDING SITE, designated SEQ ID:1165, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43784] Another function of GAM3229 is therefore inhibition of DKFZP434F0318 (Accession NP_110444.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F0318.

[43785] DKFZp434J0226 (Accession XP_051327.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZp434J0226 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp434J0226, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434J0226 BINDING SITE, designated SEQ ID:10801, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43786] Another function of GAM3229 is therefore inhibition of DKFZp434J0226 (Accession XP_051327.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434J0226.

[43787] DKFZP564J0863 (Accession NP_056274.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZP564J0863 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564J0863, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564J0863 BINDING SITE, designated SEQ ID:15802, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43788] Another function of GAM3229 is therefore inhibition of DKFZP564J0863 (Accession NP_056274.1) . Accordingly,

utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564J0863.

[43789] DKFZP566I1024 (Accession NP_056226.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZP566I1024 BINDING SITE1 and DKFZP566I1024 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DKFZP566I1024, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566I1024 BINDING SITE1 and DKFZP566I1024 BINDING SITE2, designated SEQ ID:19870 and SEQ ID:18357 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43790] Another function of GAM3229 is therefore inhibition of DKFZP566I1024 (Accession NP_056226.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566I1024.

[43791] DKFZP586A0522 (Accession NP_054752.1) is another GAM3229 target gene, herein designated TARGET GENE.

DKFZP586A0522 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586A0522, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586A0522 BINDING SITE, designated SEQ ID:15526, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43792] Another function of GAM3229 is therefore inhibition of DKFZP586A0522 (Accession NP_054752.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586A0522.

[43793] DKFZp667B1218 (Accession NP_808881.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZp667B1218 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp667B1218, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667B1218 BINDING SITE, designated SEQ ID:10537, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43794] Another function of GAM3229 is therefore inhibition of DKFZp667B1218 (Accession NP_808881.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp667B1218.

[43795] DKFZp667E0512 (Accession XP_117353.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZp667E0512 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp667E0512, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667E0512 BINDING SITE, designated SEQ ID:18552, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43796] Another function of GAM3229 is therefore inhibition of DKFZp667E0512 (Accession XP_117353.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp667E0512.

[43797] DKFZp686G052 (Accession XP_300559.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZp686G052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp686G052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp686G052 BINDING SITE, designated SEQ ID:6504, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43798] Another function of GAM3229 is therefore inhibition of DKFZp686G052 (Accession XP_300559.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp686G052.

[43799] DKFZp761H039 (Accession NP_061181.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZp761H039 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761H039, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of DKFZp761H039 BINDING SITE, designated SEQ ID:13622, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43800] Another function of GAM3229 is therefore inhibition of DKFZp761H039 (Accession NP_061181.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761H039.

[43801] DKFZp761P1121 (Accession NP_690870.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZp761P1121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761P1121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761P1121 BINDING SITE, designated SEQ ID:10832, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43802] Another function of GAM3229 is therefore inhibition of DKFZp761P1121 (Accession NP_690870.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZp761P1121.

[43803] DKFZp762C2414 (Accession NP_848637.1) is another GAM3229 target gene, herein designated TARGET GENE. DKFZp762C2414 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762C2414, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762C2414 BINDING SITE, designated SEQ ID:7031, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43804] Another function of GAM3229 is therefore inhibition of DKFZp762C2414 (Accession NP_848637.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762C2414.

[43805] DKFZp762H185 (Accession XP_172976.2) is another GAM3229 target gene, herein designated TARGET GENE. DKFZp762H185 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762H185, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762H185 BINDING SITE, designated SEQ ID:4228, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43806] Another function of GAM3229 is therefore inhibition of DKFZp762H185 (Accession XP_172976.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762H185.

[43807] Dystrophia myotonica-protein kinase (DMPK, Accession NP_004400.3) is another GAM3229 target gene, herein designated TARGET GENE. DMPK BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DMPK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DMPK BINDING SITE, designated SEQ ID:7032, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43808] Another function of GAM3229 is therefore inhibition of

Dystrophia myotonica-protein kinase (DMPK, Accession NP_004400.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMPK.

[43809] Dnaj (hsp40) homolog, subfamily a, member 3 (DNAJA3, Accession NP_005138.2) is another GAM3229 target gene, herein designated TARGET GENE. DNAJA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DNAJA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DNAJA3 BINDING SITE, designated SEQ ID:6370, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43810] Another function of GAM3229 is therefore inhibition of Dnaj (hsp40) homolog, subfamily a, member 3 (DNAJA3, Accession NP_005138.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAJA3.

[43811] DUSP18 (Accession NP_689724.2) is another GAM3229 target gene, herein designated TARGET GENE. DUSP18 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by DUSP18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP18 BINDING SITE, designated SEQ ID:7626, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43812] Another function of GAM3229 is therefore inhibition of DUSP18 (Accession NP_689724.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP18.

[43813] Dual specificity phosphatase 19 (DUSP19, Accession NP_543152.1) is another GAM3229 target gene, herein designated TARGET GENE. DUSP19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DUSP19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP19 BINDING SITE, designated SEQ ID:6797, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43814] Another function of GAM3229 is therefore inhibition of Dual specificity phosphatase 19 (DUSP19, Accession NP_543152.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP19.

[43815] Dual specificity phosphatase 7 (DUSP7, Accession XP_037430.6) is another GAM3229 target gene, herein designated TARGET GENE. DUSP7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DUSP7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP7 BINDING SITE, designated SEQ ID:6796, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43816] Another function of GAM3229 is therefore inhibition of Dual specificity phosphatase 7 (DUSP7, Accession XP_037430.6), a gene which is a member of the dual specificity protein phosphatase family . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP7.

[43817] The function of DUSP7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NP_567824.1) is another GAM3229 target gene, herein designated TARGET GENE. DYRK1A BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by DYRK1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DYRK1A BINDING SITE, designated SEQ ID:15252, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43818] Another function of GAM3229 is therefore inhibition of Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NP_567824.1), a gene which regulates cell proliferation and may be involved in brain development . and therefore may be associated with Down syndrome. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Down syndrome, and of other diseases and clinical conditions asso-

ciated with DYRK1A.

[43819] The function of DYRK1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Eukaryotic translation initiation factor 5a2 (EIF5A2, Accession NP_065123.1) is another GAM3229 target gene, herein designated TARGET GENE. EIF5A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF5A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF5A2 BINDING SITE, designated SEQ ID:14800, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43820] Another function of GAM3229 is therefore inhibition of Eukaryotic translation initiation factor 5a2 (EIF5A2, Accession NP_065123.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF5A2.

[43821] ELP3 (Accession NP_060561.3) is another GAM3229 target gene, herein designated TARGET GENE. ELP3 BINDING SITE is a target binding site found in the 3` untranslated re-

gion of mRNA encoded by ELP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ELP3 BINDING SITE, designated SEQ ID:11180, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43822] Another function of GAM3229 is therefore inhibition of ELP3 (Accession NP_060561.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELP3.

[43823] Ecotropic viral integration site 5 (EVI5, Accession NP_005656.2) is another GAM3229 target gene, herein designated TARGET GENE. EVI5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EVI5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVI5 BINDING SITE, designated SEQ ID:10675, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43824] Another function of GAM3229 is therefore inhibition of

Ecotropic viral integration site 5 (EVI5, Accession NP_005656.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVI5.

[43825] Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1) is another GAM3229 target gene, herein designated TARGET GENE. F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F3 BINDING SITE, designated SEQ ID:17533, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43826] Another function of GAM3229 is therefore inhibition of Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1), a gene which functions in normal hemostasis. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F3.

[43827] The function of F3 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM136.1.Fatty acid binding protein 2, intestinal (FABP2, Accession NP_000125.1) is another GAM3229 target gene, herein designated TARGET GENE. FABP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FABP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FABP2 BINDING SITE, designated SEQ ID:15832, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43828] Another function of GAM3229 is therefore inhibition of Fatty acid binding protein 2, intestinal (FABP2, Accession NP_000125.1), a gene which may have a role in dietary fat uptake or processing. and therefore may be associated with Cardiovascular disease and type 2 diabetes. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Cardiovascular disease and type 2 diabetes., and of other diseases and clinical conditions associated with FABP2.

[43829] The function of FABP2 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM189.1.Fanconi anemia, complementation group f (FANCF, Accession NP_073562.1) is another GAM3229 target gene, herein designated TARGET GENE. FANCF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCF BINDING SITE, designated SEQ ID:12811, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43830] Another function of GAM3229 is therefore inhibition of Fanconi anemia, complementation group f (FANCF, Accession NP_073562.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCF.

[43831] FBXW8 (Accession NP_699179.2) is another GAM3229 target gene, herein designated TARGET GENE. FBXW8 BINDING SITE1 and FBXW8 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FBXW8, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXW8 BINDING SITE1 and FBXW8 BINDING SITE2, designated SEQ ID:14800 and SEQ ID:14800 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43832] Another function of GAM3229 is therefore inhibition of FBXW8 (Accession NP_699179.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW8.

[43833] FBXW8 (Accession NP_036306.1) is another GAM3229 target gene, herein designated TARGET GENE. FBXW8 BINDING SITE1 and FBXW8 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FBXW8, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXW8 BINDING SITE1 and FBXW8 BINDING SITE2, designated SEQ ID:3077 and SEQ ID:3077 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43834] Another function of GAM3229 is therefore inhibition of

FBXW8 (Accession NP_036306.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW8.

[43835] Fc fragment of iga, receptor for (FCAR, Accession NP_579813.1) is another GAM3229 target gene, herein designated TARGET GENE. FCAR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FCAR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCAR BINDING SITE, designated SEQ ID:14078, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43836] Another function of GAM3229 is therefore inhibition of Fc fragment of iga, receptor for (FCAR, Accession NP_579813.1), a gene which binds to the fc region of immunoglobulins alpha and mediates several functions including cytokine production. and therefore may be associated with Iga nephropathy. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Iga nephropathy., and of other diseases and clinical conditions associated with FCAR.

[43837] The function of FCAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.FCRH1 (Accession NP_443170.1) is another GAM3229 target gene, herein designated TARGET GENE. FCRH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FCRH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCRH1 BINDING SITE, designated SEQ ID:10358, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43838] Another function of GAM3229 is therefore inhibition of FCRH1 (Accession NP_443170.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCRH1.

[43839] Fgd1 family, member 2 (FGD2, Accession NP_775829.1) is another GAM3229 target gene, herein designated TARGET GENE. FGD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FGD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGD2 BINDING SITE, designated SEQ ID:7015, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43840] Another function of GAM3229 is therefore inhibition of Fgd1 family, member 2 (FGD2, Accession NP_775829.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGD2.

[43841] Fragile histidine triad gene (FHIT, Accession NP_002003.1) is another GAM3229 target gene, herein designated TARGET GENE. FHIT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

FHIT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FHIT BINDING SITE, designated SEQ ID:894, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43842] Another function of GAM3229 is therefore inhibition of Fragile histidine triad gene (FHIT, Accession NP_002003.1), a gene which cleaves a- 5'- ppp- 5'a to yield amp and adp. possible tumor suppressor for specific tissues. and therefore may be associated with Cancers. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Cancers., and of other diseases and clinical conditions associated with FHIT.

[43843] The function of FHIT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM664.2.FISH (Accession NP_055446.1) is another GAM3229 target gene, herein designated TARGET GENE. FISH BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FISH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FISH BINDING SITE, designated SEQ ID:15859, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43844] Another function of GAM3229 is therefore inhibition of FISH (Accession NP_055446.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FISH.

[43845] FLJ00007 (Accession NP_258260.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ00007 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ00007, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ00007 BINDING SITE, designated SEQ ID:12711, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43846] Another function of GAM3229 is therefore inhibition of FLJ00007 (Accession NP_258260.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00007.

[43847] FLJ00060 (Accession XP_028154.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ00060 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ00060, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ00060 BINDING SITE, designated SEQ ID:717, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43848] Another function of GAM3229 is therefore inhibition of FLJ00060 (Accession XP_028154.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00060.

[43849] FLJ10276 (Accession NP_060515.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ10276 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10276, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10276 BINDING SITE, designated SEQ ID:11366, to the

nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43850] Another function of GAM3229 is therefore inhibition of FLJ10276 (Accession NP_060515.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10276.

[43851] FLJ10520 (Accession NP_060594.2) is another GAM3229 target gene, herein designated TARGET GENE. FLJ10520 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10520, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10520 BINDING SITE, designated SEQ ID:9307, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43852] Another function of GAM3229 is therefore inhibition of FLJ10520 (Accession NP_060594.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10520.

[43853] FLJ10535 (Accession NP_060599.1) is another GAM3229

target gene, herein designated TARGET GENE. FLJ10535 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10535, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10535 BINDING SITE, designated SEQ ID:6398, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43854] Another function of GAM3229 is therefore inhibition of FLJ10535 (Accession NP_060599.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10535.

[43855] FLJ10700 (Accession NP_060652.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ10700 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10700, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10700 BINDING SITE, designated SEQ ID:4483, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[43856] Another function of GAM3229 is therefore inhibition of FLJ10700 (Accession NP_060652.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10700.

[43857] FLJ10847 (Accession NP_060712.2) is another GAM3229 target gene, herein designated TARGET GENE. FLJ10847 BINDING SITE1 through FLJ10847 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by FLJ10847, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10847 BINDING SITE1 through FLJ10847 BINDING SITE3, designated SEQ ID:7550, SEQ ID:8121 and SEQ ID:3502 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43858] Another function of GAM3229 is therefore inhibition of FLJ10847 (Accession NP_060712.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10847.

[43859] FLJ11230 (Accession NP_060836.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ11230 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11230, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11230 BINDING SITE, designated SEQ ID:9182, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43860] Another function of GAM3229 is therefore inhibition of FLJ11230 (Accession NP_060836.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11230.

[43861] FLJ11323 (Accession NP_060860.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ11323 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ11323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11323 BINDING SITE, designated

SEQ ID:7842, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43862] Another function of GAM3229 is therefore inhibition of FLJ11323 (Accession NP_060860.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11323.

[43863] FLJ12610 (Accession NP_079058.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ12610 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12610, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12610 BINDING SITE, designated SEQ ID:13971, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43864] Another function of GAM3229 is therefore inhibition of FLJ12610 (Accession NP_079058.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12610.

[43865] FLJ12747 (Accession XP_290972.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ12747 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12747, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12747 BINDING SITE, designated SEQ ID:3806, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43866] Another function of GAM3229 is therefore inhibition of FLJ12747 (Accession XP_290972.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12747.

[43867] FLJ12903 (Accession NP_073590.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ12903 BINDING SITE1 and FLJ12903 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ12903, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12903 BINDING SITE1 and

FLJ12903 BINDING SITE2, designated SEQ ID:15331 and SEQ ID:19721 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43868] Another function of GAM3229 is therefore inhibition of FLJ12903 (Accession NP_073590.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12903.

[43869] FLJ12975 (Accession NP_079085.2) is another GAM3229 target gene, herein designated TARGET GENE. FLJ12975 BINDING SITE1 and FLJ12975 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ12975, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12975 BINDING SITE1 and FLJ12975 BINDING SITE2, designated SEQ ID:6872 and SEQ ID:3161 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43870] Another function of GAM3229 is therefore inhibition of FLJ12975 (Accession NP_079085.2) . Accordingly, utilities

of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12975.

[43871] FLJ12985 (Accession NP_079200.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ12985 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12985, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12985 BINDING SITE, designated SEQ ID:7712, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43872] Another function of GAM3229 is therefore inhibition of FLJ12985 (Accession NP_079200.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12985.

[43873] FLJ13072 (Accession XP_117117.2) is another GAM3229 target gene, herein designated TARGET GENE. FLJ13072 BINDING SITE1 and FLJ13072 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ13072, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13072 BINDING SITE1 and FLJ13072 BINDING SITE2, designated SEQ ID:6829 and SEQ ID:18493 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43874] Another function of GAM3229 is therefore inhibition of FLJ13072 (Accession XP_117117.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13072.

[43875] FLJ13590 (Accession NP_079116.2) is another GAM3229 target gene, herein designated TARGET GENE. FLJ13590 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13590, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13590 BINDING SITE, designated SEQ ID:6224, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43876] Another function of GAM3229 is therefore inhibition of

FLJ13590 (Accession NP_079116.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13590.

[43877] FLJ13955 (Accession NP_079035.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ13955 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13955, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13955 BINDING SITE, designated SEQ ID:7938, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43878] Another function of GAM3229 is therefore inhibition of FLJ13955 (Accession NP_079035.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13955.

[43879] FLJ14054 (Accession NP_078839.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ14054 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14054, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14054 BINDING SITE, designated SEQ ID:8656, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43880] Another function of GAM3229 is therefore inhibition of FLJ14054 (Accession NP_078839.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14054.

[43881] FLJ14351 (Accession NP_079008.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ14351 BINDING SITE1 and FLJ14351 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ14351, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14351 BINDING SITE1 and FLJ14351 BINDING SITE2, designated SEQ ID:7578 and SEQ ID:8490 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43882] Another function of GAM3229 is therefore inhibition of FLJ14351 (Accession NP_079008.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14351.

[43883] FLJ14803 (Accession NP_116231.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ14803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14803 BINDING SITE, designated SEQ ID:18549, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43884] Another function of GAM3229 is therefore inhibition of FLJ14803 (Accession NP_116231.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14803.

[43885] FLJ20038 (Accession NP_060104.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ20038 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ20038, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20038 BINDING SITE, designated SEQ ID:14023, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43886] Another function of GAM3229 is therefore inhibition of FLJ20038 (Accession NP_060104.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20038.

[43887] FLJ20045 (Accession NP_060108.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ20045 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20045 BINDING SITE, designated SEQ ID:603, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43888] Another function of GAM3229 is therefore inhibition of

FLJ20045 (Accession NP_060108.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20045.

[43889] FLJ20125 (Accession NP_060146.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ20125 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20125, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20125 BINDING SITE, designated SEQ ID:12250, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43890] Another function of GAM3229 is therefore inhibition of FLJ20125 (Accession NP_060146.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20125.

[43891] FLJ20200 (Accession NP_060178.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ20200 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20200, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20200 BINDING SITE, designated SEQ ID:18150, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43892] Another function of GAM3229 is therefore inhibition of FLJ20200 (Accession NP_060178.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20200.

[43893] FLJ20671 (Accession NP_060394.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ20671 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20671, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20671 BINDING SITE, designated SEQ ID:19922, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43894] Another function of GAM3229 is therefore inhibition of FLJ20671 (Accession NP_060394.1) . Accordingly, utilities

of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20671.

[43895] FLJ20729 (Accession NP_060423.2) is another GAM3229 target gene, herein designated TARGET GENE. FLJ20729 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20729, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20729 BINDING SITE, designated SEQ ID:7073, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43896] Another function of GAM3229 is therefore inhibition of FLJ20729 (Accession NP_060423.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20729.

[43897] FLJ21302 (Accession NP_075052.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ21302 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21302, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21302 BINDING SITE, designated SEQ ID:3479, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43898] Another function of GAM3229 is therefore inhibition of FLJ21302 (Accession NP_075052.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21302.

[43899] FLJ22347 (Accession NP_073741.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ22347 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22347, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22347 BINDING SITE, designated SEQ ID:15136, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43900] Another function of GAM3229 is therefore inhibition of FLJ22347 (Accession NP_073741.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ22347.

[43901] FLJ22529 (Accession NP_079065.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ22529 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22529, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22529 BINDING SITE, designated SEQ ID:19173, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43902] Another function of GAM3229 is therefore inhibition of FLJ22529 (Accession NP_079065.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22529.

[43903] FLJ22800 (Accession NP_079071.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ22800 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22800, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ22800 BINDING SITE, designated SEQ ID:3918, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43904] Another function of GAM3229 is therefore inhibition of FLJ22800 (Accession NP_079071.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22800.

[43905] FLJ23024 (Accession NP_079212.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ23024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23024 BINDING SITE, designated SEQ ID:2778, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43906] Another function of GAM3229 is therefore inhibition of FLJ23024 (Accession NP_079212.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ23024.

[43907] FLJ23040 (Accession NP_079450.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ23040 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23040, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23040 BINDING SITE, designated SEQ ID:7588, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43908] Another function of GAM3229 is therefore inhibition of FLJ23040 (Accession NP_079450.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23040.

[43909] FLJ23047 (Accession NP_078824.2) is another GAM3229 target gene, herein designated TARGET GENE. FLJ23047 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23047, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ23047 BINDING SITE, designated SEQ ID:11628, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43910] Another function of GAM3229 is therefore inhibition of FLJ23047 (Accession NP_078824.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23047.

[43911] FLJ23356 (Accession NP_115613.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ23356 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23356 BINDING SITE, designated SEQ ID:8065, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43912] Another function of GAM3229 is therefore inhibition of FLJ23356 (Accession NP_115613.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23356.

[43913] FLJ23416 (Accession NP_115614.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ23416 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23416, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23416 BINDING SITE, designated SEQ ID:15550, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43914] Another function of GAM3229 is therefore inhibition of FLJ23416 (Accession NP_115614.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23416.

[43915] FLJ23563 (Accession XP_041701.4) is another GAM3229 target gene, herein designated TARGET GENE. FLJ23563 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23563 BINDING SITE, designated SEQ ID:16466, to the

nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43916] Another function of GAM3229 is therefore inhibition of FLJ23563 (Accession XP_041701.4) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23563.

[43917] FLJ25286 (Accession NP_689759.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ25286 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25286, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25286 BINDING SITE, designated SEQ ID:1118, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43918] Another function of GAM3229 is therefore inhibition of FLJ25286 (Accession NP_689759.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25286.

[43919] FLJ30656 (Accession NP_689557.1) is another GAM3229

target gene, herein designated TARGET GENE. FLJ30656 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30656, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30656 BINDING SITE, designated SEQ ID:11839, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43920] Another function of GAM3229 is therefore inhibition of FLJ30656 (Accession NP_689557.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30656.

[43921] FLJ31166 (Accession NP_694567.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ31166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31166 BINDING SITE, designated SEQ ID:19706, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[43922] Another function of GAM3229 is therefore inhibition of FLJ31166 (Accession NP_694567.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31166.

[43923] FLJ31821 (Accession NP_694574.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ31821 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31821, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31821 BINDING SITE, designated SEQ ID:11267, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43924] Another function of GAM3229 is therefore inhibition of FLJ31821 (Accession NP_694574.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31821.

[43925] FLJ32096 (Accession NP_776156.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ32096

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32096, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32096 BINDING SITE, designated SEQ ID:8326, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43926] Another function of GAM3229 is therefore inhibition of FLJ32096 (Accession NP_776156.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32096.

[43927] FLJ32384 (Accession NP_653209.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ32384 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32384, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32384 BINDING SITE, designated SEQ ID:19381, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43928] Another function of GAM3229 is therefore inhibition of FLJ32384 (Accession NP_653209.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32384.

[43929] FLJ32865 (Accession NP_653214.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ32865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32865 BINDING SITE, designated SEQ ID:16336, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43930] Another function of GAM3229 is therefore inhibition of FLJ32865 (Accession NP_653214.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865.

[43931] FLJ32894 (Accession NP_653268.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ32894 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ32894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32894 BINDING SITE, designated SEQ ID:18611, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43932] Another function of GAM3229 is therefore inhibition of FLJ32894 (Accession NP_653268.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32894.

[43933] FLJ33655 (Accession NP_775912.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ33655 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33655, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33655 BINDING SITE, designated SEQ ID:2783, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43934] Another function of GAM3229 is therefore inhibition of

FLJ33655 (Accession NP_775912.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33655.

[43935] FLJ33768 (Accession NP_775881.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ33768 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33768, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33768 BINDING SITE, designated SEQ ID:1133, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43936] Another function of GAM3229 is therefore inhibition of FLJ33768 (Accession NP_775881.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33768.

[43937] FLJ33814 (Accession NP_775781.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ33814 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33814, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33814 BINDING SITE, designated SEQ ID:4586, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43938] Another function of GAM3229 is therefore inhibition of FLJ33814 (Accession NP_775781.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33814.

[43939] FLJ33860 (Accession NP_775915.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ33860 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33860, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33860 BINDING SITE, designated SEQ ID:2033, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43940] Another function of GAM3229 is therefore inhibition of FLJ33860 (Accession NP_775915.1) . Accordingly, utilities

of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33860.

[43941] FLJ33918 (Accession NP_689620.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ33918 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33918, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33918 BINDING SITE, designated SEQ ID:3095, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43942] Another function of GAM3229 is therefore inhibition of FLJ33918 (Accession NP_689620.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33918.

[43943] FLJ34817 (Accession NP_689516.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ34817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ34817, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34817 BINDING SITE, designated SEQ ID:20002, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43944] Another function of GAM3229 is therefore inhibition of FLJ34817 (Accession NP_689516.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34817.

[43945] FLJ35487 (Accession NP_776181.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ35487 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35487, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35487 BINDING SITE, designated SEQ ID:7671, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43946] Another function of GAM3229 is therefore inhibition of FLJ35487 (Accession NP_776181.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ35487.

[43947] FLJ35681 (Accession NP_787096.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ35681 BINDING SITE1 and FLJ35681 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ35681, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35681 BINDING SITE1 and FLJ35681 BINDING SITE2, designated SEQ ID:20076 and SEQ ID:14927 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43948] Another function of GAM3229 is therefore inhibition of FLJ35681 (Accession NP_787096.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35681.

[43949] FLJ35740 (Accession NP_671728.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ35740 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35740, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35740 BINDING SITE, designated SEQ ID:19097, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43950] Another function of GAM3229 is therefore inhibition of FLJ35740 (Accession NP_671728.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35740.

[43951] FLJ35848 (Accession XP_290755.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ35848 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35848, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35848 BINDING SITE, designated SEQ ID:4410, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43952] Another function of GAM3229 is therefore inhibition of FLJ35848 (Accession XP_290755.1) . Accordingly, utilities

of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35848.

[43953] FLJ36032 (Accession XP_290874.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ36032 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36032, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36032 BINDING SITE, designated SEQ ID:6274, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43954] Another function of GAM3229 is therefore inhibition of FLJ36032 (Accession XP_290874.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36032.

[43955] FLJ37078 (Accession NP_694588.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ37078 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ37078, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37078 BINDING SITE, designated SEQ ID:7587, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43956] Another function of GAM3229 is therefore inhibition of FLJ37078 (Accession NP_694588.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37078.

[43957] FLJ37433 (Accession NP_848612.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ37433 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37433, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37433 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43958] Another function of GAM3229 is therefore inhibition of FLJ37433 (Accession NP_848612.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ37433.

[43959] FLJ38149 (Accession XP_091919.5) is another GAM3229 target gene, herein designated TARGET GENE. FLJ38149 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38149 BINDING SITE, designated SEQ ID:11940, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43960] Another function of GAM3229 is therefore inhibition of FLJ38149 (Accession XP_091919.5) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38149.

[43961] FLJ38281 (Accession NP_689814.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ38281 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38281, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ38281 BINDING SITE, designated SEQ ID:1314, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43962] Another function of GAM3229 is therefore inhibition of FLJ38281 (Accession NP_689814.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38281.

[43963] FLJ38607 (Accession NP_689867.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ38607 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38607, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38607 BINDING SITE, designated SEQ ID:11533, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43964] Another function of GAM3229 is therefore inhibition of FLJ38607 (Accession NP_689867.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ38607.

[43965] FLJ38792 (Accession NP_848615.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ38792 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38792, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38792 BINDING SITE, designated SEQ ID:18663, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43966] Another function of GAM3229 is therefore inhibition of FLJ38792 (Accession NP_848615.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38792.

[43967] FLJ38819 (Accession NP_665872.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ38819 BINDING SITE1 and FLJ38819 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38819, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of FLJ38819 BINDING SITE1 and FLJ38819 BINDING SITE2, designated SEQ ID:9307 and SEQ ID:1627 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43968] Another function of GAM3229 is therefore inhibition of FLJ38819 (Accession NP_665872.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38819.

[43969] FLJ38991 (Accession NP_776188.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ38991 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38991, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38991 BINDING SITE, designated SEQ ID:12896, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43970] Another function of GAM3229 is therefore inhibition of FLJ38991 (Accession NP_776188.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ38991.

[43971] FLJ39058 (Accession NP_775851.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ39058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39058 BINDING SITE, designated SEQ ID:5123, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43972] Another function of GAM3229 is therefore inhibition of FLJ39058 (Accession NP_775851.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39058.

[43973] FLJ39426 (Accession NP_775880.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ39426 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ39426, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ39426 BINDING SITE, designated SEQ ID:16679, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43974] Another function of GAM3229 is therefore inhibition of FLJ39426 (Accession NP_775880.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39426.

[43975] FLJ39599 (Accession NP_776164.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ39599 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39599, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39599 BINDING SITE, designated SEQ ID:7239, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43976] Another function of GAM3229 is therefore inhibition of FLJ39599 (Accession NP_776164.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ39599.

[43977] FLJ39639 (Accession XP_290687.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ39639 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39639, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39639 BINDING SITE, designated SEQ ID:2704, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43978] Another function of GAM3229 is therefore inhibition of FLJ39639 (Accession XP_290687.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39639.

[43979] FLJ40137 (Accession NP_775749.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ40137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ40137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ40137 BINDING SITE, designated SEQ ID:3565, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43980] Another function of GAM3229 is therefore inhibition of FLJ40137 (Accession NP_775749.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ40137.

[43981] FLJ90119 (Accession NP_699178.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ90119 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90119, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90119 BINDING SITE, designated SEQ ID:1074, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43982] Another function of GAM3229 is therefore inhibition of FLJ90119 (Accession NP_699178.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90119.

[43983] FLJ90754 (Accession NP_699197.1) is another GAM3229 target gene, herein designated TARGET GENE. FLJ90754 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ90754, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90754 BINDING SITE, designated SEQ ID:2556, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43984] Another function of GAM3229 is therefore inhibition of FLJ90754 (Accession NP_699197.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90754.

[43985] Fragile x mental retardation 2 (FMR2, Accession NP_002016.1) is another GAM3229 target gene, herein designated TARGET GENE. FMR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FMR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FMR2 BINDING SITE, designated

SEQ ID:9034, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43986] Another function of GAM3229 is therefore inhibition of Fragile x mental retardation 2 (FMR2, Accession NP_002016.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FMR2.

[43987] FSD1 (Accession NP_077309.1) is another GAM3229 target gene, herein designated TARGET GENE. FSD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FSD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FSD1 BINDING SITE, designated SEQ ID:12959, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43988] Another function of GAM3229 is therefore inhibition of FSD1 (Accession NP_077309.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FSD1.

[43989] Follistatin-like 3 (secreted glycoprotein) (FSTL3, Accession

NP_005851.1) is another GAM3229 target gene, herein designated TARGET GENE. FSTL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FSTL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FSTL3 BINDING SITE, designated SEQ ID:13077, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43990] Another function of GAM3229 is therefore inhibition of Follistatin-like 3 (secreted glycoprotein) (FSTL3, Accession NP_005851.1), a gene which is a member of the follistatin- module- protein family and therefore may be associated with Leukemia. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Leukemia., and of other diseases and clinical conditions associated with FSTL3.

[43991] The function of FSTL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM523.2.Ftsj homolog 2 (e. coli) (FTSJ2, Accession NP_803191.1) is another GAM3229 target gene, herein

designated TARGET GENE. FTSJ2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FTSJ2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FTSJ2 BINDING SITE, designated SEQ ID:14535, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43992] Another function of GAM3229 is therefore inhibition of Ftsj homolog 2 (e. coli) (FTSJ2, Accession NP_803191.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FTSJ2.

[43993] Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) is another GAM3229 target gene, herein designated TARGET GENE. FUT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FUT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FUT1 BINDING SITE, designated SEQ ID:13673, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43994] Another function of GAM3229 is therefore inhibition of Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUT1.

[43995] Giant axonal neuropathy (gigaxonin) (GAN, Accession NP_071324.1) is another GAM3229 target gene, herein designated TARGET GENE. GAN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GAN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GAN BINDING SITE, designated SEQ ID:14322, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43996] Another function of GAM3229 is therefore inhibition of Giant axonal neuropathy (gigaxonin) (GAN, Accession

NP_071324.1), a gene which plays an important role in neurofilament architecture. and therefore may be associated with Giant axonal neuropathy 1. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Giant axonal neuropathy 1., and of other diseases and clinical conditions associated with GAN.

[43997] The function of GAN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.GBP4 (Accession NP_443173.2) is another GAM3229 target gene, herein designated TARGET GENE. GBP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GBP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GBP4 BINDING SITE, designated SEQ ID:655, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[43998] Another function of GAM3229 is therefore inhibition of GBP4 (Accession NP_443173.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GBP4.

[43999] Glial fibrillary acidic protein (GFAP, Accession NP_002046.1) is another GAM3229 target gene, herein designated TARGET GENE. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GFAP BINDING SITE, designated SEQ ID:9652, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44000] Another function of GAM3229 is therefore inhibition of Glial fibrillary acidic protein (GFAP, Accession NP_002046.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFAP.

[44001] Glyoxalase i (GLO1, Accession NP_006699.1) is another GAM3229 target gene, herein designated TARGET GENE. GLO1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

GLO1 BINDING SITE, designated SEQ ID:14826, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44002] Another function of GAM3229 is therefore inhibition of Glyoxalase i (GLO1, Accession NP_006699.1), a gene which converts methylglyoxal and glutathione to S- lactoylglutathione. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLO1.

[44003] The function of GLO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1550.1.Gm2 ganglioside activator protein (GM2A, Accession NP_000396.1) is another GAM3229 target gene, herein designated TARGET GENE. GM2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GM2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GM2A BINDING SITE, designated SEQ ID:2783, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44004] Another function of GAM3229 is therefore inhibition of Gm2 ganglioside activator protein (GM2A, Accession NP_000396.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GM2A.

[44005] GNPNAT1 (Accession XP_085119.1) is another GAM3229 target gene, herein designated TARGET GENE. GNPNAT1 BINDING SITE1 and GNPNAT1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GNPNAT1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNPNAT1 BINDING SITE1 and GNPNAT1 BINDING SITE2, designated SEQ ID:12484 and SEQ ID:13881 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44006] Another function of GAM3229 is therefore inhibition of GNPNAT1 (Accession XP_085119.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNPNAT1.

[44007] GPP34R (Accession NP_060648.2) is another GAM3229

target gene, herein designated TARGET GENE. GPP34R BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPP34R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPP34R BINDING SITE, designated SEQ ID:14018, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44008] Another function of GAM3229 is therefore inhibition of GPP34R (Accession NP_060648.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPP34R.

[44009] G protein-coupled receptor 81 (GPR81, Accession NP_115943.1) is another GAM3229 target gene, herein designated TARGET GENE. GPR81 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR81, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR81 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ

ID:221.

[44010] Another function of GAM3229 is therefore inhibition of G protein-coupled receptor 81 (GPR81, Accession NP_115943.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR81.

[44011] Glutathione peroxidase 6 (olfactory) (GPX6, Accession NP_056511.2) is another GAM3229 target gene, herein designated TARGET GENE. GPX6 BINDING SITE1 and GPX6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GPX6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPX6 BINDING SITE1 and GPX6 BINDING SITE2, designated SEQ ID:7367 and SEQ ID:19324 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44012] Another function of GAM3229 is therefore inhibition of Glutathione peroxidase 6 (olfactory) (GPX6, Accession NP_056511.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPX6.

[44013] GR6 (Accession NP_031380.1) is another GAM3229 target gene, herein designated TARGET GENE. GR6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GR6 BINDING SITE, designated SEQ ID:7906, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44014] Another function of GAM3229 is therefore inhibition of GR6 (Accession NP_031380.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GR6.

[44015] GREB1 (Accession NP_055483.2) is another GAM3229 target gene, herein designated TARGET GENE. GREB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GREB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GREB1 BINDING SITE, designated SEQ ID:11197, to the nucleotide sequence of GAM3229

RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44016] Another function of GAM3229 is therefore inhibition of GREB1 (Accession NP_055483.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GREB1.

[44017] Glutamate receptor, ionotropic, delta 1 (GRID1, Accession XP_043613.8) is another GAM3229 target gene, herein designated TARGET GENE. GRID1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRID1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRID1 BINDING SITE, designated SEQ ID:17543, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44018] Another function of GAM3229 is therefore inhibition of Glutamate receptor, ionotropic, delta 1 (GRID1, Accession XP_043613.8) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRID1.

[44019] Glutamate receptor, ionotropic, n-methyl d-aspartate 2a

(GRIN2A, Accession NP_000824.1) is another GAM3229 target gene, herein designated TARGET GENE. GRIN2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRIN2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRIN2A BINDING SITE, designated SEQ ID:13819, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44020] Another function of GAM3229 is therefore inhibition of Glutamate receptor, ionotropic, n-methyl d-aspartate 2a (GRIN2A, Accession NP_000824.1), a gene which modulates the efficiency of synaptic plasticity. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIN2A.

[44021] The function of GRIN2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.2.Glutamate receptor, metabotropic 6 (GRM6, Accession NP_000834.1) is another GAM3229 target gene, herein designated TARGET GENE. GRM6 BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by GRM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRM6 BINDING SITE, designated SEQ ID:12308, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44022] Another function of GAM3229 is therefore inhibition of Glutamate receptor, metabotropic 6 (GRM6, Accession NP_000834.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRM6.

[44023] GSDM (Accession NP_835465.1) is another GAM3229 target gene, herein designated TARGET GENE. GSDM BINDING SITE1 and GSDM BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by GSDM, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSDM BINDING SITE1 and GSDM BINDING SITE2, designated SEQ ID:10286 and SEQ ID:6398 respectively, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44024] Another function of GAM3229 is therefore inhibition of GSDM (Accession NP_835465.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSDM.

[44025] Hypermethylated in cancer 2 (HIC2, Accession NP_055909.1) is another GAM3229 target gene, herein designated TARGET GENE. HIC2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by HIC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIC2 BINDING SITE, designated SEQ ID:9438, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44026] Another function of GAM3229 is therefore inhibition of Hypermethylated in cancer 2 (HIC2, Accession NP_055909.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIC2.

[44027] Hypermethylated in cancer 2 (HIC2, Accession

XP_036937.2) is another GAM3229 target gene, herein designated TARGET GENE. HIC2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by HIC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIC2 BINDING SITE, designated SEQ ID:9438, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44028] Another function of GAM3229 is therefore inhibition of Hypermethylated in cancer 2 (HIC2, Accession XP_036937.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIC2.

[44029] HIG1 (Accession NP_054775.1) is another GAM3229 target gene, herein designated TARGET GENE. HIG1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HIG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIG1 BINDING SITE, designated SEQ ID:6969, to the nucleotide sequence

of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44030] Another function of GAM3229 is therefore inhibition of HIG1 (Accession NP_054775.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIG1.

[44031] Major histocompatibility complex, class ii, do beta (HLA-DOB, Accession NP_002111.1) is another GAM3229 target gene, herein designated TARGET GENE. HLA-DOB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HLA-DOB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HLA-DOB BINDING SITE, designated SEQ ID:14561, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44032] Another function of GAM3229 is therefore inhibition of Major histocompatibility complex, class ii, do beta (HLA-DOB, Accession NP_002111.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLA-DOB.

[44033] Homeo box b2 (HOXB2, Accession NP_002136.1) is another GAM3229 target gene, herein designated TARGET GENE. HOXB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HOXB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HOXB2 BINDING SITE, designated SEQ ID:7506, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44034] Another function of GAM3229 is therefore inhibition of Homeo box b2 (HOXB2, Accession NP_002136.1), a gene which may mediate the regulation of hematopoietic cell growth and differentiation. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXB2.

[44035] The function of HOXB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1990.1.Heparan sulfate (glucosamine) 3-o-sulfotransferase 5 (HS3ST5, Accession NP_705840.1) is another GAM3229 target gene, herein designated TAR-

GET GENE. HS3ST5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HS3ST5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HS3ST5 BINDING SITE, designated SEQ ID:8703, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44036] Another function of GAM3229 is therefore inhibition of Heparan sulfate (glucosamine) 3-o-sulfotransferase 5 (HS3ST5, Accession NP_705840.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HS3ST5.

[44037] HSD3B7 (Accession NP_079469.2) is another GAM3229 target gene, herein designated TARGET GENE. HSD3B7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSD3B7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSD3B7 BINDING SITE, designated SEQ ID:15973, to the

nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44038] Another function of GAM3229 is therefore inhibition of HSD3B7 (Accession NP_079469.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSD3B7.

[44039] HSNOV1 (Accession NP_059985.2) is another GAM3229 target gene, herein designated TARGET GENE. HSNOV1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSNOV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSNOV1 BINDING SITE, designated SEQ ID:10558, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44040] Another function of GAM3229 is therefore inhibition of HSNOV1 (Accession NP_059985.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSNOV1.

[44041] Heat shock 70kda protein 5 (glucose-regulated protein,

78kda) (HSPA5, Accession NP_005338.1) is another GAM3229 target gene, herein designated TARGET GENE. HSPA5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSPA5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPA5 BINDING SITE, designated SEQ ID:12356, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44042] Another function of GAM3229 is therefore inhibition of Heat shock 70kda protein 5 (glucose-regulated protein, 78kda) (HSPA5, Accession NP_005338.1), a gene which is involved in the folding and assembly of proteins in the endoplasmic reticulum (ER). Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPA5.

[44043] The function of HSPA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.HSPC063 (Accession NP_054874.1) is another GAM3229 target gene, herein designated TARGET GENE. HSPC063 BINDING SITE1 and HSPC063 BINDING SITE2 are

target binding sites found in untranslated regions of mRNA encoded by HSPC063, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPC063 BINDING SITE1 and HSPC063 BINDING SITE2, designated SEQ ID:7180 and SEQ ID:5789 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44044] Another function of GAM3229 is therefore inhibition of HSPC063 (Accession NP_054874.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC063.

[44045] HSPC065 (Accession NP_054876.2) is another GAM3229 target gene, herein designated TARGET GENE. HSPC065 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSPC065, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPC065 BINDING SITE, designated SEQ ID:9903, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[44046] Another function of GAM3229 is therefore inhibition of HSPC065 (Accession NP_054876.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC065.

[44047] HSRNAFEV (Accession NP_059991.1) is another GAM3229 target gene, herein designated TARGET GENE. HSRNAFEV BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSRNAFEV, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSRNAFEV BINDING SITE, designated SEQ ID:5540, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44048] Another function of GAM3229 is therefore inhibition of HSRNAFEV (Accession NP_059991.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSRNAFEV.

[44049] HT009 (Accession NP_060940.1) is another GAM3229 target gene, herein designated TARGET GENE. HT009 BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HT009, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HT009 BINDING SITE, designated SEQ ID:10585, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44050] Another function of GAM3229 is therefore inhibition of HT009 (Accession NP_060940.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HT009.

[44051] HTCD37 (Accession NP_067045.1) is another GAM3229 target gene, herein designated TARGET GENE. HTCD37 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HTCD37, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTCD37 BINDING SITE, designated SEQ ID:10478, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44052] Another function of GAM3229 is therefore inhibition of

HTCD37 (Accession NP_067045.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTCD37.

[44053] Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1) is another GAM3229 target gene, herein designated TARGET GENE. HUS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HUS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUS1 BINDING SITE, designated SEQ ID:10277, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44054] Another function of GAM3229 is therefore inhibition of Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1), a gene which May form DNA damage- responsive protein complex . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUS1.

[44055] The function of HUS1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM189.1.Intercellular adhesion molecule 1 (cd54), human rhinovirus receptor (ICAM1, Accession NP_000192.1) is another GAM3229 target gene, herein designated TARGET GENE. ICAM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ICAM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ICAM1 BINDING SITE, designated SEQ ID:9491, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44056] Another function of GAM3229 is therefore inhibition of Intercellular adhesion molecule 1 (cd54), human rhinovirus receptor (ICAM1, Accession NP_000192.1), a gene which binds the integrin LFA- 1 (ITGB2) and promotes adhesion; member of the immunoglobulin superfamily and therefore may be associated with Malaria, cerebral, susceptibility to. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Malaria, cerebral, susceptibility to, and of other diseases and clinical conditions associated with ICAM1.

[44057] The function of ICAM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Insulin-like growth factor binding protein 5 (IGFBP5, Accession NP_000590.1) is another GAM3229 target gene, herein designated TARGET GENE. IGFBP5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IGFBP5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IGFBP5 BINDING SITE, designated SEQ ID:512, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44058] Another function of GAM3229 is therefore inhibition of Insulin-like growth factor binding protein 5 (IGFBP5, Accession NP_000590.1), a gene which either inhibits or stimulates the growth promoting effects of the igfs on cell culture. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IGFBP5.

[44059] The function of IGFBP5 has been established by previous studies. See 146733. Allander et al. (1994) cloned the

IGFBP5 gene from a human genomic library and showed that it is divided into 4 exons which, primarily due to a first intron of approximately 25 kb, span about 33 kb of DNA. Southern analysis identified a single copy of the IGFBP5 gene in the haploid human genome. By PCR amplification of DNA from somatic human/rodent cell hybrids, by fluorescence in situ hybridization, and by hybridization to pulsed field gel electrophoresis fragments, they showed that the gene is located on 2q33- q34. The IGFBP2 gene (OMIM Ref. No. 146731) and the IGFBP5 gene are transcribed convergently and are separated by approximately 20 to 40 kb of DNA. Primer extension studies identified the IGFBP5 mRNA cap site 772 bp 5- prime to the first nucleotide of the translation start codon. A potential TATA element beginning 33 bp 5- prime to the mRNA cap site was identified. When a DNA fragment containing this cap site and 461 bp of upstream sequence was placed 5-prime to the chloramphenicol acetyltransferase (CAT) reporter gene and transfected into human breast cancer cells, it directed CAT expression in an orientation- specific manner, suggesting that this region contains elements essential for IGFBP5 promoter activity. Kou et al. (1994) demonstrated that, in the mouse, Igfbp2 and

Igfbp5 colocalize to a proximal region of chromosome 1 that is syntenic with human chromosome 2q33- q36 and that the 2 genes are 5 kb apart in a tail- to- tail orientation. This suggests that the human IGFBP5 gene is located on 2q33- q36. Kou et al. (1994) also used interspecific backcross mapping and gene cloning to demonstrate that the Igfbp1 and Igfbp3 are located in the proximal part of chromosome 11. In the human genome, these 2 loci map within 20 kb of one another on 7p14- p12, and the genes are organized in a tail- to- tail configuration. The results suggested to Kou et al. (1994) an evolutionary scheme in which a primordial IGFBP gene duplicated to form a cluster that was later replicated to create a second linkage group.

[44060]

[44061] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[44062] Allander, S. V.; Larsson, C.; Ehrenborg, E.; Suwanichkul, A.; Weber, G.; Morris, S. L.; Bajalica, S.; Kiefer, M. C.; Luthman, H.; Powell, D. R. : Characterization of the chromosomal gene and promoter for human insulin- like growth factor binding protein- 5. J. Biol. Chem. 269: 10891-10898, 1994. ; and

[44063] Kou, K.; James, P. L.; Clemmons, D. R.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Rotwein, P. : Identification of two clusters of mouse insulin- like growth factor binding protein.

[44064] Further studies establishing the function and utilities of IGFBP5 are found in John Hopkins OMIM database record ID 146734, and in cited publications listed in Table 5, which are hereby incorporated by reference.Interleukin 11 (IL11, Accession NP_000632.1) is another GAM3229 target gene, herein designated TARGET GENE. IL11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL11 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44065] Another function of GAM3229 is therefore inhibition of Interleukin 11 (IL11, Accession NP_000632.1), a gene which stimulates the proliferation of hematopoietic stem cells and megakaryocyte progenitor cells and induces megakaryocyte maturation. Accordingly, utilities of

GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL11.

[44066] The function of IL11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM41.1.Interleukin 12 receptor, beta 1 (IL12RB1, Accession NP_714912.1) is another GAM3229 target gene, herein designated TARGET GENE. IL12RB1 BINDING SITE1 and IL12RB1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by IL12RB1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL12RB1 BINDING SITE1 and IL12RB1 BINDING SITE2, designated SEQ ID:8116 and SEQ ID:9835 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44067] Another function of GAM3229 is therefore inhibition of Interleukin 12 receptor, beta 1 (IL12RB1, Accession NP_714912.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL12RB1.

[44068] Interleukin 19 (IL19, Accession NP_037503.2) is another GAM3229 target gene, herein designated TARGET GENE. IL19 BINDING SITE1 and IL19 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by IL19, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL19 BINDING SITE1 and IL19 BINDING SITE2, designated SEQ ID:11633 and SEQ ID:14348 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44069] Another function of GAM3229 is therefore inhibition of Interleukin 19 (IL19, Accession NP_037503.2), a gene which may play a role in B- cell activation and autoantibody production. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL19.

[44070] The function of IL19 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Interleukin 1, alpha (IL1A, Accession NP_000566.3) is another GAM3229 target gene, herein

designated TARGET GENE. IL1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL1A BINDING SITE, designated SEQ ID:13186, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44071] Another function of GAM3229 is therefore inhibition of Interleukin 1, alpha (IL1A, Accession NP_000566.3), a gene which stimulates thymocyte proliferation by inducing il- 2 release, b- cell maturation & proliferation, & fibroblast growth factor activity. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1A.

[44072] The function of IL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM933.1.Interleukin 8 (IL8, Accession NP_000575.1) is another GAM3229 target gene, herein designated TARGET GENE. IL8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL8,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL8 BINDING SITE, designated SEQ ID:16050, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44073] Another function of GAM3229 is therefore inhibition of Interleukin 8 (IL8, Accession NP_000575.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL8.

[44074] Potassium voltage-gated channel, isk-related family, member 3 (KCNE3, Accession NP_005463.1) is another GAM3229 target gene, herein designated TARGET GENE. KCNE3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KCNE3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNE3 BINDING SITE, designated SEQ ID:19681, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44075] Another function of GAM3229 is therefore inhibition of

Potassium voltage-gated channel, isk-related family, member 3 (KCNE3, Accession NP_005463.1), a gene which ancillary protein that co- assemble with a potassium channel alpha- subunit to modulate the gating kinetics and enhance stability of the multimeric complex (by similarity). and therefore may be associated with Hypokalemic periodic paralysis. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Hypokalemic periodic paralysis, and of other diseases and clinical conditions associated with KCNE3.

[44076] The function of KCNE3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM234.1.Kinase insert domain receptor (a type iii receptor tyrosine kinase) (KDR, Accession NP_002244.1) is another GAM3229 target gene, herein designated TARGET GENE. KDR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KDR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KDR BINDING SITE, designated SEQ ID:618, to the nucleotide sequence of GAM3229 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:221.

[44077] Another function of GAM3229 is therefore inhibition of Kinase insert domain receptor (a type iii receptor tyrosine kinase) (KDR, Accession NP_002244.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KDR.

[44078] KENAE (Accession NP_789786.1) is another GAM3229 target gene, herein designated TARGET GENE. KENAE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KENAE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KENAE BINDING SITE, designated SEQ ID:3881, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44079] Another function of GAM3229 is therefore inhibition of KENAE (Accession NP_789786.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KENAE.

[44080] Kh-type splicing regulatory protein (fuse binding protein 2) (KHSRP, Accession NP_003676.1) is another GAM3229

target gene, herein designated TARGET GENE. KHSRP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KHSRP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KHSRP BINDING SITE, designated SEQ ID:10161, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44081] Another function of GAM3229 is therefore inhibition of Kh-type splicing regulatory protein (fuse binding protein 2) (KHSRP, Accession NP_003676.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KHSRP.

[44082] KIAA0186 (Accession NP_066545.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0186 BINDING SITE, designated SEQ ID:8187, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[44083] Another function of GAM3229 is therefore inhibition of KIAA0186 (Accession NP_066545.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0186.

[44084] KIAA0193 (Accession NP_055581.2) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0193, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0193 BINDING SITE, designated SEQ ID:9437, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44085] Another function of GAM3229 is therefore inhibition of KIAA0193 (Accession NP_055581.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0193.

[44086] KIAA0205 (Accession NP_055688.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0205

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0205, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0205 BINDING SITE, designated SEQ ID:5448, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44087] Another function of GAM3229 is therefore inhibition of KIAA0205 (Accession NP_055688.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0205.

[44088] KIAA0280 (Accession XP_166238.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0280 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0280, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0280 BINDING SITE, designated SEQ ID:18647, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44089] Another function of GAM3229 is therefore inhibition of KIAA0280 (Accession XP_166238.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0280.

[44090] KIAA0391 (Accession NP_055487.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0391 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0391, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0391 BINDING SITE, designated SEQ ID:9624, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44091] Another function of GAM3229 is therefore inhibition of KIAA0391 (Accession NP_055487.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0391.

[44092] KIAA0446 (Accession XP_044155.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0446 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by KIAA0446, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0446 BINDING SITE, designated SEQ ID:12906, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44093] Another function of GAM3229 is therefore inhibition of KIAA0446 (Accession XP_044155.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0446.

[44094] KIAA0469 (Accession NP_055666.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0469 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0469, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0469 BINDING SITE, designated SEQ ID:5867, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44095] Another function of GAM3229 is therefore inhibition of

KIAA0469 (Accession NP_055666.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469.

[44096] KIAA0478 (Accession NP_055685.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0478, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0478 BINDING SITE, designated SEQ ID:6356, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44097] Another function of GAM3229 is therefore inhibition of KIAA0478 (Accession NP_055685.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0478.

[44098] KIAA0493 (Accession XP_034717.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0493 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0493, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0493 BINDING SITE, designated SEQ ID:13205, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44099] Another function of GAM3229 is therefore inhibition of KIAA0493 (Accession XP_034717.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0493.

[44100] KIAA0513 (Accession NP_055547.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0513 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0513, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44101] Another function of GAM3229 is therefore inhibition of KIAA0513 (Accession NP_055547.1) . Accordingly, utilities

of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513.

[44102] KIAA0527 (Accession XP_171054.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0527 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0527, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0527 BINDING SITE, designated SEQ ID:9370, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44103] Another function of GAM3229 is therefore inhibition of KIAA0527 (Accession XP_171054.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0527.

[44104] KIAA0532 (Accession XP_047659.6) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0532, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0532 BINDING SITE, designated SEQ ID:3516, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44105] Another function of GAM3229 is therefore inhibition of KIAA0532 (Accession XP_047659.6) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0532.

[44106] KIAA0562 (Accession NP_055519.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0562 BINDING SITE, designated SEQ ID:3797, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44107] Another function of GAM3229 is therefore inhibition of KIAA0562 (Accession NP_055519.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA0562.

[44108] KIAA0605 (Accession NP_055509.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0605 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0605, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0605 BINDING SITE, designated SEQ ID:1515, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44109] Another function of GAM3229 is therefore inhibition of KIAA0605 (Accession NP_055509.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0605.

[44110] KIAA0828 (Accession NP_056143.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0828 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0828, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA0828 BINDING SITE, designated SEQ ID:15963, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44111] Another function of GAM3229 is therefore inhibition of KIAA0828 (Accession NP_056143.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0828.

[44112] KIAA0841 (Accession XP_049237.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0841 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0841, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0841 BINDING SITE, designated SEQ ID:4565, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44113] Another function of GAM3229 is therefore inhibition of KIAA0841 (Accession XP_049237.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0841.

[44114] KIAA0924 (Accession NP_055712.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0924 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0924, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0924 BINDING SITE, designated SEQ ID:7195, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44115] Another function of GAM3229 is therefore inhibition of KIAA0924 (Accession NP_055712.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0924.

[44116] KIAA0935 (Accession XP_052620.6) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0935 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0935, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA0935 BINDING SITE, designated SEQ ID:12234, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44117] Another function of GAM3229 is therefore inhibition of KIAA0935 (Accession XP_052620.6) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0935.

[44118] KIAA0982 (Accession NP_054742.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA0982 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0982, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0982 BINDING SITE, designated SEQ ID:19897, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44119] Another function of GAM3229 is therefore inhibition of KIAA0982 (Accession NP_054742.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0982.

[44120] KIAA1010 (Accession XP_050742.5) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1010 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1010, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1010 BINDING SITE, designated SEQ ID:845, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44121] Another function of GAM3229 is therefore inhibition of KIAA1010 (Accession XP_050742.5) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1010.

[44122] KIAA1040 (Accession XP_051091.3) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1040 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1040, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1040 BINDING SITE, designated SEQ ID:11317, to the

nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44123] Another function of GAM3229 is therefore inhibition of KIAA1040 (Accession XP_051091.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1040.

[44124] KIAA1041 (Accession NP_055762.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1041 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1041, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1041 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44125] Another function of GAM3229 is therefore inhibition of KIAA1041 (Accession NP_055762.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1041.

[44126] KIAA1054 (Accession XP_043493.5) is another GAM3229

target gene, herein designated TARGET GENE. KIAA1054 BINDING SITE1 and KIAA1054 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1054, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1054 BINDING SITE1 and KIAA1054 BINDING SITE2, designated SEQ ID:4043 and SEQ ID:15902 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44127] Another function of GAM3229 is therefore inhibition of KIAA1054 (Accession XP_043493.5) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1054.

[44128] KIAA1145 (Accession NP_065749.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1145 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1145, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1145 BINDING SITE, designated SEQ ID:10272, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44129] Another function of GAM3229 is therefore inhibition of KIAA1145 (Accession NP_065749.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1145.

[44130] KIAA1155 (Accession XP_030864.2) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1155 BINDING SITE1 and KIAA1155 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1155, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1155 BINDING SITE1 and KIAA1155 BINDING SITE2, designated SEQ ID:9308 and SEQ ID:4896 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44131] Another function of GAM3229 is therefore inhibition of KIAA1155 (Accession XP_030864.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA1155.

[44132] KIAA1198 (Accession NP_065765.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by KIAA1198, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE4, designated SEQ ID:4779, SEQ ID:7372, SEQ ID:1315 and SEQ ID:12313 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44133] Another function of GAM3229 is therefore inhibition of KIAA1198 (Accession NP_065765.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1198.

[44134] KIAA1200 (Accession XP_031054.4) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1200 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1200, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1200 BINDING SITE, designated SEQ ID:13574, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44135] Another function of GAM3229 is therefore inhibition of KIAA1200 (Accession XP_031054.4) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1200.

[44136] KIAA1257 (Accession XP_031577.2) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1257 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1257, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1257 BINDING SITE, designated SEQ ID:9371, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44137] Another function of GAM3229 is therefore inhibition of KIAA1257 (Accession XP_031577.2) . Accordingly, utilities

of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1257.

[44138] KIAA1318 (Accession NP_065820.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1318 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1318 BINDING SITE, designated SEQ ID:1457, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44139] Another function of GAM3229 is therefore inhibition of KIAA1318 (Accession NP_065820.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1318.

[44140] KIAA1396 (Accession XP_032054.2) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1396 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1396, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1396 BINDING SITE, designated SEQ ID:14141, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44141] Another function of GAM3229 is therefore inhibition of KIAA1396 (Accession XP_032054.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1396.

[44142] KIAA1493 (Accession XP_034415.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1493 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1493 BINDING SITE, designated SEQ ID:4891, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44143] Another function of GAM3229 is therefore inhibition of KIAA1493 (Accession XP_034415.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA1493.

[44144] KIAA1571 (Accession XP_027744.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1571 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1571, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1571 BINDING SITE, designated SEQ ID:13416, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44145] Another function of GAM3229 is therefore inhibition of KIAA1571 (Accession XP_027744.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1571.

[44146] KIAA1671 (Accession XP_037809.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1671 BINDING SITE1 through KIAA1671 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by KIAA1671, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1671 BINDING SITE1 through KIAA1671 BINDING SITE3, designated SEQ ID:19751, SEQ ID:17241 and SEQ ID:5639 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44147] Another function of GAM3229 is therefore inhibition of KIAA1671 (Accession XP_037809.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1671.

[44148] KIAA1727 (Accession XP_034262.4) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1727 BINDING SITE1 and KIAA1727 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1727, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1727 BINDING SITE1 and KIAA1727 BINDING SITE2, designated SEQ ID:8253 and SEQ ID:7550 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44149] Another function of GAM3229 is therefore inhibition of KIAA1727 (Accession XP_034262.4) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1727.

[44150] KIAA1765 (Accession XP_047355.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1765 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1765, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1765 BINDING SITE, designated SEQ ID:2344, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44151] Another function of GAM3229 is therefore inhibition of KIAA1765 (Accession XP_047355.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1765.

[44152] KIAA1784 (Accession NP_115820.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1784 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1784, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1784 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44153] Another function of GAM3229 is therefore inhibition of KIAA1784 (Accession NP_115820.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1784.

[44154] KIAA1827 (Accession XP_290834.1) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1827 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1827, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1827 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44155] Another function of GAM3229 is therefore inhibition of

KIAA1827 (Accession XP_290834.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1827.

[44156] KIAA1829 (Accession XP_030378.2) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1829 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1829, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1829 BINDING SITE, designated SEQ ID:15973, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44157] Another function of GAM3229 is therefore inhibition of KIAA1829 (Accession XP_030378.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1829.

[44158] KIAA1924 (Accession NP_694971.2) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1924 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1924, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1924 BINDING SITE, designated SEQ ID:7589, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44159] Another function of GAM3229 is therefore inhibition of KIAA1924 (Accession NP_694971.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1924.

[44160] KIAA1971 (Accession XP_058720.4) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1971 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1971, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1971 BINDING SITE, designated SEQ ID:7601, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44161] Another function of GAM3229 is therefore inhibition of KIAA1971 (Accession XP_058720.4) . Accordingly, utilities

of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1971.

[44162] KIAA1998 (Accession XP_068710.3) is another GAM3229 target gene, herein designated TARGET GENE. KIAA1998 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1998, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1998 BINDING SITE, designated SEQ ID:19071, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44163] Another function of GAM3229 is therefore inhibition of KIAA1998 (Accession XP_068710.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1998.

[44164] KIAA2025 (Accession XP_086409.4) is another GAM3229 target gene, herein designated TARGET GENE. KIAA2025 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA2025, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA2025 BINDING SITE, designated SEQ ID:7899, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44165] Another function of GAM3229 is therefore inhibition of KIAA2025 (Accession XP_086409.4) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2025.

[44166] KIAA2028 (Accession XP_059415.2) is another GAM3229 target gene, herein designated TARGET GENE. KIAA2028 BINDING SITE1 through KIAA2028 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by KIAA2028, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA2028 BINDING SITE1 through KIAA2028 BINDING SITE3, designated SEQ ID:17589, SEQ ID:18073 and SEQ ID:19988 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44167] Another function of GAM3229 is therefore inhibition of

KIAA2028 (Accession XP_059415.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2028.

[44168] Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NP_003670.1) is another GAM3229 target gene, herein designated TARGET GENE. KMO BINDING SITE1 and KMO BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KMO, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KMO BINDING SITE1 and KMO BINDING SITE2, designated SEQ ID:9048 and SEQ ID:15859 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44169] Another function of GAM3229 is therefore inhibition of Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NP_003670.1), a gene which may play a role in encephalic photoreception. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KMO.

[44170] The function of KMO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Keratin, hair, basic, 2 (KRTHB2, Accession NP_149022.3) is another GAM3229 target gene, herein designated TARGET GENE. KRTHB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KRTHB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KRTHB2 BINDING SITE, designated SEQ ID:12235, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44171] Another function of GAM3229 is therefore inhibition of Keratin, hair, basic, 2 (KRTHB2, Accession NP_149022.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KRTHB2.

[44172] Kinase suppressor of ras (KSR, Accession XP_290793.1) is another GAM3229 target gene, herein designated TARGET GENE. KSR BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KSR, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KSR BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44173] Another function of GAM3229 is therefore inhibition of Kinase suppressor of ras (KSR, Accession XP_290793.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KSR.

[44174] Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) is another GAM3229 target gene, herein designated TARGET GENE. LAMP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAMP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMP3 BINDING SITE, designated SEQ ID:3841, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44175] Another function of GAM3229 is therefore inhibition of

Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP3.

[44176] LAT1-3TM (Accession NP_112488.1) is another GAM3229 target gene, herein designated TARGET GENE. LAT1-3TM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LAT1-3TM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAT1-3TM BINDING SITE, designated SEQ ID:13820, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44177] Another function of GAM3229 is therefore inhibition of LAT1-3TM (Accession NP_112488.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAT1-3TM.

[44178] Lipocalin 7 (LCN7, Accession NP_071447.1) is another GAM3229 target gene, herein designated TARGET GENE. LCN7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCN7, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCN7 BINDING SITE, designated SEQ ID:7234, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44179] Another function of GAM3229 is therefore inhibition of Lipocalin 7 (LCN7, Accession NP_071447.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCN7.

[44180] Lim homeobox protein 3 (LHX3, Accession NP_055379.1) is another GAM3229 target gene, herein designated TARGET GENE. LHX3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LHX3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LHX3 BINDING SITE, designated SEQ ID:20146, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44181] Another function of GAM3229 is therefore inhibition of

Lim homeobox protein 3 (LHX3, Accession NP_055379.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHX3.

[44182] Leukemia inhibitory factor (cholinergic differentiation factor) (LIF, Accession NP_002300.1) is another GAM3229 target gene, herein designated TARGET GENE. LIF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LIF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LIF BINDING SITE, designated SEQ ID:4988, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44183] Another function of GAM3229 is therefore inhibition of Leukemia inhibitory factor (cholinergic differentiation factor) (LIF, Accession NP_002300.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIF.

[44184] LNIR (Accession NP_112178.1) is another GAM3229 target gene, herein designated TARGET GENE. LNIR BINDING SITE is a target binding site found in the 3` untranslated re-

gion of mRNA encoded by LNIR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LNIR BINDING SITE, designated SEQ ID:6798, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44185] Another function of GAM3229 is therefore inhibition of LNIR (Accession NP_112178.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNIR.

[44186] LOC112687 (Accession XP_053145.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC112687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112687 BINDING SITE, designated SEQ ID:10726, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44187] Another function of GAM3229 is therefore inhibition of

LOC112687 (Accession XP_053145.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112687.

[44188] LOC115098 (Accession NP_612451.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC115098 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC115098, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115098 BINDING SITE, designated SEQ ID:15832, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44189] Another function of GAM3229 is therefore inhibition of LOC115098 (Accession NP_612451.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115098.

[44190] LOC115219 (Accession XP_055499.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC115219 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC115219, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115219 BINDING SITE, designated SEQ ID:12851, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44191] Another function of GAM3229 is therefore inhibition of LOC115219 (Accession XP_055499.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115219.

[44192] LOC117584 (Accession NP_476519.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC117584 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC117584, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC117584 BINDING SITE, designated SEQ ID:3964, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[44193] Another function of GAM3229 is therefore inhibition of LOC117584 (Accession NP_476519.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC117584.

[44194] LOC118812 (Accession XP_058346.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:16805, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44195] Another function of GAM3229 is therefore inhibition of LOC118812 (Accession XP_058346.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118812.

[44196] LOC118812 (Accession NP_849154.1) is another

GAM3229 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:16805, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44197] Another function of GAM3229 is therefore inhibition of LOC118812 (Accession NP_849154.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118812.

[44198] LOC119392 (Accession NP_660290.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC119392 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC119392, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC119392 BINDING SITE, desig-

nated SEQ ID:9142, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44199] Another function of GAM3229 is therefore inhibition of LOC119392 (Accession NP_660290.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC119392.

[44200] LOC120526 (Accession XP_058475.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC120526 BINDING SITE1 and LOC120526 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC120526, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC120526 BINDING SITE1 and LOC120526 BINDING SITE2, designated SEQ ID:10538 and SEQ ID:2073 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44201] Another function of GAM3229 is therefore inhibition of LOC120526 (Accession XP_058475.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC120526.

[44202] LOC121838 (Accession XP_071772.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC121838 BINDING SITE1 and LOC121838 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC121838, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC121838 BINDING SITE1 and LOC121838 BINDING SITE2, designated SEQ ID:14349 and SEQ ID:1458 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44203] Another function of GAM3229 is therefore inhibition of LOC121838 (Accession XP_071772.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121838.

[44204] LOC125061 (Accession XP_058889.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC125061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC125061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC125061 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44205] Another function of GAM3229 is therefore inhibition of LOC125061 (Accession XP_058889.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125061.

[44206] LOC126669 (Accession XP_060121.4) is another GAM3229 target gene, herein designated TARGET GENE. LOC126669 BINDING SITE1 and LOC126669 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC126669, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126669 BINDING SITE1 and LOC126669 BINDING SITE2, designated SEQ ID:13284 and SEQ ID:11629 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[44207] Another function of GAM3229 is therefore inhibition of LOC126669 (Accession XP_060121.4) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126669.

[44208] LOC130639 (Accession XP_059464.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC130639 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC130639, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130639 BINDING SITE, designated SEQ ID:13129, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44209] Another function of GAM3229 is therefore inhibition of LOC130639 (Accession XP_059464.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130639.

[44210] LOC130813 (Accession XP_065904.1) is another

GAM3229 target gene, herein designated TARGET GENE. LOC130813 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC130813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:12421, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44211] Another function of GAM3229 is therefore inhibition of LOC130813 (Accession XP_065904.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813.

[44212] LOC132241 (Accession XP_059583.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC132241 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC132241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC132241 BINDING SITE, desig-

nated SEQ ID:15759, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44213] Another function of GAM3229 is therefore inhibition of LOC132241 (Accession XP_059583.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132241.

[44214] LOC135293 (Accession XP_072402.4) is another GAM3229 target gene, herein designated TARGET GENE. LOC135293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135293 BINDING SITE, designated SEQ ID:12656, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44215] Another function of GAM3229 is therefore inhibition of LOC135293 (Accession XP_072402.4) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC135293.

[44216] LOC135818 (Accession XP_059804.4) is another GAM3229 target gene, herein designated TARGET GENE. LOC135818 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135818 BINDING SITE, designated SEQ ID:19721, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44217] Another function of GAM3229 is therefore inhibition of LOC135818 (Accession XP_059804.4) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135818.

[44218] LOC136345 (Accession XP_072455.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC136345 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC136345, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC136345 BINDING SITE, designated SEQ ID:6455, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44219] Another function of GAM3229 is therefore inhibition of LOC136345 (Accession XP_072455.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC136345.

[44220] LOC137886 (Accession XP_059929.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC137886 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC137886, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC137886 BINDING SITE, designated SEQ ID:9666, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44221] Another function of GAM3229 is therefore inhibition of LOC137886 (Accession XP_059929.3) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137886.

[44222] LOC139422 (Accession XP_066687.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC139422 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC139422, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC139422 BINDING SITE, designated SEQ ID:16130, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44223] Another function of GAM3229 is therefore inhibition of LOC139422 (Accession XP_066687.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139422.

[44224] LOC143677 (Accession XP_096471.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC143677 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC143677, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143677 BINDING SITE, designated SEQ ID:14289, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44225] Another function of GAM3229 is therefore inhibition of LOC143677 (Accession XP_096471.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143677.

[44226] LOC144404 (Accession XP_084852.6) is another GAM3229 target gene, herein designated TARGET GENE. LOC144404 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144404, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144404 BINDING SITE, designated SEQ ID:19677, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44227] Another function of GAM3229 is therefore inhibition of LOC144404 (Accession XP_084852.6) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144404.

[44228] LOC144481 (Accession XP_096611.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC144481 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144481, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144481 BINDING SITE, designated SEQ ID:3550, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44229] Another function of GAM3229 is therefore inhibition of LOC144481 (Accession XP_096611.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144481.

[44230] LOC144871 (Accession XP_096698.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC144871 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144871, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144871 BINDING SITE, designated SEQ ID:15802, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44231] Another function of GAM3229 is therefore inhibition of LOC144871 (Accession XP_096698.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144871.

[44232] LOC145188 (Accession XP_085049.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC145188 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145188, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145188 BINDING SITE, designated SEQ ID:15484, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44233] Another function of GAM3229 is therefore inhibition of LOC145188 (Accession XP_085049.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145188.

[44234] LOC145268 (Accession XP_085072.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC145268 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145268 BINDING SITE, designated SEQ ID:10524, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44235] Another function of GAM3229 is therefore inhibition of LOC145268 (Accession XP_085072.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145268.

[44236] LOC145387 (Accession XP_096791.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC145387 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145387, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145387 BINDING SITE, designated SEQ ID:12820, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44237] Another function of GAM3229 is therefore inhibition of LOC145387 (Accession XP_096791.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145387.

[44238] LOC145601 (Accession XP_096816.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC145601 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145601, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC145601 BINDING SITE, designated SEQ ID:10802, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44239] Another function of GAM3229 is therefore inhibition of LOC145601 (Accession XP_096816.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145601.

[44240] LOC145988 (Accession XP_085290.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC145988 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145988, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145988 BINDING SITE, designated SEQ ID:15535, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44241] Another function of GAM3229 is therefore inhibition of LOC145988 (Accession XP_085290.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC145988.

[44242] LOC146229 (Accession XP_085387.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC146229 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146229, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146229 BINDING SITE, designated SEQ ID:15411, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44243] Another function of GAM3229 is therefore inhibition of LOC146229 (Accession XP_085387.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146229.

[44244] LOC146336 (Accession XP_085421.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC146336 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146336, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146336 BINDING SITE, designated SEQ ID:5123, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44245] Another function of GAM3229 is therefore inhibition of LOC146336 (Accession XP_085421.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146336.

[44246] LOC146346 (Accession XP_085430.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC146346 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146346 BINDING SITE, designated SEQ ID:3401, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44247] Another function of GAM3229 is therefore inhibition of

LOC146346 (Accession XP_085430.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146346.

[44248] LOC146443 (Accession XP_085461.6) is another GAM3229 target gene, herein designated TARGET GENE. LOC146443 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146443, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146443 BINDING SITE, designated SEQ ID:9729, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44249] Another function of GAM3229 is therefore inhibition of LOC146443 (Accession XP_085461.6) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146443.

[44250] LOC146713 (Accession XP_097071.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC146713 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC146713, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146713 BINDING SITE, designated SEQ ID:19578, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44251] Another function of GAM3229 is therefore inhibition of LOC146713 (Accession XP_097071.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146713.

[44252] LOC146850 (Accession XP_097109.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC146850 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146850, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146850 BINDING SITE, designated SEQ ID:15412, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[44253] Another function of GAM3229 is therefore inhibition of LOC146850 (Accession XP_097109.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146850.

[44254] LOC146909 (Accession XP_085634.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC146909 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146909, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146909 BINDING SITE, designated SEQ ID:11082, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44255] Another function of GAM3229 is therefore inhibition of LOC146909 (Accession XP_085634.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146909.

[44256] LOC147004 (Accession XP_097155.1) is another

GAM3229 target gene, herein designated TARGET GENE. LOC147004 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147004, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147004 BINDING SITE, designated SEQ ID:11470, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44257] Another function of GAM3229 is therefore inhibition of LOC147004 (Accession XP_097155.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147004.

[44258] LOC147166 (Accession XP_085722.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC147166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147166 BINDING SITE, desig-

nated SEQ ID:14800, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44259] Another function of GAM3229 is therefore inhibition of LOC147166 (Accession XP_085722.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147166.

[44260] LOC147343 (Accession XP_097225.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC147343 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147343, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147343 BINDING SITE, designated SEQ ID:7551, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44261] Another function of GAM3229 is therefore inhibition of LOC147343 (Accession XP_097225.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC147343.

[44262] LOC147817 (Accession XP_085903.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC147817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147817 BINDING SITE, designated SEQ ID:5287, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44263] Another function of GAM3229 is therefore inhibition of LOC147817 (Accession XP_085903.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147817.

[44264] LOC147947 (Accession XP_085974.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC147947 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147947, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147947 BINDING SITE, designated SEQ ID:4263, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44265] Another function of GAM3229 is therefore inhibition of LOC147947 (Accession XP_085974.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147947.

[44266] LOC148203 (Accession XP_086095.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC148203 BINDING SITE1 and LOC148203 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC148203, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148203 BINDING SITE1 and LOC148203 BINDING SITE2, designated SEQ ID:18261 and SEQ ID:6399 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44267] Another function of GAM3229 is therefore inhibition of

LOC148203 (Accession XP_086095.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148203.

[44268] LOC148709 (Accession XP_086281.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC148709 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148709, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148709 BINDING SITE, designated SEQ ID:6483, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44269] Another function of GAM3229 is therefore inhibition of LOC148709 (Accession XP_086281.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148709.

[44270] LOC148918 (Accession XP_086361.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC148918 BINDING SITE1 and LOC148918 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC148918, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148918 BINDING SITE1 and LOC148918 BINDING SITE2, designated SEQ ID:7157 and SEQ ID:15411 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44271] Another function of GAM3229 is therefore inhibition of LOC148918 (Accession XP_086361.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148918.

[44272] LOC149149 (Accession XP_097598.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC149149 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149149 BINDING SITE, designated SEQ ID:4780, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44273] Another function of GAM3229 is therefore inhibition of LOC149149 (Accession XP_097598.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149149.

[44274] LOC149371 (Accession NP_787072.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC149371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149371 BINDING SITE, designated SEQ ID:4008, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44275] Another function of GAM3229 is therefore inhibition of LOC149371 (Accession NP_787072.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149371.

[44276] LOC149466 (Accession XP_086546.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC149466 BINDING SITE1 and LOC149466 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC149466, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149466 BINDING SITE1 and LOC149466 BINDING SITE2, designated SEQ ID:10865 and SEQ ID:12245 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44277] Another function of GAM3229 is therefore inhibition of LOC149466 (Accession XP_086546.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149466.

[44278] LOC149670 (Accession XP_086647.4) is another GAM3229 target gene, herein designated TARGET GENE. LOC149670 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149670, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149670 BINDING SITE, designated SEQ ID:10537, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44279] Another function of GAM3229 is therefore inhibition of LOC149670 (Accession XP_086647.4) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149670.

[44280] LOC149692 (Accession XP_097706.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC149692 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149692, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149692 BINDING SITE, designated SEQ ID:619, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44281] Another function of GAM3229 is therefore inhibition of LOC149692 (Accession XP_097706.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149692.

[44282] LOC149821 (Accession XP_097751.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC149821 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149821, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149821 BINDING SITE, designated SEQ ID:7976, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44283] Another function of GAM3229 is therefore inhibition of LOC149821 (Accession XP_097751.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149821.

[44284] LOC150166 (Accession XP_097824.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC150166 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC150166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150166 BINDING SITE, designated SEQ ID:2705, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44285] Another function of GAM3229 is therefore inhibition of LOC150166 (Accession XP_097824.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150166.

[44286] LOC150407 (Accession XP_086906.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC150407 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150407, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150407 BINDING SITE, designated SEQ ID:7746, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44287] Another function of GAM3229 is therefore inhibition of LOC150407 (Accession XP_086906.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150407.

[44288] LOC150587 (Accession XP_097917.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC150587 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150587 BINDING SITE, designated SEQ ID:6798, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44289] Another function of GAM3229 is therefore inhibition of LOC150587 (Accession XP_097917.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150587.

[44290] LOC150946 (Accession XP_097977.2) is another GAM3229 target gene, herein designated TARGET GENE.

LOC150946 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150946, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150946 BINDING SITE, designated SEQ ID:13021, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44291] Another function of GAM3229 is therefore inhibition of LOC150946 (Accession XP_097977.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150946.

[44292] LOC151196 (Accession XP_098019.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC151196 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151196, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151196 BINDING SITE, designated SEQ ID:2041, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44293] Another function of GAM3229 is therefore inhibition of LOC151196 (Accession XP_098019.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151196.

[44294] LOC151201 (Accession XP_098021.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC151201 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE, designated SEQ ID:2056, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44295] Another function of GAM3229 is therefore inhibition of LOC151201 (Accession XP_098021.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151201.

[44296] LOC151636 (Accession NP_612144.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC151636 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151636, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151636 BINDING SITE, designated SEQ ID:15373, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44297] Another function of GAM3229 is therefore inhibition of LOC151636 (Accession NP_612144.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151636.

[44298] LOC151657 (Accession XP_098100.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC151657 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151657, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC151657 BINDING SITE, designated SEQ ID:12136, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44299] Another function of GAM3229 is therefore inhibition of LOC151657 (Accession XP_098100.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151657.

[44300] LOC152445 (Accession XP_098231.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC152445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE, designated SEQ ID:10071, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44301] Another function of GAM3229 is therefore inhibition of LOC152445 (Accession XP_098231.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC152445.

[44302] LOC152620 (Accession XP_011108.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC152620 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152620, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152620 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44303] Another function of GAM3229 is therefore inhibition of LOC152620 (Accession XP_011108.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152620.

[44304] LOC152719 (Accession XP_098257.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC152719 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152719, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152719 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44305] Another function of GAM3229 is therefore inhibition of LOC152719 (Accession XP_098257.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152719.

[44306] LOC152804 (Accession XP_098266.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC152804 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152804, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152804 BINDING SITE, designated SEQ ID:6723, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44307] Another function of GAM3229 is therefore inhibition of

LOC152804 (Accession XP_098266.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152804.

[44308] LOC153139 (Accession XP_098318.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC153139 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153139, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153139 BINDING SITE, designated SEQ ID:4758, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44309] Another function of GAM3229 is therefore inhibition of LOC153139 (Accession XP_098318.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153139.

[44310] LOC154184 (Accession XP_098488.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC154184 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC154184, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154184 BINDING SITE, designated SEQ ID:4758, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44311] Another function of GAM3229 is therefore inhibition of LOC154184 (Accession XP_098488.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154184.

[44312] LOC154282 (Accession XP_098505.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC154282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154282 BINDING SITE, designated SEQ ID:18644, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[44313] Another function of GAM3229 is therefore inhibition of LOC154282 (Accession XP_098505.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154282.

[44314] LOC154822 (Accession XP_098618.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC154822 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154822 BINDING SITE, designated SEQ ID:1820, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44315] Another function of GAM3229 is therefore inhibition of LOC154822 (Accession XP_098618.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154822.

[44316] LOC154877 (Accession XP_098626.1) is another

GAM3229 target gene, herein designated TARGET GENE. LOC154877 BINDING SITE1 and LOC154877 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC154877, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE1 and LOC154877 BINDING SITE2, designated SEQ ID:14674 and SEQ ID:10615 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44317] Another function of GAM3229 is therefore inhibition of LOC154877 (Accession XP_098626.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877.

[44318] LOC155032 (Accession XP_098647.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC155032 BINDING SITE1 and LOC155032 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC155032, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC155032 BINDING SITE1 and LOC155032 BINDING SITE2, designated SEQ ID:6455 and SEQ ID:16924 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44319] Another function of GAM3229 is therefore inhibition of LOC155032 (Accession XP_098647.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155032.

[44320] LOC157226 (Accession XP_033876.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC157226 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC157226, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157226 BINDING SITE, designated SEQ ID:5282, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44321] Another function of GAM3229 is therefore inhibition of LOC157226 (Accession XP_033876.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157226.

[44322] LOC158014 (Accession XP_088442.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC158014 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158014, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158014 BINDING SITE, designated SEQ ID:16148, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44323] Another function of GAM3229 is therefore inhibition of LOC158014 (Accession XP_088442.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158014.

[44324] LOC158257 (Accession XP_098908.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC158257 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC158257, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158257 BINDING SITE, designated SEQ ID:19341, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44325] Another function of GAM3229 is therefore inhibition of LOC158257 (Accession XP_098908.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158257.

[44326] LOC158373 (Accession XP_048539.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC158373 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158373, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158373 BINDING SITE, designated SEQ ID:18514, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44327] Another function of GAM3229 is therefore inhibition of LOC158373 (Accession XP_048539.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158373.

[44328] LOC158402 (Accession XP_098936.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC158402 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158402, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158402 BINDING SITE, designated SEQ ID:2018, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44329] Another function of GAM3229 is therefore inhibition of LOC158402 (Accession XP_098936.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158402.

[44330] LOC158476 (Accession XP_098955.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC158476 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158476, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158476 BINDING SITE, designated SEQ ID:6246, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44331] Another function of GAM3229 is therefore inhibition of LOC158476 (Accession XP_098955.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158476.

[44332] LOC158563 (Accession XP_088606.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC158563 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158563 BINDING SITE, designated SEQ ID:9836, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44333] Another function of GAM3229 is therefore inhibition of LOC158563 (Accession XP_088606.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158563.

[44334] LOC158865 (Accession XP_099000.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC158865 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158865 BINDING SITE, designated SEQ ID:1389, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44335] Another function of GAM3229 is therefore inhibition of LOC158865 (Accession XP_099000.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158865.

[44336] LOC161145 (Accession XP_101622.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC161145 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC161145, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC161145 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44337] Another function of GAM3229 is therefore inhibition of LOC161145 (Accession XP_101622.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161145.

[44338] LOC162967 (Accession XP_091890.6) is another GAM3229 target gene, herein designated TARGET GENE. LOC162967 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC162967, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC162967 BINDING SITE, designated SEQ ID:18580, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44339] Another function of GAM3229 is therefore inhibition of LOC162967 (Accession XP_091890.6) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162967.

[44340] LOC163227 (Accession NP_775802.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC163227, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2, designated SEQ ID:19173 and SEQ ID:8466 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44341] Another function of GAM3229 is therefore inhibition of LOC163227 (Accession NP_775802.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163227.

[44342] LOC163590 (Accession NP_659471.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC163590 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC163590, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163590 BINDING SITE, designated SEQ ID:2345, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44343] Another function of GAM3229 is therefore inhibition of LOC163590 (Accession NP_659471.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163590.

[44344] LOC164153 (Accession XP_089415.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC164153 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC164153, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC164153 BINDING SITE, designated SEQ ID:17694, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44345] Another function of GAM3229 is therefore inhibition of LOC164153 (Accession XP_089415.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164153.

[44346] LOC196214 (Accession XP_116897.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC196214 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196214, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196214 BINDING SITE, designated SEQ ID:12821, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44347] Another function of GAM3229 is therefore inhibition of LOC196214 (Accession XP_116897.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196214.

[44348] LOC196463 (Accession NP_775813.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC196463 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196463, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196463 BINDING SITE, designated SEQ ID:10525, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44349] Another function of GAM3229 is therefore inhibition of LOC196463 (Accession NP_775813.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196463.

[44350] LOC197358 (Accession XP_113872.2) is another GAM3229 target gene, herein designated TARGET GENE.

LOC197358 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC197358, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC197358 BINDING SITE, designated SEQ ID:8630, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44351] Another function of GAM3229 is therefore inhibition of LOC197358 (Accession XP_113872.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197358.

[44352] LOC199899 (Accession XP_117153.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC199899 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC199899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199899 BINDING SITE, designated SEQ ID:940, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44353] Another function of GAM3229 is therefore inhibition of LOC199899 (Accession XP_117153.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199899.

[44354] LOC200860 (Accession XP_117289.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC200860 BINDING SITE1 and LOC200860 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC200860, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200860 BINDING SITE1 and LOC200860 BINDING SITE2, designated SEQ ID:6951 and SEQ ID:18373 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44355] Another function of GAM3229 is therefore inhibition of LOC200860 (Accession XP_117289.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC200860.

[44356] LOC200895 (Accession NP_789785.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC200895 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200895, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200895 BINDING SITE, designated SEQ ID:13587, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44357] Another function of GAM3229 is therefore inhibition of LOC200895 (Accession NP_789785.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200895.

[44358] LOC200916 (Accession XP_114317.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC200916 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200916, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200916 BINDING SITE, designated SEQ ID:5449, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44359] Another function of GAM3229 is therefore inhibition of LOC200916 (Accession XP_114317.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200916.

[44360] LOC201292 (Accession NP_775818.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC201292 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201292, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201292 BINDING SITE, designated SEQ ID:11829, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44361] Another function of GAM3229 is therefore inhibition of LOC201292 (Accession NP_775818.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201292.

[44362] LOC201868 (Accession XP_114393.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC201868 BINDING SITE1 and LOC201868 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC201868, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201868 BINDING SITE1 and LOC201868 BINDING SITE2, designated SEQ ID:542 and SEQ ID:7507 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44363] Another function of GAM3229 is therefore inhibition of LOC201868 (Accession XP_114393.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201868.

[44364] LOC202459 (Accession NP_660346.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC202459 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC202459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202459 BINDING SITE, designated SEQ ID:4939, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44365] Another function of GAM3229 is therefore inhibition of LOC202459 (Accession NP_660346.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202459.

[44366] LOC202934 (Accession XP_117486.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC202934 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC202934, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE, designated SEQ ID:6398, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[44367] Another function of GAM3229 is therefore inhibition of LOC202934 (Accession XP_117486.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934.

[44368] LOC203547 (Accession XP_114719.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC203547 BINDING SITE1 and LOC203547 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC203547, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC203547 BINDING SITE1 and LOC203547 BINDING SITE2, designated SEQ ID:828 and SEQ ID:17521 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44369] Another function of GAM3229 is therefore inhibition of LOC203547 (Accession XP_114719.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203547.

[44370] LOC219293 (Accession XP_166599.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC219293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219293 BINDING SITE, designated SEQ ID:14079, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44371] Another function of GAM3229 is therefore inhibition of LOC219293 (Accession XP_166599.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219293.

[44372] LOC219731 (Accession XP_167596.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC219731 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC219731, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC219731 BINDING SITE, designated SEQ ID:4505, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44373] Another function of GAM3229 is therefore inhibition of LOC219731 (Accession XP_167596.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219731.

[44374] LOC220074 (Accession NP_660352.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC220074 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC220074, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220074 BINDING SITE, designated SEQ ID:9729, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44375] Another function of GAM3229 is therefore inhibition of LOC220074 (Accession NP_660352.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC220074.

[44376] LOC220980 (Accession XP_167629.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC220980 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC220980, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220980 BINDING SITE, designated SEQ ID:4661, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44377] Another function of GAM3229 is therefore inhibition of LOC220980 (Accession XP_167629.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220980.

[44378] LOC221405 (Accession XP_168138.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC221405 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221405, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221405 BINDING SITE, designated SEQ ID:14485, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44379] Another function of GAM3229 is therefore inhibition of LOC221405 (Accession XP_168138.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221405.

[44380] LOC221601 (Accession XP_168071.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC221601 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221601, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221601 BINDING SITE, designated SEQ ID:4758, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44381] Another function of GAM3229 is therefore inhibition of

LOC221601 (Accession XP_168071.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221601.

[44382] LOC221663 (Accession XP_168131.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC221663 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221663 BINDING SITE, designated SEQ ID:4068, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44383] Another function of GAM3229 is therefore inhibition of LOC221663 (Accession XP_168131.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221663.

[44384] LOC221946 (Accession XP_168340.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC221946 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC221946, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221946 BINDING SITE, designated SEQ ID:17132, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44385] Another function of GAM3229 is therefore inhibition of LOC221946 (Accession XP_168340.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221946.

[44386] LOC221960 (Accession XP_165859.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC221960 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221960, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221960 BINDING SITE, designated SEQ ID:3459, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[44387] Another function of GAM3229 is therefore inhibition of LOC221960 (Accession XP_165859.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221960.

[44388] LOC222057 (Accession XP_166594.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC222057 BINDING SITE1 and LOC222057 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC222057, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222057 BINDING SITE1 and LOC222057 BINDING SITE2, designated SEQ ID:8135 and SEQ ID:9877 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44389] Another function of GAM3229 is therefore inhibition of LOC222057 (Accession XP_166594.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222057.

[44390] LOC222224 (Accession XP_168473.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC222224 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222224, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222224 BINDING SITE, designated SEQ ID:18096, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44391] Another function of GAM3229 is therefore inhibition of LOC222224 (Accession XP_168473.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222224.

[44392] LOC252983 (Accession XP_170858.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC252983 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC252983, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC252983 BINDING SITE, designated SEQ ID:17884, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44393] Another function of GAM3229 is therefore inhibition of LOC252983 (Accession XP_170858.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC252983.

[44394] LOC255131 (Accession XP_171131.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC255131 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255131, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255131 BINDING SITE, designated SEQ ID:1329, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44395] Another function of GAM3229 is therefore inhibition of LOC255131 (Accession XP_171131.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC255131.

[44396] LOC255338 (Accession XP_171105.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC255338 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255338, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255338 BINDING SITE, designated SEQ ID:10003, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44397] Another function of GAM3229 is therefore inhibition of LOC255338 (Accession XP_171105.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255338.

[44398] LOC255458 (Accession XP_173150.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC255458 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC255458, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255458 BINDING SITE, designated SEQ ID:5123, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44399] Another function of GAM3229 is therefore inhibition of LOC255458 (Accession XP_173150.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255458.

[44400] LOC255975 (Accession XP_171083.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC255975 BINDING SITE1 and LOC255975 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC255975, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255975 BINDING SITE1 and LOC255975 BINDING SITE2, designated SEQ ID:829 and SEQ ID:8135 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44401] Another function of GAM3229 is therefore inhibition of LOC255975 (Accession XP_171083.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255975.

[44402] LOC256614 (Accession XP_172864.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC256614 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC256614, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256614 BINDING SITE, designated SEQ ID:14850, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44403] Another function of GAM3229 is therefore inhibition of LOC256614 (Accession XP_172864.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256614.

[44404] LOC282919 (Accession XP_212607.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC282919 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282919, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282919 BINDING SITE, designated SEQ ID:9471, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44405] Another function of GAM3229 is therefore inhibition of LOC282919 (Accession XP_212607.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282919.

[44406] LOC282956 (Accession XP_212649.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC282956 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282956, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282956 BINDING SITE, designated SEQ ID:9471, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44407] Another function of GAM3229 is therefore inhibition of LOC282956 (Accession XP_212649.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282956.

[44408] LOC282980 (Accession XP_210840.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC282980 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282980, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282980 BINDING SITE, designated SEQ ID:3959, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44409] Another function of GAM3229 is therefore inhibition of LOC282980 (Accession XP_210840.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282980.

[44410] LOC282997 (Accession XP_208473.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC282997 BINDING SITE1 and LOC282997 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC282997, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282997 BINDING SITE1 and LOC282997 BINDING SITE2, designated SEQ ID:18319 and SEQ ID:3573 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44411] Another function of GAM3229 is therefore inhibition of LOC282997 (Accession XP_208473.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282997.

[44412] LOC283031 (Accession XP_210859.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283031 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283031, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283031 BINDING SITE, designated SEQ ID:7798, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44413] Another function of GAM3229 is therefore inhibition of LOC283031 (Accession XP_210859.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283031.

[44414] LOC283046 (Accession XP_208495.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283046 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283046, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283046 BINDING SITE, designated SEQ ID:9872, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44415] Another function of GAM3229 is therefore inhibition of LOC283046 (Accession XP_208495.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283046.

[44416] LOC283061 (Accession XP_210875.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283061 BINDING SITE, designated SEQ ID:8704, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44417] Another function of GAM3229 is therefore inhibition of LOC283061 (Accession XP_210875.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283061.

[44418] LOC283089 (Accession XP_210885.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283089 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC283089, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283089 BINDING SITE, designated SEQ ID:2783, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44419] Another function of GAM3229 is therefore inhibition of LOC283089 (Accession XP_210885.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283089.

[44420] LOC283112 (Accession XP_210890.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC283112 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283112, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283112 BINDING SITE, designated SEQ ID:12579, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44421] Another function of GAM3229 is therefore inhibition of LOC283112 (Accession XP_210890.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283112.

[44422] LOC283119 (Accession XP_210895.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283119 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283119, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283119 BINDING SITE, designated SEQ ID:1059, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44423] Another function of GAM3229 is therefore inhibition of LOC283119 (Accession XP_210895.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283119.

[44424] LOC283120 (Accession XP_208516.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC283120 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283120, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283120 BINDING SITE, designated SEQ ID:18374, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44425] Another function of GAM3229 is therefore inhibition of LOC283120 (Accession XP_208516.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283120.

[44426] LOC283130 (Accession XP_208525.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC283130 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283130, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283130 BINDING SITE, designated SEQ ID:13623, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44427] Another function of GAM3229 is therefore inhibition of LOC283130 (Accession XP_208525.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283130.

[44428] LOC283177 (Accession XP_210903.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283177 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283177 BINDING SITE, designated SEQ ID:3801, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44429] Another function of GAM3229 is therefore inhibition of LOC283177 (Accession XP_210903.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283177.

[44430] LOC283215 (Accession XP_208555.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC283215 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283215, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283215 BINDING SITE, designated SEQ ID:7550, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44431] Another function of GAM3229 is therefore inhibition of LOC283215 (Accession XP_208555.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283215.

[44432] LOC283293 (Accession XP_210962.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC283293 BINDING SITE, designated SEQ ID:3960, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44433] Another function of GAM3229 is therefore inhibition of LOC283293 (Accession XP_210962.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283293.

[44434] LOC283323 (Accession XP_210973.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283323 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283323 BINDING SITE, designated SEQ ID:620, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44435] Another function of GAM3229 is therefore inhibition of LOC283323 (Accession XP_210973.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283323.

[44436] LOC283336 (Accession XP_208620.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283336 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283336 BINDING SITE, designated SEQ ID:6969, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44437] Another function of GAM3229 is therefore inhibition of LOC283336 (Accession XP_208620.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283336.

[44438] LOC283387 (Accession XP_211007.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283387 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283387, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283387 BINDING SITE, designated SEQ ID:19818, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44439] Another function of GAM3229 is therefore inhibition of LOC283387 (Accession XP_211007.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283387.

[44440] LOC283394 (Accession XP_211021.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283394 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283394, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283394 BINDING SITE, designated SEQ ID:9191, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44441] Another function of GAM3229 is therefore inhibition of

LOC283394 (Accession XP_211021.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283394.

[44442] LOC283484 (Accession XP_211053.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283484 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283484, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283484 BINDING SITE, designated SEQ ID:14686, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44443] Another function of GAM3229 is therefore inhibition of LOC283484 (Accession XP_211053.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283484.

[44444] LOC283487 (Accession XP_211062.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283487 BINDING SITE is a target binding site found in

the 3` untranslated region of multiple transcripts of mRNA encoded by LOC283487, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283487 BINDING SITE, designated SEQ ID:4891, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44445] Another function of GAM3229 is therefore inhibition of LOC283487 (Accession XP_211062.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283487.

[44446] LOC283551 (Accession XP_211110.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283551 BINDING SITE1 and LOC283551 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283551, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283551 BINDING SITE1 and LOC283551 BINDING SITE2, designated SEQ ID:17293 and SEQ ID:18515 respectively, to the

nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44447] Another function of GAM3229 is therefore inhibition of LOC283551 (Accession XP_211110.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283551.

[44448] LOC283575 (Accession XP_211095.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283575 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283575, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283575 BINDING SITE, designated SEQ ID:6798, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44449] Another function of GAM3229 is therefore inhibition of LOC283575 (Accession XP_211095.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283575.

[44450] LOC283590 (Accession XP_208741.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283590 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283590, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283590 BINDING SITE, designated SEQ ID:1550, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44451] Another function of GAM3229 is therefore inhibition of LOC283590 (Accession XP_208741.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283590.

[44452] LOC283641 (Accession XP_208764.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283641 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283641, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC283641 BINDING SITE, designated SEQ ID:10286, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44453] Another function of GAM3229 is therefore inhibition of LOC283641 (Accession XP_208764.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283641.

[44454] LOC283655 (Accession XP_211144.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283655 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283655, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283655 BINDING SITE, designated SEQ ID:3252, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44455] Another function of GAM3229 is therefore inhibition of LOC283655 (Accession XP_211144.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283655.

[44456] LOC283728 (Accession XP_211183.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC283728 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283728, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283728 BINDING SITE, designated SEQ ID:19012, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44457] Another function of GAM3229 is therefore inhibition of LOC283728 (Accession XP_211183.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283728.

[44458] LOC283767 (Accession XP_208835.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283767 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283767, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283767 BINDING SITE, designated SEQ ID:1069, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44459] Another function of GAM3229 is therefore inhibition of LOC283767 (Accession XP_208835.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283767.

[44460] LOC283889 (Accession XP_208899.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283889 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283889, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283889 BINDING SITE, designated SEQ ID:12163, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44461] Another function of GAM3229 is therefore inhibition of

LOC283889 (Accession XP_208899.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283889.

[44462] LOC283928 (Accession XP_208909.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC283928 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283928, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283928 BINDING SITE, designated SEQ ID:8866, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44463] Another function of GAM3229 is therefore inhibition of LOC283928 (Accession XP_208909.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283928.

[44464] LOC284001 (Accession XP_208958.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC284001 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC284001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284001 BINDING SITE, designated SEQ ID:14012, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44465] Another function of GAM3229 is therefore inhibition of LOC284001 (Accession XP_208958.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284001.

[44466] LOC284016 (Accession XP_211298.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284016 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284016, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284016 BINDING SITE, designated SEQ ID:2783, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[44467] Another function of GAM3229 is therefore inhibition of LOC284016 (Accession XP_211298.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284016.

[44468] LOC284041 (Accession XP_211309.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284041 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284041, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284041 BINDING SITE, designated SEQ ID:17544, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44469] Another function of GAM3229 is therefore inhibition of LOC284041 (Accession XP_211309.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284041.

[44470] LOC284063 (Accession XP_208992.1) is another

GAM3229 target gene, herein designated TARGET GENE. LOC284063 BINDING SITE1 and LOC284063 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284063, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284063 BINDING SITE1 and LOC284063 BINDING SITE2, designated SEQ ID:7960 and SEQ ID:9729 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44471] Another function of GAM3229 is therefore inhibition of LOC284063 (Accession XP_208992.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284063.

[44472] LOC284074 (Accession XP_211321.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284074 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284074, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284074 BINDING SITE, designated SEQ ID:1935, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44473] Another function of GAM3229 is therefore inhibition of LOC284074 (Accession XP_211321.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284074.

[44474] LOC284095 (Accession XP_211324.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284095 BINDING SITE1 through LOC284095 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284095, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284095 BINDING SITE1 through LOC284095 BINDING SITE3, designated SEQ ID:6762, SEQ ID:11871 and SEQ ID:3941 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44475] Another function of GAM3229 is therefore inhibition of LOC284095 (Accession XP_211324.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284095.

[44476] LOC284098 (Accession XP_209008.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC284098 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284098, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284098 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44477] Another function of GAM3229 is therefore inhibition of LOC284098 (Accession XP_209008.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284098.

[44478] LOC284101 (Accession XP_209019.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284101 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC284101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284101 BINDING SITE, designated SEQ ID:2800, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44479] Another function of GAM3229 is therefore inhibition of LOC284101 (Accession XP_209019.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284101.

[44480] LOC284102 (Accession XP_211327.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC284102 BINDING SITE1 through LOC284102 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC284102, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284102 BINDING SITE1 through LOC284102 BINDING SITE4, designated SEQ ID:6048, SEQ ID:9397, SEQ ID:4684 and SEQ ID:15652 respectively, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44481] Another function of GAM3229 is therefore inhibition of LOC284102 (Accession XP_211327.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284102.

[44482] LOC284117 (Accession XP_209024.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284117 BINDING SITE, designated SEQ ID:3205, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44483] Another function of GAM3229 is therefore inhibition of LOC284117 (Accession XP_209024.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284117.

[44484] LOC284135 (Accession XP_209032.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284135 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284135 BINDING SITE, designated SEQ ID:2340, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44485] Another function of GAM3229 is therefore inhibition of LOC284135 (Accession XP_209032.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284135.

[44486] LOC284183 (Accession XP_209059.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284183 BINDING SITE1 and LOC284183 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284183, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC284183 BINDING SITE1 and LOC284183 BINDING SITE2, designated SEQ ID:4891 and SEQ ID:9729 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44487] Another function of GAM3229 is therefore inhibition of LOC284183 (Accession XP_209059.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284183.

[44488] LOC284186 (Accession XP_209060.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC284186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284186 BINDING SITE, designated SEQ ID:18663, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44489] Another function of GAM3229 is therefore inhibition of LOC284186 (Accession XP_209060.2) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284186.

[44490] LOC284191 (Accession XP_211377.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284191 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284191, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284191 BINDING SITE, designated SEQ ID:6160, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44491] Another function of GAM3229 is therefore inhibition of LOC284191 (Accession XP_211377.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284191.

[44492] LOC284260 (Accession XP_211408.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284260 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC284260, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284260 BINDING SITE, designated SEQ ID:8657, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44493] Another function of GAM3229 is therefore inhibition of LOC284260 (Accession XP_211408.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284260.

[44494] LOC284276 (Accession XP_211412.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284276 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284276, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284276 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44495] Another function of GAM3229 is therefore inhibition of LOC284276 (Accession XP_211412.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284276.

[44496] LOC284294 (Accession XP_211421.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284294 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284294, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284294 BINDING SITE, designated SEQ ID:13205, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44497] Another function of GAM3229 is therefore inhibition of LOC284294 (Accession XP_211421.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284294.

[44498] LOC284305 (Accession XP_211425.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC284305 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284305, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284305 BINDING SITE, designated SEQ ID:4957, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44499] Another function of GAM3229 is therefore inhibition of LOC284305 (Accession XP_211425.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284305.

[44500] LOC284317 (Accession XP_209162.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284317 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284317, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284317 BINDING SITE, designated SEQ ID:16453, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44501] Another function of GAM3229 is therefore inhibition of LOC284317 (Accession XP_209162.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284317.

[44502] LOC284337 (Accession XP_211434.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284337 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284337, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284337 BINDING SITE, designated SEQ ID:12960, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44503] Another function of GAM3229 is therefore inhibition of LOC284337 (Accession XP_211434.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284337.

[44504] LOC284361 (Accession NP_778233.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC284361 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284361, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284361 BINDING SITE, designated SEQ ID:11166, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44505] Another function of GAM3229 is therefore inhibition of LOC284361 (Accession NP_778233.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284361.

[44506] LOC284362 (Accession XP_211435.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284362 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284362, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284362 BINDING SITE, designated SEQ ID:941, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44507] Another function of GAM3229 is therefore inhibition of LOC284362 (Accession XP_211435.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284362.

[44508] LOC284421 (Accession XP_209200.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284421 BINDING SITE1 and LOC284421 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284421, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284421 BINDING SITE1 and LOC284421 BINDING SITE2, designated SEQ ID:10044 and SEQ ID:2187 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44509] Another function of GAM3229 is therefore inhibition of LOC284421 (Accession XP_209200.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284421.

[44510] LOC284426 (Accession XP_209198.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284426 BINDING SITE1 through LOC284426 BINDING SITE4 are target binding sites found in untranslated regions of mRNA encoded by LOC284426, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284426 BINDING SITE1 through LOC284426 BINDING SITE4, designated SEQ ID:20053, SEQ ID:19721, SEQ ID:9681 and SEQ ID:7372 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44511] Another function of GAM3229 is therefore inhibition of LOC284426 (Accession XP_209198.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284426.

[44512] LOC284436 (Accession XP_290862.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC284436 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284436 BINDING SITE, designated SEQ ID:19435, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44513] Another function of GAM3229 is therefore inhibition of LOC284436 (Accession XP_290862.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284436.

[44514] LOC284454 (Accession XP_209216.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284454 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284454, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284454 BINDING SITE, designated SEQ ID:9887, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44515] Another function of GAM3229 is therefore inhibition of LOC284454 (Accession XP_209216.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284454.

[44516] LOC284456 (Accession XP_211470.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284456 BINDING SITE, designated SEQ ID:18780, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44517] Another function of GAM3229 is therefore inhibition of LOC284456 (Accession XP_211470.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284456.

[44518] LOC284464 (Accession XP_209221.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284464 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284464, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284464 BINDING SITE, designated SEQ ID:6969, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44519] Another function of GAM3229 is therefore inhibition of LOC284464 (Accession XP_209221.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284464.

[44520] LOC284471 (Accession XP_209225.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284471 BINDING SITE1 and LOC284471 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284471, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC284471 BINDING SITE1 and LOC284471 BINDING SITE2, designated SEQ ID:6824 and SEQ ID:6873 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44521] Another function of GAM3229 is therefore inhibition of LOC284471 (Accession XP_209225.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284471.

[44522] LOC284475 (Accession XP_211478.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284475 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284475 BINDING SITE, designated SEQ ID:6825, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44523] Another function of GAM3229 is therefore inhibition of LOC284475 (Accession XP_211478.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284475.

[44524] LOC284512 (Accession XP_211500.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284512 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284512, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284512 BINDING SITE, designated SEQ ID:13007, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44525] Another function of GAM3229 is therefore inhibition of LOC284512 (Accession XP_211500.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284512.

[44526] LOC284514 (Accession XP_209244.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284514 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC284514, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284514 BINDING SITE, designated SEQ ID:16576, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44527] Another function of GAM3229 is therefore inhibition of LOC284514 (Accession XP_209244.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284514.

[44528] LOC284568 (Accession XP_209263.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284568 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284568, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284568 BINDING SITE, designated SEQ ID:4506, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44529] Another function of GAM3229 is therefore inhibition of LOC284568 (Accession XP_209263.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284568.

[44530] LOC284587 (Accession XP_209278.3) is another GAM3229 target gene, herein designated TARGET GENE. LOC284587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284587 BINDING SITE, designated SEQ ID:9877, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44531] Another function of GAM3229 is therefore inhibition of LOC284587 (Accession XP_209278.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284587.

[44532] LOC284630 (Accession XP_211562.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC284630 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284630, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284630 BINDING SITE, designated SEQ ID:15653, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44533] Another function of GAM3229 is therefore inhibition of LOC284630 (Accession XP_211562.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284630.

[44534] LOC284701 (Accession XP_294994.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284701 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284701, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284701 BINDING SITE, designated SEQ ID:8135, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44535] Another function of GAM3229 is therefore inhibition of LOC284701 (Accession XP_294994.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284701.

[44536] LOC284723 (Accession XP_211602.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284723 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284723, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284723 BINDING SITE, designated SEQ ID:1735, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44537] Another function of GAM3229 is therefore inhibition of LOC284723 (Accession XP_211602.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284723.

[44538] LOC284745 (Accession XP_211620.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284745 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284745, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284745 BINDING SITE, designated SEQ ID:9999, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44539] Another function of GAM3229 is therefore inhibition of LOC284745 (Accession XP_211620.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284745.

[44540] LOC284837 (Accession XP_211658.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284837 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284837, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284837 BINDING SITE, designated SEQ ID:18808, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44541] Another function of GAM3229 is therefore inhibition of LOC284837 (Accession XP_211658.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284837.

[44542] LOC284865 (Accession XP_211672.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284865 BINDING SITE1 and LOC284865 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284865, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284865 BINDING SITE1 and LOC284865 BINDING SITE2, designated SEQ ID:10282 and SEQ ID:16817 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44543] Another function of GAM3229 is therefore inhibition of LOC284865 (Accession XP_211672.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284865.

[44544] LOC284934 (Accession XP_211696.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC284934 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284934, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284934 BINDING SITE, designated SEQ ID:18766, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44545] Another function of GAM3229 is therefore inhibition of LOC284934 (Accession XP_211696.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284934.

[44546] LOC285001 (Accession XP_211730.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285001 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC285001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285001 BINDING SITE, designated SEQ ID:18439, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44547] Another function of GAM3229 is therefore inhibition of LOC285001 (Accession XP_211730.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285001.

[44548] LOC285026 (Accession XP_209440.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285026 BINDING SITE1 and LOC285026 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285026, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285026 BINDING SITE1 and LOC285026 BINDING SITE2, designated SEQ ID:3961 and SEQ ID:6793 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[44549] Another function of GAM3229 is therefore inhibition of LOC285026 (Accession XP_209440.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285026.

[44550] LOC285033 (Accession XP_211739.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285033 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285033, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285033 BINDING SITE, designated SEQ ID:16976, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44551] Another function of GAM3229 is therefore inhibition of LOC285033 (Accession XP_211739.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285033.

[44552] LOC285058 (Accession XP_211753.1) is another

GAM3229 target gene, herein designated TARGET GENE. LOC285058 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285058 BINDING SITE, designated SEQ ID:9309, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44553] Another function of GAM3229 is therefore inhibition of LOC285058 (Accession XP_211753.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285058.

[44554] LOC285083 (Accession XP_209464.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285083 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285083, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285083 BINDING SITE, desig-

nated SEQ ID:2096, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44555] Another function of GAM3229 is therefore inhibition of LOC285083 (Accession XP_209464.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285083.

[44556] LOC285088 (Accession XP_209465.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285088 BINDING SITE1 and LOC285088 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285088, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285088 BINDING SITE1 and LOC285088 BINDING SITE2, designated SEQ ID:9680 and SEQ ID:10075 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44557] Another function of GAM3229 is therefore inhibition of LOC285088 (Accession XP_209465.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285088.

[44558] LOC285136 (Accession XP_211777.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285136 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285136 BINDING SITE, designated SEQ ID:14792, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44559] Another function of GAM3229 is therefore inhibition of LOC285136 (Accession XP_211777.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285136.

[44560] LOC285221 (Accession XP_209521.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285221 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285221, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285221 BINDING SITE, designated SEQ ID:6398, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44561] Another function of GAM3229 is therefore inhibition of LOC285221 (Accession XP_209521.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285221.

[44562] LOC285231 (Accession XP_211813.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285231 BINDING SITE1 through LOC285231 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC285231, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285231 BINDING SITE1 through LOC285231 BINDING SITE3, designated SEQ ID:7578, SEQ ID:16034 and SEQ ID:8476 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44563] Another function of GAM3229 is therefore inhibition of LOC285231 (Accession XP_211813.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285231.

[44564] LOC285299 (Accession XP_209554.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285299 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285299, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285299 BINDING SITE, designated SEQ ID:2404, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44565] Another function of GAM3229 is therefore inhibition of LOC285299 (Accession XP_209554.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285299.

[44566] LOC285334 (Accession XP_211844.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC285334 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285334 BINDING SITE, designated SEQ ID:16422, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44567] Another function of GAM3229 is therefore inhibition of LOC285334 (Accession XP_211844.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285334.

[44568] LOC285344 (Accession XP_211853.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285344 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285344, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285344 BINDING SITE, designated SEQ ID:4229, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44569] Another function of GAM3229 is therefore inhibition of LOC285344 (Accession XP_211853.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285344.

[44570] LOC285345 (Accession XP_211854.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285345 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285345, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285345 BINDING SITE, designated SEQ ID:2368, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44571] Another function of GAM3229 is therefore inhibition of LOC285345 (Accession XP_211854.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285345.

[44572] LOC285363 (Accession XP_211870.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285363 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285363, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285363 BINDING SITE, designated SEQ ID:14046, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44573] Another function of GAM3229 is therefore inhibition of LOC285363 (Accession XP_211870.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285363.

[44574] LOC285398 (Accession XP_209593.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285398 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285398, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC285398 BINDING SITE, designated SEQ ID:10964, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44575] Another function of GAM3229 is therefore inhibition of LOC285398 (Accession XP_209593.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285398.

[44576] LOC285540 (Accession XP_209654.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285540 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285540, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285540 BINDING SITE, designated SEQ ID:18955, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44577] Another function of GAM3229 is therefore inhibition of LOC285540 (Accession XP_209654.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285540.

[44578] LOC285587 (Accession XP_211947.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285587 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285587 BINDING SITE, designated SEQ ID:12848, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44579] Another function of GAM3229 is therefore inhibition of LOC285587 (Accession XP_211947.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285587.

[44580] LOC285589 (Accession XP_209671.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285589 BINDING SITE1 and LOC285589 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285589, corresponding to

target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285589 BINDING SITE1 and LOC285589 BINDING SITE2, designated SEQ ID:11982 and SEQ ID:6398 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44581] Another function of GAM3229 is therefore inhibition of LOC285589 (Accession XP_209671.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285589.

[44582] LOC285626 (Accession XP_211959.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285626 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285626, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285626 BINDING SITE, designated SEQ ID:14142, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44583] Another function of GAM3229 is therefore inhibition of LOC285626 (Accession XP_211959.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285626.

[44584] LOC285638 (Accession XP_209693.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285638 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285638, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285638 BINDING SITE, designated SEQ ID:1800, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44585] Another function of GAM3229 is therefore inhibition of LOC285638 (Accession XP_209693.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285638.

[44586] LOC285683 (Accession XP_211980.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC285683 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285683, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285683 BINDING SITE, designated SEQ ID:14636, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44587] Another function of GAM3229 is therefore inhibition of LOC285683 (Accession XP_211980.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285683.

[44588] LOC285722 (Accession XP_211997.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285722 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285722, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285722 BINDING SITE, designated SEQ ID:19086, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44589] Another function of GAM3229 is therefore inhibition of LOC285722 (Accession XP_211997.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285722.

[44590] LOC285744 (Accession XP_209743.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285744 BINDING SITE1 and LOC285744 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285744, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285744 BINDING SITE1 and LOC285744 BINDING SITE2, designated SEQ ID:8764 and SEQ ID:17380 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44591] Another function of GAM3229 is therefore inhibition of LOC285744 (Accession XP_209743.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285744.

[44592] LOC285747 (Accession XP_209742.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285747 BINDING SITE1 and LOC285747 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285747, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285747 BINDING SITE1 and LOC285747 BINDING SITE2, designated SEQ ID:6072 and SEQ ID:13313 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44593] Another function of GAM3229 is therefore inhibition of LOC285747 (Accession XP_209742.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285747.

[44594] LOC285749 (Accession XP_212010.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285749 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285749, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285749 BINDING SITE, designated SEQ ID:4758, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44595] Another function of GAM3229 is therefore inhibition of LOC285749 (Accession XP_212010.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285749.

[44596] LOC285760 (Accession XP_209750.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285760 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285760, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285760 BINDING SITE, designated SEQ ID:10409, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44597] Another function of GAM3229 is therefore inhibition of

LOC285760 (Accession XP_209750.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285760.

[44598] LOC285822 (Accession XP_209777.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285822 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285822 BINDING SITE, designated SEQ ID:6398, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44599] Another function of GAM3229 is therefore inhibition of LOC285822 (Accession XP_209777.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285822.

[44600] LOC285835 (Accession XP_212057.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285835 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC285835, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285835 BINDING SITE, designated SEQ ID:9471, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44601] Another function of GAM3229 is therefore inhibition of LOC285835 (Accession XP_212057.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285835.

[44602] LOC285842 (Accession XP_212041.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285842 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285842 BINDING SITE, designated SEQ ID:10492, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[44603] Another function of GAM3229 is therefore inhibition of LOC285842 (Accession XP_212041.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285842.

[44604] LOC285843 (Accession XP_212034.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285843 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285843, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285843 BINDING SITE, designated SEQ ID:10152, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44605] Another function of GAM3229 is therefore inhibition of LOC285843 (Accession XP_212034.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285843.

[44606] LOC285847 (Accession XP_212045.1) is another

GAM3229 target gene, herein designated TARGET GENE. LOC285847 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285847, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285847 BINDING SITE, designated SEQ ID:10601, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44607] Another function of GAM3229 is therefore inhibition of LOC285847 (Accession XP_212045.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285847.

[44608] LOC285922 (Accession XP_209822.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285922 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285922 BINDING SITE, desig-

nated SEQ ID:8542, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44609] Another function of GAM3229 is therefore inhibition of LOC285922 (Accession XP_209822.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285922.

[44610] LOC285923 (Accession XP_212104.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285923 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285923, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285923 BINDING SITE, designated SEQ ID:7843, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44611] Another function of GAM3229 is therefore inhibition of LOC285923 (Accession XP_212104.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285923.

[44612] LOC285930 (Accession XP_209818.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285930 BINDING SITE1 and LOC285930 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285930, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285930 BINDING SITE1 and LOC285930 BINDING SITE2, designated SEQ ID:6763 and SEQ ID:18902 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44613] Another function of GAM3229 is therefore inhibition of LOC285930 (Accession XP_209818.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285930.

[44614] LOC285958 (Accession XP_212099.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285958 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285958, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285958 BINDING SITE, designated SEQ ID:10240, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44615] Another function of GAM3229 is therefore inhibition of LOC285958 (Accession XP_212099.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285958.

[44616] LOC285961 (Accession XP_209833.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285961 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285961, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285961 BINDING SITE, designated SEQ ID:12547, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44617] Another function of GAM3229 is therefore inhibition of

LOC285961 (Accession XP_209833.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285961.

[44618] LOC285969 (Accession XP_209842.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285969 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285969, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285969 BINDING SITE, designated SEQ ID:1953, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44619] Another function of GAM3229 is therefore inhibition of LOC285969 (Accession XP_209842.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285969.

[44620] LOC285972 (Accession XP_212105.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285972 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC285972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285972 BINDING SITE, designated SEQ ID:9694, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44621] Another function of GAM3229 is therefore inhibition of LOC285972 (Accession XP_212105.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285972.

[44622] LOC285999 (Accession XP_212120.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC285999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285999 BINDING SITE, designated SEQ ID:11099, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[44623] Another function of GAM3229 is therefore inhibition of LOC285999 (Accession XP_212120.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285999.

[44624] LOC286029 (Accession XP_209866.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286029 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286029, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286029 BINDING SITE, designated SEQ ID:3117, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44625] Another function of GAM3229 is therefore inhibition of LOC286029 (Accession XP_209866.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286029.

[44626] LOC286058 (Accession XP_212158.1) is another

GAM3229 target gene, herein designated TARGET GENE. LOC286058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286058 BINDING SITE, designated SEQ ID:15856, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44627] Another function of GAM3229 is therefore inhibition of LOC286058 (Accession XP_212158.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286058.

[44628] LOC286078 (Accession XP_212163.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286078 BINDING SITE1 and LOC286078 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC286078, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286078

BINDING SITE1 and LOC286078 BINDING SITE2, designated SEQ ID:8047 and SEQ ID:13047 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44629] Another function of GAM3229 is therefore inhibition of LOC286078 (Accession XP_212163.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286078.

[44630] LOC286103 (Accession NP_848630.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286103 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC286103, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286103 BINDING SITE, designated SEQ ID:5123, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44631] Another function of GAM3229 is therefore inhibition of LOC286103 (Accession NP_848630.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC286103.

[44632] LOC286103 (Accession XP_209897.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286103 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC286103, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286103 BINDING SITE, designated SEQ ID:5123, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44633] Another function of GAM3229 is therefore inhibition of LOC286103 (Accession XP_209897.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286103.

[44634] LOC286186 (Accession XP_212219.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286186 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286186, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286186 BINDING SITE, designated SEQ ID:5503, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44635] Another function of GAM3229 is therefore inhibition of LOC286186 (Accession XP_212219.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286186.

[44636] LOC286191 (Accession XP_212217.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286191 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286191, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286191 BINDING SITE, designated SEQ ID:5905, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44637] Another function of GAM3229 is therefore inhibition of

LOC286191 (Accession XP_212217.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286191.

[44638] LOC286207 (Accession XP_209941.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286207 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286207, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286207 BINDING SITE, designated SEQ ID:15150, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44639] Another function of GAM3229 is therefore inhibition of LOC286207 (Accession XP_209941.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286207.

[44640] LOC286208 (Accession XP_212230.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286208 BINDING SITE1 and LOC286208 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC286208, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286208 BINDING SITE1 and LOC286208 BINDING SITE2, designated SEQ ID:12103 and SEQ ID:18679 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44641] Another function of GAM3229 is therefore inhibition of LOC286208 (Accession XP_212230.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286208.

[44642] LOC286334 (Accession XP_303033.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286334 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286334 BINDING SITE, designated SEQ ID:10661, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44643] Another function of GAM3229 is therefore inhibition of LOC286334 (Accession XP_303033.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286334.

[44644] LOC286341 (Accession XP_212278.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286341 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286341, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286341 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44645] Another function of GAM3229 is therefore inhibition of LOC286341 (Accession XP_212278.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286341.

[44646] LOC286356 (Accession XP_212290.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286356 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286356 BINDING SITE, designated SEQ ID:13314, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44647] Another function of GAM3229 is therefore inhibition of LOC286356 (Accession XP_212290.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286356.

[44648] LOC286359 (Accession XP_212288.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286359 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286359, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC286359 BINDING SITE, designated SEQ ID:16003, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44649] Another function of GAM3229 is therefore inhibition of LOC286359 (Accession XP_212288.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286359.

[44650] LOC286401 (Accession XP_212310.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286401 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286401, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286401 BINDING SITE, designated SEQ ID:1364, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44651] Another function of GAM3229 is therefore inhibition of LOC286401 (Accession XP_212310.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC286401.

[44652] LOC286435 (Accession XP_210047.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286435 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286435, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286435 BINDING SITE, designated SEQ ID:6220, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44653] Another function of GAM3229 is therefore inhibition of LOC286435 (Accession XP_210047.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286435.

[44654] LOC286437 (Accession XP_210050.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286437 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286437, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286437 BINDING SITE, designated SEQ ID:15960, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44655] Another function of GAM3229 is therefore inhibition of LOC286437 (Accession XP_210050.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286437.

[44656] LOC286441 (Accession XP_212319.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC286441 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286441, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286441 BINDING SITE, designated SEQ ID:9998, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44657] Another function of GAM3229 is therefore inhibition of

LOC286441 (Accession XP_212319.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286441.

[44658] LOC338575 (Accession XP_290473.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC338575 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338575, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338575 BINDING SITE, designated SEQ ID:16337, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44659] Another function of GAM3229 is therefore inhibition of LOC338575 (Accession XP_290473.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338575.

[44660] LOC338612 (Accession XP_294668.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC338612 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC338612, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338612 BINDING SITE, designated SEQ ID:5199, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44661] Another function of GAM3229 is therefore inhibition of LOC338612 (Accession XP_294668.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338612.

[44662] LOC338645 (Accession XP_290494.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC338645 BINDING SITE1 and LOC338645 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC338645, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338645 BINDING SITE1 and LOC338645 BINDING SITE2, designated SEQ ID:13444 and SEQ ID:2827 respectively, to the

nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44663] Another function of GAM3229 is therefore inhibition of LOC338645 (Accession XP_290494.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338645.

[44664] LOC338709 (Accession XP_211595.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC338709 BINDING SITE1 and LOC338709 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC338709, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338709 BINDING SITE1 and LOC338709 BINDING SITE2, designated SEQ ID:8135 and SEQ ID:9877 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44665] Another function of GAM3229 is therefore inhibition of LOC338709 (Accession XP_211595.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC338709.

[44666] LOC338773 (Accession XP_290570.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC338773 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338773, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338773 BINDING SITE, designated SEQ ID:9515, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44667] Another function of GAM3229 is therefore inhibition of LOC338773 (Accession XP_290570.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338773.

[44668] LOC338799 (Accession NP_848633.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC338799 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC338799, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338799 BINDING SITE, designated SEQ ID:14539, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44669] Another function of GAM3229 is therefore inhibition of LOC338799 (Accession NP_848633.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338799.

[44670] LOC338817 (Accession XP_290588.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC338817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338817 BINDING SITE, designated SEQ ID:19436, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44671] Another function of GAM3229 is therefore inhibition of LOC338817 (Accession XP_290588.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338817.

[44672] LOC338864 (Accession XP_294731.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC338864 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338864, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338864 BINDING SITE, designated SEQ ID:16899, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44673] Another function of GAM3229 is therefore inhibition of LOC338864 (Accession XP_294731.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338864.

[44674] LOC338899 (Accession XP_294740.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC338899 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC338899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338899 BINDING SITE, designated SEQ ID:8395, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44675] Another function of GAM3229 is therefore inhibition of LOC338899 (Accession XP_294740.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338899.

[44676] LOC338917 (Accession XP_290610.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC338917 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338917, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338917 BINDING SITE, designated SEQ ID:8024, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44677] Another function of GAM3229 is therefore inhibition of LOC338917 (Accession XP_290610.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338917.

[44678] LOC338991 (Accession XP_290663.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC338991 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338991, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338991 BINDING SITE, designated SEQ ID:1069, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44679] Another function of GAM3229 is therefore inhibition of LOC338991 (Accession XP_290663.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338991.

[44680] LOC338999 (Accession XP_290659.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC338999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338999 BINDING SITE, designated SEQ ID:1069, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44681] Another function of GAM3229 is therefore inhibition of LOC338999 (Accession XP_290659.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338999.

[44682] LOC339077 (Accession XP_294802.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC339077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339077 BINDING SITE, designated SEQ ID:9695, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44683] Another function of GAM3229 is therefore inhibition of LOC339077 (Accession XP_294802.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339077.

[44684] LOC339078 (Accession XP_290692.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339078 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339078 BINDING SITE, designated SEQ ID:9304, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44685] Another function of GAM3229 is therefore inhibition of LOC339078 (Accession XP_290692.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339078.

[44686] LOC339091 (Accession XP_290239.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339091 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339091, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339091 BINDING SITE, designated SEQ ID:13820, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44687] Another function of GAM3229 is therefore inhibition of LOC339091 (Accession XP_290239.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339091.

[44688] LOC339146 (Accession XP_294825.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339146 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC339146 BINDING SITE, designated SEQ ID:2752, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44689] Another function of GAM3229 is therefore inhibition of LOC339146 (Accession XP_294825.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339146.

[44690] LOC339178 (Accession XP_290742.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339178 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339178, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339178 BINDING SITE, designated SEQ ID:19259, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44691] Another function of GAM3229 is therefore inhibition of LOC339178 (Accession XP_290742.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC339178.

[44692] LOC339201 (Accession XP_290756.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339201 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339201 BINDING SITE, designated SEQ ID:7031, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44693] Another function of GAM3229 is therefore inhibition of LOC339201 (Accession XP_290756.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339201.

[44694] LOC339216 (Accession XP_290762.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC339216 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339216, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339216 BINDING SITE, designated SEQ ID:2800, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44695] Another function of GAM3229 is therefore inhibition of LOC339216 (Accession XP_290762.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339216.

[44696] LOC339282 (Accession XP_294900.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC339282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339282 BINDING SITE, designated SEQ ID:2800, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44697] Another function of GAM3229 is therefore inhibition of

LOC339282 (Accession XP_294900.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339282.

[44698] LOC339283 (Accession XP_294899.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC339283 BINDING SITE1 and LOC339283 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339283, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339283 BINDING SITE1 and LOC339283 BINDING SITE2, designated SEQ ID:12131 and SEQ ID:2800 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44699] Another function of GAM3229 is therefore inhibition of LOC339283 (Accession XP_294899.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339283.

[44700] LOC339325 (Accession XP_290830.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC339325 BINDING SITE1 and LOC339325 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339325, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339325 BINDING SITE1 and LOC339325 BINDING SITE2, designated SEQ ID:20083 and SEQ ID:9527 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44701] Another function of GAM3229 is therefore inhibition of LOC339325 (Accession XP_290830.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339325.

[44702] LOC339400 (Accession XP_294926.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339400 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339400 BINDING SITE, desig-

nated SEQ ID:17876, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44703] Another function of GAM3229 is therefore inhibition of LOC339400 (Accession XP_294926.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339400.

[44704] LOC339459 (Accession XP_290907.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC339459 BINDING SITE1 and LOC339459 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339459, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339459 BINDING SITE1 and LOC339459 BINDING SITE2, designated SEQ ID:537 and SEQ ID:4044 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44705] Another function of GAM3229 is therefore inhibition of LOC339459 (Accession XP_290907.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC339459.

[44706] LOC339492 (Accession XP_290919.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339492 BINDING SITE1 and LOC339492 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339492, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339492 BINDING SITE1 and LOC339492 BINDING SITE2, designated SEQ ID:3503 and SEQ ID:1590 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44707] Another function of GAM3229 is therefore inhibition of LOC339492 (Accession XP_290919.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339492.

[44708] LOC339577 (Accession XP_295005.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339577 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC339577, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339577 BINDING SITE, designated SEQ ID:18440, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44709] Another function of GAM3229 is therefore inhibition of LOC339577 (Accession XP_295005.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339577.

[44710] LOC339600 (Accession XP_295014.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339600 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339600, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339600 BINDING SITE, designated SEQ ID:18533, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44711] Another function of GAM3229 is therefore inhibition of LOC339600 (Accession XP_295014.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339600.

[44712] LOC339635 (Accession XP_293210.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC339635 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339635, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339635 BINDING SITE, designated SEQ ID:19918, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44713] Another function of GAM3229 is therefore inhibition of LOC339635 (Accession XP_293210.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339635.

[44714] LOC339685 (Accession XP_295032.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC339685 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339685, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339685 BINDING SITE, designated SEQ ID:19789, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44715] Another function of GAM3229 is therefore inhibition of LOC339685 (Accession XP_295032.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339685.

[44716] LOC339694 (Accession XP_295035.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339694 BINDING SITE1 and LOC339694 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC339694, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339694 BINDING SITE1 and LOC339694 BINDING SITE2, desig-

nated SEQ ID:7230 and SEQ ID:12466 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44717] Another function of GAM3229 is therefore inhibition of LOC339694 (Accession XP_295035.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339694.

[44718] LOC339720 (Accession XP_295041.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339720 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339720, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339720 BINDING SITE, designated SEQ ID:9730, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44719] Another function of GAM3229 is therefore inhibition of LOC339720 (Accession XP_295041.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC339720.

[44720] LOC339738 (Accession XP_295048.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339738 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339738, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339738 BINDING SITE, designated SEQ ID:7722, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44721] Another function of GAM3229 is therefore inhibition of LOC339738 (Accession XP_295048.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339738.

[44722] LOC339751 (Accession XP_295053.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339751 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339751, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339751 BINDING SITE, designated SEQ ID:13172, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44723] Another function of GAM3229 is therefore inhibition of LOC339751 (Accession XP_295053.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339751.

[44724] LOC339803 (Accession XP_295072.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339803 BINDING SITE, designated SEQ ID:10537, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44725] Another function of GAM3229 is therefore inhibition of LOC339803 (Accession XP_295072.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339803.

[44726] LOC339807 (Accession XP_295070.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339807 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339807, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339807 BINDING SITE, designated SEQ ID:11926, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44727] Another function of GAM3229 is therefore inhibition of LOC339807 (Accession XP_295070.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339807.

[44728] LOC339809 (Accession XP_291020.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339809 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC339809, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339809 BINDING SITE, designated SEQ ID:17851, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44729] Another function of GAM3229 is therefore inhibition of LOC339809 (Accession XP_291020.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339809.

[44730] LOC339813 (Accession XP_295074.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339813 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339813 BINDING SITE, designated SEQ ID:10359, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44731] Another function of GAM3229 is therefore inhibition of LOC339813 (Accession XP_295074.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339813.

[44732] LOC339833 (Accession XP_291031.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339833 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339833, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339833 BINDING SITE, designated SEQ ID:17042, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44733] Another function of GAM3229 is therefore inhibition of LOC339833 (Accession XP_291031.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339833.

[44734] LOC339907 (Accession XP_291065.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC339907 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339907, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339907 BINDING SITE, designated SEQ ID:8327, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44735] Another function of GAM3229 is therefore inhibition of LOC339907 (Accession XP_291065.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339907.

[44736] LOC339942 (Accession XP_295107.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC339942 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339942, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339942 BINDING SITE, designated SEQ ID:11400, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44737] Another function of GAM3229 is therefore inhibition of LOC339942 (Accession XP_295107.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339942.

[44738] LOC340125 (Accession XP_291150.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340125 BINDING SITE1 and LOC340125 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC340125, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340125 BINDING SITE1 and LOC340125 BINDING SITE2, designated SEQ ID:9877 and SEQ ID:8135 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44739] Another function of GAM3229 is therefore inhibition of LOC340125 (Accession XP_291150.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC340125.

[44740] LOC340138 (Accession XP_291153.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340138 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340138 BINDING SITE, designated SEQ ID:2497, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44741] Another function of GAM3229 is therefore inhibition of LOC340138 (Accession XP_291153.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340138.

[44742] LOC340170 (Accession XP_291160.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340170 BINDING SITE, designated SEQ ID:1195, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44743] Another function of GAM3229 is therefore inhibition of LOC340170 (Accession XP_291160.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340170.

[44744] LOC340227 (Accession XP_291203.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340227 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340227, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340227 BINDING SITE, designated SEQ ID:8135, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44745] Another function of GAM3229 is therefore inhibition of LOC340227 (Accession XP_291203.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340227.

[44746] LOC340249 (Accession XP_291211.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340249 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340249, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340249 BINDING SITE, designated SEQ ID:20021, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44747] Another function of GAM3229 is therefore inhibition of LOC340249 (Accession XP_291211.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340249.

[44748] LOC340290 (Accession XP_291214.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340290 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC340290, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340290 BINDING SITE, designated SEQ ID:8135, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44749] Another function of GAM3229 is therefore inhibition of LOC340290 (Accession XP_291214.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340290.

[44750] LOC340321 (Accession XP_295212.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340321 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340321, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340321 BINDING SITE, designated SEQ ID:1655, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44751] Another function of GAM3229 is therefore inhibition of LOC340321 (Accession XP_295212.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340321.

[44752] LOC340390 (Accession XP_291269.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340390 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340390, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340390 BINDING SITE, designated SEQ ID:1473, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44753] Another function of GAM3229 is therefore inhibition of LOC340390 (Accession XP_291269.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340390.

[44754] LOC340414 (Accession XP_295240.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC340414 BINDING SITE1 and LOC340414 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC340414, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340414 BINDING SITE1 and LOC340414 BINDING SITE2, designated SEQ ID:7368 and SEQ ID:13658 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44755] Another function of GAM3229 is therefore inhibition of LOC340414 (Accession XP_295240.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340414.

[44756] LOC340494 (Accession XP_290428.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340494 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340494, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340494 BINDING SITE, desig-

nated SEQ ID:19097, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44757] Another function of GAM3229 is therefore inhibition of LOC340494 (Accession XP_290428.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340494.

[44758] LOC340512 (Accession XP_295262.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340512 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340512, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340512 BINDING SITE, designated SEQ ID:9452, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44759] Another function of GAM3229 is therefore inhibition of LOC340512 (Accession XP_295262.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC340512.

[44760] LOC340528 (Accession XP_295268.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC340528 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340528, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340528 BINDING SITE, designated SEQ ID:14406, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44761] Another function of GAM3229 is therefore inhibition of LOC340528 (Accession XP_295268.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340528.

[44762] LOC342926 (Accession XP_292790.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC342926 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC342926, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC342926 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44763] Another function of GAM3229 is therefore inhibition of LOC342926 (Accession XP_292790.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC342926.

[44764] LOC343803 (Accession XP_297895.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC343803 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC343803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC343803 BINDING SITE, designated SEQ ID:14285, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44765] Another function of GAM3229 is therefore inhibition of LOC343803 (Accession XP_297895.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC343803.

[44766] LOC346653 (Accession XP_294357.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC346653 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC346653, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC346653 BINDING SITE, designated SEQ ID:19528, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44767] Another function of GAM3229 is therefore inhibition of LOC346653 (Accession XP_294357.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC346653.

[44768] LOC347848 (Accession XP_302609.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC347848 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC347848, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347848 BINDING SITE, designated SEQ ID:16961, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44769] Another function of GAM3229 is therefore inhibition of LOC347848 (Accession XP_302609.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347848.

[44770] LOC347918 (Accession XP_300565.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC347918 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347918, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347918 BINDING SITE, designated SEQ ID:955, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44771] Another function of GAM3229 is therefore inhibition of LOC347918 (Accession XP_300565.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347918.

[44772] LOC348094 (Accession XP_300615.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348094 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348094, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348094 BINDING SITE, designated SEQ ID:16020, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44773] Another function of GAM3229 is therefore inhibition of LOC348094 (Accession XP_300615.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348094.

[44774] LOC348113 (Accession XP_300623.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC348113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348113 BINDING SITE, designated SEQ ID:1069, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44775] Another function of GAM3229 is therefore inhibition of LOC348113 (Accession XP_300623.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348113.

[44776] LOC348137 (Accession XP_300635.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348137 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348137, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348137 BINDING SITE, designated SEQ ID:1069, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44777] Another function of GAM3229 is therefore inhibition of LOC348137 (Accession XP_300635.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348137.

[44778] LOC348142 (Accession XP_300636.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348142 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348142, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348142 BINDING SITE, designated SEQ ID:1069, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44779] Another function of GAM3229 is therefore inhibition of LOC348142 (Accession XP_300636.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348142.

[44780] LOC348235 (Accession XP_300670.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348235 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348235 BINDING SITE, designated SEQ ID:16390, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44781] Another function of GAM3229 is therefore inhibition of LOC348235 (Accession XP_300670.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348235.

[44782] LOC348262 (Accession XP_300683.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348262 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC348262 BINDING SITE, designated SEQ ID:19609, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44783] Another function of GAM3229 is therefore inhibition of LOC348262 (Accession XP_300683.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348262.

[44784] LOC348378 (Accession XP_300723.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348378 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348378, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348378 BINDING SITE, designated SEQ ID:10183, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44785] Another function of GAM3229 is therefore inhibition of LOC348378 (Accession XP_300723.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348378.

[44786] LOC348393 (Accession XP_302741.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348393 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348393 BINDING SITE, designated SEQ ID:10000, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44787] Another function of GAM3229 is therefore inhibition of LOC348393 (Accession XP_302741.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348393.

[44788] LOC348396 (Accession XP_300729.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348396 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348396, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348396 BINDING SITE, designated SEQ ID:17091, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44789] Another function of GAM3229 is therefore inhibition of LOC348396 (Accession XP_300729.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348396.

[44790] LOC348402 (Accession XP_300730.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348402 BINDING SITE1 and LOC348402 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348402, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348402 BINDING SITE1 and LOC348402 BINDING SITE2, designated SEQ ID:3503 and SEQ ID:1590 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44791] Another function of GAM3229 is therefore inhibition of LOC348402 (Accession XP_300730.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348402.

[44792] LOC348474 (Accession XP_209299.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC348474 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348474, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348474 BINDING SITE, designated SEQ ID:13205, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44793] Another function of GAM3229 is therefore inhibition of LOC348474 (Accession XP_209299.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348474.

[44794] LOC348488 (Accession XP_300352.1) is another GAM3229 target gene, herein designated TARGET GENE.

LOC348488 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348488, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348488 BINDING SITE, designated SEQ ID:7579, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44795] Another function of GAM3229 is therefore inhibition of LOC348488 (Accession XP_300352.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348488.

[44796] LOC348503 (Accession XP_300762.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348503 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348503, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348503 BINDING SITE, designated SEQ ID:14079, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44797] Another function of GAM3229 is therefore inhibition of LOC348503 (Accession XP_300762.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348503.

[44798] LOC348504 (Accession XP_300769.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348504 BINDING SITE1 and LOC348504 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348504, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348504 BINDING SITE1 and LOC348504 BINDING SITE2, designated SEQ ID:542 and SEQ ID:7507 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44799] Another function of GAM3229 is therefore inhibition of LOC348504 (Accession XP_300769.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC348504.

[44800] LOC348508 (Accession XP_302806.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348508 BINDING SITE1 and LOC348508 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348508, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348508 BINDING SITE1 and LOC348508 BINDING SITE2, designated SEQ ID:8135 and SEQ ID:9877 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44801] Another function of GAM3229 is therefore inhibition of LOC348508 (Accession XP_302806.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348508.

[44802] LOC348532 (Accession XP_302818.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348532, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348532 BINDING SITE, designated SEQ ID:10000, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44803] Another function of GAM3229 is therefore inhibition of LOC348532 (Accession XP_302818.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348532.

[44804] LOC348567 (Accession XP_300378.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348567 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348567, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348567 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44805] Another function of GAM3229 is therefore inhibition of

LOC348567 (Accession XP_300378.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348567.

[44806] LOC348687 (Accession XP_302853.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348687 BINDING SITE, designated SEQ ID:4582, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44807] Another function of GAM3229 is therefore inhibition of LOC348687 (Accession XP_302853.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348687.

[44808] LOC348790 (Accession XP_300843.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348790 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC348790, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348790 BINDING SITE, designated SEQ ID:18680, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44809] Another function of GAM3229 is therefore inhibition of LOC348790 (Accession XP_300843.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348790.

[44810] LOC348797 (Accession XP_302888.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348797 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348797, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348797 BINDING SITE, designated SEQ ID:750, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[44811] Another function of GAM3229 is therefore inhibition of LOC348797 (Accession XP_302888.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348797.

[44812] LOC348842 (Accession XP_300861.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348842 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348842 BINDING SITE, designated SEQ ID:9877, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44813] Another function of GAM3229 is therefore inhibition of LOC348842 (Accession XP_300861.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348842.

[44814] LOC348843 (Accession XP_302903.1) is another

GAM3229 target gene, herein designated TARGET GENE. LOC348843 BINDING SITE1 and LOC348843 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348843, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348843 BINDING SITE1 and LOC348843 BINDING SITE2, designated SEQ ID:542 and SEQ ID:7507 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44815] Another function of GAM3229 is therefore inhibition of LOC348843 (Accession XP_302903.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348843.

[44816] LOC348909 (Accession XP_300875.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348909 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348909, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC348909 BINDING SITE, designated SEQ ID:9882, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44817] Another function of GAM3229 is therefore inhibition of LOC348909 (Accession XP_300875.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348909.

[44818] LOC348938 (Accession XP_300883.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348938 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348938, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348938 BINDING SITE, designated SEQ ID:15195, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44819] Another function of GAM3229 is therefore inhibition of LOC348938 (Accession XP_300883.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348938.

[44820] LOC348995 (Accession XP_300434.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC348995 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348995, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348995 BINDING SITE, designated SEQ ID:6161, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44821] Another function of GAM3229 is therefore inhibition of LOC348995 (Accession XP_300434.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348995.

[44822] LOC349075 (Accession XP_300932.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC349075 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349075, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349075 BINDING SITE, designated SEQ ID:8631, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44823] Another function of GAM3229 is therefore inhibition of LOC349075 (Accession XP_300932.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349075.

[44824] LOC349101 (Accession XP_173186.2) is another GAM3229 target gene, herein designated TARGET GENE. LOC349101 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349101 BINDING SITE, designated SEQ ID:3432, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44825] Another function of GAM3229 is therefore inhibition of

LOC349101 (Accession XP_173186.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349101.

[44826] LOC349169 (Accession XP_302978.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC349169 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349169, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349169 BINDING SITE, designated SEQ ID:7284, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44827] Another function of GAM3229 is therefore inhibition of LOC349169 (Accession XP_302978.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349169.

[44828] LOC349170 (Accession XP_300969.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC349170 BINDING SITE1 through LOC349170 BINDING

SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC349170, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349170 BINDING SITE1 through LOC349170 BINDING SITE3, designated SEQ ID:14615, SEQ ID:20159 and SEQ ID:20022 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44829] Another function of GAM3229 is therefore inhibition of LOC349170 (Accession XP_300969.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349170.

[44830] LOC349236 (Accession XP_300988.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC349236 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349236, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349236 BINDING SITE, desig-

nated SEQ ID:17381, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44831] Another function of GAM3229 is therefore inhibition of LOC349236 (Accession XP_300988.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349236.

[44832] LOC349261 (Accession XP_300998.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC349261 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349261, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349261 BINDING SITE, designated SEQ ID:2783, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44833] Another function of GAM3229 is therefore inhibition of LOC349261 (Accession XP_300998.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC349261.

[44834] LOC349360 (Accession XP_088528.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC349360 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349360, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349360 BINDING SITE, designated SEQ ID:6478, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44835] Another function of GAM3229 is therefore inhibition of LOC349360 (Accession XP_088528.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349360.

[44836] LOC349430 (Accession XP_301084.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC349430 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349430, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349430 BINDING SITE, designated SEQ ID:6220, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44837] Another function of GAM3229 is therefore inhibition of LOC349430 (Accession XP_301084.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349430.

[44838] LOC349440 (Accession XP_300513.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC349440 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349440, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349440 BINDING SITE, designated SEQ ID:9876, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44839] Another function of GAM3229 is therefore inhibition of LOC349440 (Accession XP_300513.1) . Accordingly, utili-

ties of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349440.

[44840] LOC51193 (Accession NP_057415.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC51193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51193, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51193 BINDING SITE, designated SEQ ID:4293, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44841] Another function of GAM3229 is therefore inhibition of LOC51193 (Accession NP_057415.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51193.

[44842] LOC55954 (Accession NP_061976.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC55954 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC55954, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC55954 BINDING SITE, designated SEQ ID:5283, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44843] Another function of GAM3229 is therefore inhibition of LOC55954 (Accession NP_061976.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC55954.

[44844] LOC90408 (Accession XP_031517.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC90408 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC90408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90408 BINDING SITE, designated SEQ ID:16149, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44845] Another function of GAM3229 is therefore inhibition of LOC90408 (Accession XP_031517.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC90408.

[44846] LOC90485 (Accession XP_032059.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC90485 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90485, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90485 BINDING SITE, designated SEQ ID:2914, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44847] Another function of GAM3229 is therefore inhibition of LOC90485 (Accession XP_032059.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90485.

[44848] LOC91250 (Accession XP_037135.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC91250 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC91250, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of LOC91250 BINDING SITE, designated SEQ ID:18320, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44849] Another function of GAM3229 is therefore inhibition of LOC91250 (Accession XP_037135.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91250.

[44850] LOC92597 (Accession NP_775739.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC92597 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92597, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92597 BINDING SITE, designated SEQ ID:4501, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44851] Another function of GAM3229 is therefore inhibition of LOC92597 (Accession NP_775739.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC92597.

[44852] LOC93463 (Accession XP_051528.1) is another GAM3229 target gene, herein designated TARGET GENE. LOC93463 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC93463, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC93463 BINDING SITE, designated SEQ ID:1098, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44853] Another function of GAM3229 is therefore inhibition of LOC93463 (Accession XP_051528.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93463.

[44854] Low density lipoprotein receptor-related protein 4 (LRP4, Accession XP_035037.2) is another GAM3229 target gene, herein designated TARGET GENE. LRP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of LRP4 BINDING SITE, designated SEQ ID:16726, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44855] Another function of GAM3229 is therefore inhibition of Low density lipoprotein receptor-related protein 4 (LRP4, Accession XP_035037.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP4.

[44856] Lymphocyte antigen 6 complex, locus g6c (LY6G6C, Accession NP_079537.1) is another GAM3229 target gene, herein designated TARGET GENE. LY6G6C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LY6G6C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LY6G6C BINDING SITE, designated SEQ ID:11181, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44857] Another function of GAM3229 is therefore inhibition of Lymphocyte antigen 6 complex, locus g6c (LY6G6C, Accession NP_079537.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LY6G6C.

[44858] Leucine zipper, putative tumor suppressor 1 (LZTS1, Accession NP_066300.1) is another GAM3229 target gene, herein designated TARGET GENE. LZTS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LZTS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LZTS1 BINDING SITE, designated SEQ ID:1073, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44859] Another function of GAM3229 is therefore inhibition of Leucine zipper, putative tumor suppressor 1 (LZTS1, Accession NP_066300.1), a gene which is an essential component of the nucleoskeleton. potential role in crosslinking filaments or anchoring other molecules. it is essential for growth. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical

conditions associated with LZTS1.

[44860] The function of LZTS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.MAC30 (Accession XP_031536.2) is another GAM3229 target gene, herein designated TARGET GENE. MAC30 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAC30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAC30 BINDING SITE, designated SEQ ID:15124, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44861] Another function of GAM3229 is therefore inhibition of MAC30 (Accession XP_031536.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAC30.

[44862] Mannosidase, beta a, lysosomal-like (MANBAL, Accession NP_071360.1) is another GAM3229 target gene, herein designated TARGET GENE. MANBAL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MANBAL, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MANBAL BINDING SITE, designated SEQ ID:18033, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44863] Another function of GAM3229 is therefore inhibition of Mannosidase, beta a, lysosomal-like (MANBAL, Accession NP_071360.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MANBAL.

[44864] Microtubule-associated protein 1 light chain 3 beta (MAP1LC3B, Accession NP_073729.1) is another GAM3229 target gene, herein designated TARGET GENE. MAP1LC3B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAP1LC3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAP1LC3B BINDING SITE, designated SEQ ID:18525, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44865] Another function of GAM3229 is therefore inhibition of

Microtubule-associated protein 1 light chain 3 beta (MAP1LC3B, Accession NP_073729.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP1LC3B.

[44866] MAPA (Accession NP_660299.1) is another GAM3229 target gene, herein designated TARGET GENE. MAPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPA BINDING SITE, designated SEQ ID:17799, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44867] Another function of GAM3229 is therefore inhibition of MAPA (Accession NP_660299.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPA.

[44868] Microtubule-associated protein tau (MAPT, Accession NP_776088.1) is another GAM3229 target gene, herein designated TARGET GENE. MAPT BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by MAPT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPT BINDING SITE, designated SEQ ID:18784, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44869] Another function of GAM3229 is therefore inhibition of Microtubule-associated protein tau (MAPT, Accession NP_776088.1), a gene which Microtubule- associated protein tau; promotes microtubule assembly. and therefore is associated with Frontotemporal dementia, pallidopontonigral degeneration, pick disease- like dementia, pick disease. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Frontotemporal dementia, pallidopontonigral degeneration, pick disease- like dementia, pick disease, and of other diseases and clinical conditions associated with MAPT.

[44870] The function of MAPT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM200.2.Map/microtubule affinity-regulating kinase 2 (MARK2, Accession NP_059672.1) is another GAM3229

target gene, herein designated TARGET GENE. MARK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MARK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MARK2 BINDING SITE, designated SEQ ID:8182, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44871] Another function of GAM3229 is therefore inhibition of Map/microtubule affinity-regulating kinase 2 (MARK2, Accession NP_059672.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MARK2.

[44872] Map/microtubule affinity-regulating kinase 2 (MARK2, Accession NP_004945.2) is another GAM3229 target gene, herein designated TARGET GENE. MARK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MARK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of MARK2 BINDING SITE, designated SEQ ID:8182, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44873] Another function of GAM3229 is therefore inhibition of Map/microtubule affinity-regulating kinase 2 (MARK2, Accession NP_004945.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MARK2.

[44874] Mcm10 minichromosome maintenance deficient 10 (s. cerevisiae) (MCM10, Accession NP_060988.2) is another GAM3229 target gene, herein designated TARGET GENE. MCM10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MCM10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCM10 BINDING SITE, designated SEQ ID:6797, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44875] Another function of GAM3229 is therefore inhibition of Mcm10 minichromosome maintenance deficient 10 (s. cerevisiae) (MCM10, Accession NP_060988.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with MCM10.

[44876] Mediterranean fever (MEFV, Accession NP_000234.1) is another GAM3229 target gene, herein designated TARGET GENE. MEFV BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MEFV, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MEFV BINDING SITE, designated SEQ ID:5889, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44877] Another function of GAM3229 is therefore inhibition of Mediterranean fever (MEFV, Accession NP_000234.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEFV.

[44878] MGC10200 (Accession NP_659497.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC10200 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10200, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC10200 BINDING SITE, designated SEQ ID:5932, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44879] Another function of GAM3229 is therefore inhibition of MGC10200 (Accession NP_659497.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10200.

[44880] MGC10818 (Accession NP_085045.2) is another GAM3229 target gene, herein designated TARGET GENE. MGC10818 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10818, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10818 BINDING SITE, designated SEQ ID:14416, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44881] Another function of GAM3229 is therefore inhibition of MGC10818 (Accession NP_085045.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC10818.

[44882] MGC10986 (Accession NP_085053.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC10986 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10986, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10986 BINDING SITE, designated SEQ ID:6559, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44883] Another function of GAM3229 is therefore inhibition of MGC10986 (Accession NP_085053.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10986.

[44884] MGC11386 (Accession NP_116322.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC11386 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC11386, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC11386 BINDING SITE, designated SEQ ID:4993, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44885] Another function of GAM3229 is therefore inhibition of MGC11386 (Accession NP_116322.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11386.

[44886] MGC13024 (Accession NP_689501.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC13024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13024 BINDING SITE, designated SEQ ID:16302, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44887] Another function of GAM3229 is therefore inhibition of MGC13024 (Accession NP_689501.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13024.

[44888] MGC13138 (Accession NP_219363.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC13138 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13138 BINDING SITE, designated SEQ ID:10825, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44889] Another function of GAM3229 is therefore inhibition of MGC13138 (Accession NP_219363.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13138.

[44890] MGC14289 (Accession NP_542391.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC14289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14289 BINDING SITE, designated SEQ ID:13575, to

the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44891] Another function of GAM3229 is therefore inhibition of MGC14289 (Accession NP_542391.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14289.

[44892] MGC14386 (Accession NP_291022.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC14386 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14386, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14386 BINDING SITE, designated SEQ ID:10978, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44893] Another function of GAM3229 is therefore inhibition of MGC14386 (Accession NP_291022.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14386.

[44894] MGC14836 (Accession NP_219480.1) is another GAM3229

target gene, herein designated TARGET GENE. MGC14836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14836 BINDING SITE, designated SEQ ID:12819, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44895] Another function of GAM3229 is therefore inhibition of MGC14836 (Accession NP_219480.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14836.

[44896] MGC15606 (Accession NP_659474.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC15606 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC15606, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15606 BINDING SITE, designated SEQ ID:9411, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[44897] Another function of GAM3229 is therefore inhibition of MGC15606 (Accession NP_659474.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15606.

[44898] MGC21675 (Accession NP_443093.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC21675 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC21675, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC21675 BINDING SITE, designated SEQ ID:1835, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44899] Another function of GAM3229 is therefore inhibition of MGC21675 (Accession NP_443093.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21675.

[44900] MGC2452 (Accession NP_116033.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC2452

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC2452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2452 BINDING SITE, designated SEQ ID:6351, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44901] Another function of GAM3229 is therefore inhibition of MGC2452 (Accession NP_116033.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2452.

[44902] MGC2474 (Accession NP_076420.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC2474 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2474, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2474 BINDING SITE, designated SEQ ID:5948, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44903] Another function of GAM3229 is therefore inhibition of MGC2474 (Accession NP_076420.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2474.

[44904] MGC26979 (Accession NP_714915.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC26979 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC26979, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC26979 BINDING SITE, designated SEQ ID:15483, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44905] Another function of GAM3229 is therefore inhibition of MGC26979 (Accession NP_714915.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC26979.

[44906] MGC27345 (Accession XP_300964.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC27345 BINDING SITE1 and MGC27345 BINDING SITE2 are target

binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MGC27345, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC27345 BINDING SITE1 and MGC27345 BINDING SITE2, designated SEQ ID:10537 and SEQ ID:8394 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44907] Another function of GAM3229 is therefore inhibition of MGC27345 (Accession XP_300964.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC27345.

[44908] MGC27345 (Accession NP_787076.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC27345 BINDING SITE1 and MGC27345 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MGC27345, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC27345 BINDING SITE1 and MGC27345 BINDING SITE2,

designated SEQ ID:10537 and SEQ ID:10712 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44909] Another function of GAM3229 is therefore inhibition of MGC27345 (Accession NP_787076.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC27345.

[44910] MGC3113 (Accession NP_076940.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC3113 BINDING SITE1 and MGC3113 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MGC3113, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3113 BINDING SITE1 and MGC3113 BINDING SITE2, designated SEQ ID:2387 and SEQ ID:18526 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44911] Another function of GAM3229 is therefore inhibition of MGC3113 (Accession NP_076940.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MGC3113.

[44912] MGC33637 (Accession NP_689809.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC33637 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC33637, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC33637 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44913] Another function of GAM3229 is therefore inhibition of MGC33637 (Accession NP_689809.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33637.

[44914] MGC34132 (Accession XP_291029.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC34132 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC34132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC34132 BINDING SITE, designated SEQ ID:17411, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44915] Another function of GAM3229 is therefore inhibition of MGC34132 (Accession XP_291029.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34132.

[44916] MGC35163 (Accession NP_689765.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC35163 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35163, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35163 BINDING SITE, designated SEQ ID:2119, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44917] Another function of GAM3229 is therefore inhibition of MGC35163 (Accession NP_689765.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC35163.

[44918] MGC35308 (Accession NP_787118.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC35308 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35308, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC35308 BINDING SITE, designated SEQ ID:14998, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44919] Another function of GAM3229 is therefore inhibition of MGC35308 (Accession NP_787118.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35308.

[44920] MGC35468 (Accession NP_694976.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC35468 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC35468, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC35468 BINDING SITE, designated SEQ ID:12471, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44921] Another function of GAM3229 is therefore inhibition of MGC35468 (Accession NP_694976.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC35468.

[44922] MGC46336 (Accession XP_290712.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC46336 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC46336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC46336 BINDING SITE, designated SEQ ID:8629, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44923] Another function of GAM3229 is therefore inhibition of MGC46336 (Accession XP_290712.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC46336.

[44924] MGC50337 (Accession NP_848604.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC50337 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC50337, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC50337 BINDING SITE, designated SEQ ID:17884, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44925] Another function of GAM3229 is therefore inhibition of MGC50337 (Accession NP_848604.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC50337.

[44926] MGC5149 (Accession XP_051200.2) is another GAM3229 target gene, herein designated TARGET GENE. MGC5149 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC5149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC5149 BINDING SITE, designated SEQ ID:940, to the

nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44927] Another function of GAM3229 is therefore inhibition of MGC5149 (Accession XP_051200.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5149.

[44928] MGC9726 (Accession NP_796377.1) is another GAM3229 target gene, herein designated TARGET GENE. MGC9726 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC9726, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC9726 BINDING SITE, designated SEQ ID:18506, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44929] Another function of GAM3229 is therefore inhibition of MGC9726 (Accession NP_796377.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC9726.

[44930] Mhc class ii transactivator (MHC2TA, Accession

NP_000237.1) is another GAM3229 target gene, herein designated TARGET GENE. MHC2TA BINDING SITE1 and MHC2TA BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MHC2TA, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MHC2TA BINDING SITE1 and MHC2TA BINDING SITE2, designated SEQ ID:12501 and SEQ ID:14620 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44931] Another function of GAM3229 is therefore inhibition of Mhc class ii transactivator (MHC2TA, Accession NP_000237.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MHC2TA.

[44932] Mhc class i polypeptide-related sequence b (MICB, Accession NP_005922.1) is another GAM3229 target gene, herein designated TARGET GENE. MICB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MICB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of MICB BINDING SITE, designated SEQ ID:11538, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44933] Another function of GAM3229 is therefore inhibition of Mhc class i polypeptide-related sequence b (MICB, Accession NP_005922.1), a gene which involved in the presentation of foreign antigens to the immune system. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MICB.

[44934] The function of MICB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM258.1.MIDORI (Accession NP_065829.1) is another GAM3229 target gene, herein designated TARGET GENE. MIDORI BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MIDORI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIDORI BINDING SITE, designated SEQ ID:7016, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[44935] Another function of GAM3229 is therefore inhibition of MIDORI (Accession NP_065829.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIDORI.

[44936] MIZF (Accession NP_056332.1) is another GAM3229 target gene, herein designated TARGET GENE. MIZF BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MIZF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MIZF BINDING SITE, designated SEQ ID:6430, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44937] Another function of GAM3229 is therefore inhibition of MIZF (Accession NP_056332.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIZF.

[44938] Melan-a (MLANA, Accession NP_005502.1) is another GAM3229 target gene, herein designated TARGET GENE. MLANA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MLANA, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLANA BINDING SITE, designated SEQ ID:12846, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44939] Another function of GAM3229 is therefore inhibition of Melan-a (MLANA, Accession NP_005502.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLANA.

[44940] Melanoma-derived leucine zipper, extra-nuclear factor (MLZE, Accession NP_113603.1) is another GAM3229 target gene, herein designated TARGET GENE. MLZE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MLZE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MLZE BINDING SITE, designated SEQ ID:2064, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44941] Another function of GAM3229 is therefore inhibition of

Melanoma-derived leucine zipper, extra-nuclear factor (MLZE, Accession NP_113603.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLZE.

[44942] Matrix metalloproteinase-like 1 (MMPL1, Accession NP_004133.1) is another GAM3229 target gene, herein designated TARGET GENE. MMPL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MMPL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MMPL1 BINDING SITE, designated SEQ ID:18579, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44943] Another function of GAM3229 is therefore inhibition of Matrix metalloproteinase-like 1 (MMPL1, Accession NP_004133.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMPL1.

[44944] Mitochondrial ribosomal protein l30 (MRPL30, Accession NP_660213.1) is another GAM3229 target gene, herein designated TARGET GENE. MRPL30 BINDING SITE1 and

MRPL30 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MRPL30, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL30 BINDING SITE1 and MRPL30 BINDING SITE2, designated SEQ ID:4263 and SEQ ID:4509 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44945] Another function of GAM3229 is therefore inhibition of Mitochondrial ribosomal protein l30 (MRPL30, Accession NP_660213.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL30.

[44946] Mitochondrial ribosomal protein s27 (MRPS27, Accession NP_055899.1) is another GAM3229 target gene, herein designated TARGET GENE. MRPS27 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPS27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPS27 BINDING

SITE, designated SEQ ID:10070, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44947] Another function of GAM3229 is therefore inhibition of Mitochondrial ribosomal protein s27 (MRPS27, Accession NP_055899.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS27.

[44948] MRS3/4 (Accession NP_112489.2) is another GAM3229 target gene, herein designated TARGET GENE. MRS3/4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRS3/4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRS3/4 BINDING SITE, designated SEQ ID:7253, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44949] Another function of GAM3229 is therefore inhibition of MRS3/4 (Accession NP_112489.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRS3/4.

[44950] MtFMT (Accession NP_640335.1) is another GAM3229 target gene, herein designated TARGET GENE. MtFMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MtFMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MtFMT BINDING SITE, designated SEQ ID:6398, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44951] Another function of GAM3229 is therefore inhibition of MtFMT (Accession NP_640335.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MtFMT.

[44952] MTH2 (Accession NP_060753.1) is another GAM3229 target gene, herein designated TARGET GENE. MTH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MTH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MTH2 BINDING SITE, designated SEQ ID:18725, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA,

also designated SEQ ID:221.

[44953] Another function of GAM3229 is therefore inhibition of MTH2 (Accession NP_060753.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTH2.

[44954] MYLC2PL (Accession NP_612412.1) is another GAM3229 target gene, herein designated TARGET GENE. MYLC2PL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MYLC2PL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYLC2PL BINDING SITE, designated SEQ ID:13697, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44955] Another function of GAM3229 is therefore inhibition of MYLC2PL (Accession NP_612412.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLC2PL.

[44956] Myosin 5c (MYO5C, Accession NP_061198.1) is another GAM3229 target gene, herein designated TARGET GENE. MYO5C BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by MYO5C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYO5C BINDING SITE, designated SEQ ID:12851, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44957] Another function of GAM3229 is therefore inhibition of Myosin 5c (MYO5C, Accession NP_061198.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYO5C.

[44958] N-ethylmaleimide-sensitive factor attachment protein, alpha (NAPA, Accession NP_003818.1) is another GAM3229 target gene, herein designated TARGET GENE. NAPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NAPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NAPA BINDING SITE, designated SEQ ID:5619, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44959] Another function of GAM3229 is therefore inhibition of N-ethylmaleimide-sensitive factor attachment protein, alpha (NAPA, Accession NP_003818.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAPA.

[44960] Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1) is another GAM3229 target gene, herein designated TARGET GENE. NCOA6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NCOA6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE, designated SEQ ID:18704, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44961] Another function of GAM3229 is therefore inhibition of Nuclear receptor coactivator 6 (NCOA6, Accession NP_054790.1), a gene which activates gene transcription through ligand- dependent association with coactivators. and therefore may be associated with Breast cancer. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Breast cancer., and of other diseases

and clinical conditions associated with NCOA6.

[44962] The function of NCOA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NP_079107.5) is another GAM3229 target gene, herein designated TARGET GENE. NCOA6IP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCOA6IP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA6IP BINDING SITE, designated SEQ ID:14417, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44963] Another function of GAM3229 is therefore inhibition of Nuclear receptor coactivator 6 interacting protein (NCOA6IP, Accession NP_079107.5) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6IP.

[44964] Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) is

another GAM3229 target gene, herein designated TARGET GENE. NDUFC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDUFC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDUFC2 BINDING SITE, designated SEQ ID:2783, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44965] Another function of GAM3229 is therefore inhibition of Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDUFC2.

[44966] Neural precursor cell expressed, developmentally downregulated 4 (NEDD4, Accession XP_046129.4) is another GAM3229 target gene, herein designated TARGET GENE. NEDD4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NEDD4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of NEDD4 BINDING SITE, designated SEQ ID:16923, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44967] Another function of GAM3229 is therefore inhibition of Neural precursor cell expressed, developmentally down-regulated 4 (NEDD4, Accession XP_046129.4), a gene which ubiquitinates regulatory proteins involved in transcription. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEDD4.

[44968] The function of NEDD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM48.2.Nei like 2 (e. coli) (NEIL2, Accession NP_659480.1) is another GAM3229 target gene, herein designated TARGET GENE. NEIL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NEIL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEIL2 BINDING SITE, designated SEQ ID:9514, to the nucleotide sequence of GAM3229

RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44969] Another function of GAM3229 is therefore inhibition of Nei like 2 (e. coli) (NEIL2, Accession NP_659480.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEIL2.

[44970] Neurogenic differentiation 1 (NEUROD1, Accession NP_002491.1) is another GAM3229 target gene, herein designated TARGET GENE. NEUROD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NEUROD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEUROD1 BINDING SITE, designated SEQ ID:14176, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44971] Another function of GAM3229 is therefore inhibition of Neurogenic differentiation 1 (NEUROD1, Accession NP_002491.1), a gene which acts as a differentiation factor during neurogenesis and therefore may be associated with Type ii diabetes mellitus. Accordingly, utilities of

GAM3229 include diagnosis, prevention and treatment of Type ii diabetes mellitus, and of other diseases and clinical conditions associated with NEUROD1.

[44972] The function of NEUROD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1035.1.Neurofibromin 2 (bilateral acoustic neuroma) (NF2, Accession NP_057502.1) is another GAM3229 target gene, herein designated TARGET GENE. NF2 BINDING SITE1 and NF2 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by NF2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NF2 BINDING SITE1 and NF2 BINDING SITE2, designated SEQ ID:11182 and SEQ ID:8254 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44973] Another function of GAM3229 is therefore inhibition of Neurofibromin 2 (bilateral acoustic neuroma) (NF2, Accession NP_057502.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with NF2.

[44974] Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1) is another GAM3229 target gene, herein designated TARGET GENE. NQO1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NQO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NQO1 BINDING SITE, designated SEQ ID:19166, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44975] Another function of GAM3229 is therefore inhibition of Nad(p)h dehydrogenase, quinone 1 (NQO1, Accession NP_000894.1), a gene which is cytochrome b5 reductase which reduces redox dyes and quinones. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NQO1.

[44976] The function of NQO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.NUP43 (Accession NP_078923.2) is another

GAM3229 target gene, herein designated TARGET GENE. NUP43 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NUP43, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NUP43 BINDING SITE, designated SEQ ID:16948, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44977] Another function of GAM3229 is therefore inhibition of NUP43 (Accession NP_078923.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUP43.

[44978] Opioid receptor, mu 1 (OPRM1, Accession NP_000905.1) is another GAM3229 target gene, herein designated TARGET GENE. OPRM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OPRM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OPRM1 BINDING SITE, designated SEQ ID:17047, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ

ID:221.

[44979] Another function of GAM3229 is therefore inhibition of Opioid receptor, mu 1 (OPRM1, Accession NP_000905.1), a gene which inhibits neurotransmitter release by reducing calcium ion currents and increasing potassium ion conductance. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OPRM1.

[44980] The function of OPRM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM883.1.Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663164.1) is another GAM3229 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:8465, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44981] Another function of GAM3229 is therefore inhibition of

Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663164.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[44982] Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663160.1) is another GAM3229 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:8465, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44983] Another function of GAM3229 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663160.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[44984] Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663163.1) is another GAM3229 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:8465, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44985] Another function of GAM3229 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663163.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[44986] Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663161.1) is another GAM3229 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:8465, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[44987] Another function of GAM3229 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663161.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[44988] Oxysterol binding protein-like 3 (OSBPL3, Accession NP_056365.1) is another GAM3229 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:8465, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44989] Another function of GAM3229 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_056365.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[44990] Oxysterol binding protein-like 3 (OSBPL3, Accession

NP_663162.1) is another GAM3229 target gene, herein designated TARGET GENE. OSBPL3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSBPL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:8465, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44991] Another function of GAM3229 is therefore inhibition of Oxysterol binding protein-like 3 (OSBPL3, Accession NP_663162.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3.

[44992] Oxysterol binding protein-like 8 (OSBPL8, Accession NP_065892.1) is another GAM3229 target gene, herein designated TARGET GENE. OSBPL8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OSBPL8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL8 BINDING SITE, desig-

nated SEQ ID:1446, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44993] Another function of GAM3229 is therefore inhibition of Oxysterol binding protein-like 8 (OSBPL8, Accession NP_065892.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL8.

[44994] Oncostatin m (OSM, Accession NP_065391.1) is another GAM3229 target gene, herein designated TARGET GENE. OSM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OSM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSM BINDING SITE, designated SEQ ID:15290, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44995] Another function of GAM3229 is therefore inhibition of Oncostatin m (OSM, Accession NP_065391.1), a gene which inhibits the proliferation of a number of tumor cell lines, caused an acute inflammatory reaction. Accordingly, utilities of GAM3229 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with OSM.

[44996] The function of OSM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.2.Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS, Accession NP_006443.1) is another GAM3229 target gene, herein designated TARGET GENE. PAICS BINDING SITE1 and PAICS BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by PAICS, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PAICS BINDING SITE1 and PAICS BINDING SITE2, designated SEQ ID:963 and SEQ ID:12311 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44997] Another function of GAM3229 is therefore inhibition of Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase (PAICS, Accession NP_006443.1), a gene which is required

for purine biosynthesis. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAICS.

[44998] The function of PAICS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Protocadherin alpha 9 (PCDHA9, Accession NP_054724.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHA9 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA9 BINDING SITE, designated SEQ ID:2783, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[44999] Another function of GAM3229 is therefore inhibition of Protocadherin alpha 9 (PCDHA9, Accession NP_054724.1), a gene which is a calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA9.

[45000] The function of PCDHA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Protocadherin beta 11 (PCDHB11, Accession NP_061754.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHB11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB11 BINDING SITE, designated SEQ ID:3153, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45001] Another function of GAM3229 is therefore inhibition of Protocadherin beta 11 (PCDHB11, Accession NP_061754.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB11.

[45002] Protocadherin beta 16 (PCDHB16, Accession NP_066008.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHB16 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by PCDHB16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB16 BINDING SITE, designated SEQ ID:5101, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45003] Another function of GAM3229 is therefore inhibition of Protocadherin beta 16 (PCDHB16, Accession NP_066008.1), a gene which is a potential calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB16.

[45004] The function of PCDHB16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Protocadherin gamma subfamily a, 1 (PCDHGA1, Accession NP_061735.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of PCDHGA1 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45005] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 1 (PCDHGA1, Accession NP_061735.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA1.

[45006] Protocadherin gamma subfamily a, 10 (PCDHGA10, Accession NP_061736.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGA10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA10 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45007] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 10 (PCDHGA10, Accession NP_061736.1) . Accordingly, utilities of GAM3229 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA10.

[45008] Protocadherin gamma subfamily a, 11 (PCDHGA11, Accession NP_061737.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHGA11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA11 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45009] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 11 (PCDHGA11, Accession NP_061737.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA11.

[45010] Protocadherin gamma subfamily a, 11 (PCDHGA11, Accession NP_114481.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA11 BINDING SITE is a target binding site found in the 3` untranslated re-

gion of multiple transcripts of mRNA encoded by PCDHGA11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA11 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45011] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 11 (PCDHGA11, Accession NP_114481.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA11.

[45012] Protocadherin gamma subfamily a, 12 (PCDHGA12, Accession NP_003726.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHGA12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA12 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45013] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 12 (PCDHGA12, Accession NP_003726.1), a gene which potential calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA12.

[45014] The function of PCDHGA12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM607.2.Protocadherin gamma subfamily a, 2 (PCDHGA2, Accession NP_061738.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA2 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ

ID:221.

[45015] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 2 (PCDHGA2, Accession NP_061738.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA2.

[45016] Protocadherin gamma subfamily a, 3 (PCDHGA3, Accession NP_061739.2) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA3 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45017] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 3 (PCDHGA3, Accession NP_061739.2), a gene which is a potential calcium-dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA3.

[45018] The function of PCDHGA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM607.2.Protocadherin gamma subfamily a, 4 (PCDHGA4, Accession NP_061740.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHGA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA4 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45019] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 4 (PCDHGA4, Accession NP_061740.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA4.

[45020] Protocadherin gamma subfamily a, 5 (PCDHGA5, Accession NP_061741.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA5 BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGA5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA5 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45021] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 5 (PCDHGA5, Accession NP_061741.1), a gene which is a potential calcium-dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA5.

[45022] The function of PCDHGA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM607.2.Protocadherin gamma subfamily a, 6 (PCDHGA6, Accession NP_061742.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGA6, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA6 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45023] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 6 (PCDHGA6, Accession NP_061742.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA6.

[45024] Protocadherin gamma subfamily a, 7 (PCDHGA7, Accession NP_061743.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHGA7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA7 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45025] Another function of GAM3229 is therefore inhibition of

Protocadherin gamma subfamily a, 7 (PCDHGA7, Accession NP_061743.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA7.

[45026] Protocadherin gamma subfamily a, 8 (PCDHGA8, Accession NP_114477.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHGA8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA8 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45027] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 8 (PCDHGA8, Accession NP_114477.1), a gene which is a potential calcium-dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA8.

[45028] The function of PCDHGA8 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM607.2.Protocadherin gamma subfamily a, 9 (PCDHGA9, Accession NP_061744.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGA9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGA9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGA9 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45029] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily a, 9 (PCDHGA9, Accession NP_061744.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGA9.

[45030] Protocadherin gamma subfamily b, 1 (PCDHGB1, Accession NP_061745.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGB1, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGB1 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45031] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily b, 1 (PCDHGB1, Accession NP_061745.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGB1.

[45032] Protocadherin gamma subfamily b, 2 (PCDHGB2, Accession NP_061746.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGB2 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45033] Another function of GAM3229 is therefore inhibition of

Protocadherin gamma subfamily b, 2 (PCDHGB2, Accession NP_061746.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGB2.

[45034] Protocadherin gamma subfamily b, 3 (PCDHGB3, Accession NP_061747.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGB3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGB3 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45035] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily b, 3 (PCDHGB3, Accession NP_061747.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGB3.

[45036] Protocadherin gamma subfamily b, 4 (PCDHGB4, Accession NP_003727.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGB4 BINDING SITE

is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGB4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGB4 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45037] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily b, 4 (PCDHGB4, Accession NP_003727.1), a gene which is a potential calcium-dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGB4.

[45038] The function of PCDHGB4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM607.2.Protocadherin gamma subfamily b, 5 (PCDHGB5, Accession NP_061748.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGB5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGB5, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGB5 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45039] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily b, 5 (PCDHGB5, Accession NP_061748.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGB5.

[45040] Protocadherin gamma subfamily b, 6 (PCDHGB6, Accession NP_061749.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGB6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGB6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGB6 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45041] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily b, 6 (PCDHGB6, Acces-

sion NP_061749.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGB6.

[45042] Protocadherin gamma subfamily b, 7 (PCDHGB7, Accession NP_061750.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGB7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHGB7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGB7 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45043] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily b, 7 (PCDHGB7, Accession NP_061750.1), a gene which is a potential calcium-dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGB7.

[45044] The function of PCDHGB7 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM607.2.Protocadherin gamma subfamily c, 3 (PCDHGC3, Accession NP_115779.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHGC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGC3 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45045] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily c, 3 (PCDHGC3, Accession NP_115779.1), a gene which is a potential calcium-dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGC3.

[45046] The function of PCDHGC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM607.2.Protocadherin gamma subfamily c, 3

(PCDHGC3, Accession NP_002579.2) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHGC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGC3 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45047] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily c, 3 (PCDHGC3, Accession NP_002579.2), a gene which is a potential calcium-dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGC3.

[45048] The function of PCDHGC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM607.2.Protocadherin gamma subfamily c, 4 (PCDHGC4, Accession NP_061751.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGC4

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGC4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGC4 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45049] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily c, 4 (PCDHGC4, Accession NP_061751.1), a gene which is a potential calcium-dependent cell- adhesion protein. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGC4.

[45050] The function of PCDHGC4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM607.2.Protocadherin gamma subfamily c, 5 (PCDHGC5, Accession NP_061752.1) is another GAM3229 target gene, herein designated TARGET GENE. PCDHGC5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHGC5, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHGC5 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45051] Another function of GAM3229 is therefore inhibition of Protocadherin gamma subfamily c, 5 (PCDHGC5, Accession NP_061752.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHGC5.

[45052] Phosducin-like (PDCL, Accession NP_005379.2) is another GAM3229 target gene, herein designated TARGET GENE. PDCL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDCL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDCL BINDING SITE, designated SEQ ID:18230, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45053] Another function of GAM3229 is therefore inhibition of Phosducin-like (PDCL, Accession NP_005379.2), a gene which may regulate G- protein signaling and similar to

phosducins. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDCL.

[45054] The function of PDCL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.PDZRN1 (Accession NP_699202.1) is another GAM3229 target gene, herein designated TARGET GENE. PDZRN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDZRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDZRN1 BINDING SITE, designated SEQ ID:19980, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45055] Another function of GAM3229 is therefore inhibition of PDZRN1 (Accession NP_699202.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDZRN1.

[45056] PEPP3 (Accession NP_055750.1) is another GAM3229 target gene, herein designated TARGET GENE. PEPP3 BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PEPP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PEPP3 BINDING SITE, designated SEQ ID:17981, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45057] Another function of GAM3229 is therefore inhibition of PEPP3 (Accession NP_055750.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEPP3.

[45058] Period homolog 1 (drosophila) (PER1, Accession NP_002607.1) is another GAM3229 target gene, herein designated TARGET GENE. PER1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PER1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PER1 BINDING SITE, designated SEQ ID:4346, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45059] Another function of GAM3229 is therefore inhibition of Period homolog 1 (drosophila) (PER1, Accession NP_002607.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PER1.

[45060] Period homolog 2 (drosophila) (PER2, Accession NP_073728.1) is another GAM3229 target gene, herein designated TARGET GENE. PER2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PER2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PER2 BINDING SITE, designated SEQ ID:10711, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45061] Another function of GAM3229 is therefore inhibition of Period homolog 2 (drosophila) (PER2, Accession NP_073728.1), a gene which Period homolog 2; putative circadian clock protein; has a PAS dimerization domain and therefore may be associated with Familial advanced sleep- phase syndrome. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Familial

advanced sleep- phase syndrome, and of other diseases and clinical conditions associated with PER2.

[45062] The function of PER2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Phosphoribosylformylglycinamidine synthase (fgar amidotransferase) (PFAS, Accession NP_036525.1) is another GAM3229 target gene, herein designated TARGET GENE. PFAS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PFAS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PFAS BINDING SITE, designated SEQ ID:19259, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45063] Another function of GAM3229 is therefore inhibition of Phosphoribosylformylglycinamidine synthase (fgar amidotransferase) (PFAS, Accession NP_036525.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFAS.

[45064] Putative homeodomain transcription factor 2 (PHTF2, Accession NP_065165.1) is another GAM3229 target gene, herein designated TARGET GENE. PHTF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PHTF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PHTF2 BINDING SITE, designated SEQ ID:18794, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45065] Another function of GAM3229 is therefore inhibition of Putative homeodomain transcription factor 2 (PHTF2, Accession NP_065165.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHTF2.

[45066] PIK3AP1 (Accession NP_689522.1) is another GAM3229 target gene, herein designated TARGET GENE. PIK3AP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PIK3AP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

PIK3AP1 BINDING SITE, designated SEQ ID:4110, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45067] Another function of GAM3229 is therefore inhibition of PIK3AP1 (Accession NP_689522.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3AP1.

[45068] Pbx/knotted 1 homeobox 1 (PKNOX1, Accession NP_004562.2) is another GAM3229 target gene, herein designated TARGET GENE. PKNOX1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PKNOX1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PKNOX1 BINDING SITE, designated SEQ ID:18518, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45069] Another function of GAM3229 is therefore inhibition of Pbx/knotted 1 homeobox 1 (PKNOX1, Accession NP_004562.2), a gene which may regulate gene expression and control cell differentiation. Accordingly, utilities

of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKNOX1.

[45070] The function of PKNOX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Phospholipase a2, group iid (PLA2G2D, Accession NP_036532.1) is another GAM3229 target gene, herein designated TARGET GENE. PLA2G2D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLA2G2D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PLA2G2D BINDING SITE, designated SEQ ID:12102, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45071] Another function of GAM3229 is therefore inhibition of Phospholipase a2, group iid (PLA2G2D, Accession NP_036532.1), a gene which is involved in phospholipid digestion, remodeling of cell membranes, and host defense, as well as pathophysiologic processes. Accordingly, utilities of GAM3229 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with PLA2G2D.

[45072] The function of PLA2G2D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.PLB (Accession NP_694566.1) is another GAM3229 target gene, herein designated TARGET GENE. PLB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PLB BINDING SITE, designated SEQ ID:16989, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45073] Another function of GAM3229 is therefore inhibition of PLB (Accession NP_694566.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLB.

[45074] Pro-melanin-concentrating hormone-like 1 (PMCHL1, Accession NP_114093.1) is another GAM3229 target gene, herein designated TARGET GENE. PMCHL1 BINDING SITE is a target binding site found in the 3` untranslated region

of mRNA encoded by PMCHL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMCHL1 BINDING SITE, designated SEQ ID:2034, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45075] Another function of GAM3229 is therefore inhibition of Pro-melanin-concentrating hormone-like 1 (PMCHL1, Accession NP_114093.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMCHL1.

[45076] Pro-melanin-concentrating hormone-like 2 (PMCHL2, Accession NP_114094.1) is another GAM3229 target gene, herein designated TARGET GENE. PMCHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMCHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMCHL2 BINDING SITE, designated SEQ ID:7283, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45077] Another function of GAM3229 is therefore inhibition of Pro-melanin-concentrating hormone-like 2 (PMCHL2, Accession NP_114094.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMCHL2.

[45078] POLD3 (Accession XP_166243.1) is another GAM3229 target gene, herein designated TARGET GENE. POLD3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLD3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLD3 BINDING SITE, designated SEQ ID:11834, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45079] Another function of GAM3229 is therefore inhibition of POLD3 (Accession XP_166243.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLD3.

[45080] POLR1B (Accession NP_115588.1) is another GAM3229 target gene, herein designated TARGET GENE. POLR1B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded

by POLR1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLR1B BINDING SITE, designated SEQ ID:14540, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45081] Another function of GAM3229 is therefore inhibition of POLR1B (Accession NP_115588.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLR1B.

[45082] POLR1B (Accession NP_061887.1) is another GAM3229 target gene, herein designated TARGET GENE. POLR1B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by POLR1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLR1B BINDING SITE, designated SEQ ID:14540, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45083] Another function of GAM3229 is therefore inhibition of

POLR1B (Accession NP_061887.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLR1B.

[45084] Ptprf interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1, Accession NP_003613.2) is another GAM3229 target gene, herein designated TARGET GENE. PPFIBP1 BINDING SITE1 and PPFIBP1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PPFIBP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPFIBP1 BINDING SITE1 and PPFIBP1 BINDING SITE2, designated SEQ ID:15585 and SEQ ID:7102 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45085] Another function of GAM3229 is therefore inhibition of Ptprf interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1, Accession NP_003613.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPFIBP1.

[45086] Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession

NP_005029.1) is another GAM3229 target gene, herein designated TARGET GENE. PPID BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPID, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPID BINDING SITE, designated SEQ ID:8015, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45087] Another function of GAM3229 is therefore inhibition of Peptidylprolyl isomerase d (cyclophilin d) (PPID, Accession NP_005029.1), a gene which catalyzes the cis- trans isomerization of proline imidic peptide bonds in oligopeptides. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPID.

[45088] The function of PPID and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) is another GAM3229 target gene, herein designated TARGET GENE. PPIL2 BINDING

SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPIL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPIL2 BINDING SITE, designated SEQ ID:6798, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45089] Another function of GAM3229 is therefore inhibition of Peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2, Accession NP_055152.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPIL2.

[45090] PRICKLE2 (Accession XP_093799.2) is another GAM3229 target gene, herein designated TARGET GENE. PRICKLE2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRICKLE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRICKLE2 BINDING SITE, designated SEQ ID:1859, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45091] Another function of GAM3229 is therefore inhibition of PRICKLE2 (Accession XP_093799.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRICKLE2.

[45092] Protamine 2 (PRM2, Accession NP_002753.1) is another GAM3229 target gene, herein designated TARGET GENE. PRM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRM2 BINDING SITE, designated SEQ ID:15684, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45093] Another function of GAM3229 is therefore inhibition of Protamine 2 (PRM2, Accession NP_002753.1), a gene which compacts sperm dna into a highly condensed, stable and inactive complex. and therefore may be associated with Infertility. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Infertility, and of other diseases and clinical conditions associated with PRM2.

[45094] The function of PRM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.2.PRO0233 (Accession NP_054840.1) is another GAM3229 target gene, herein designated TARGET GENE. PRO0233 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO0233, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0233 BINDING SITE, designated SEQ ID:7103, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45095] Another function of GAM3229 is therefore inhibition of PRO0233 (Accession NP_054840.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0233.

[45096] PRO0297 (Accession NP_054800.1) is another GAM3229 target gene, herein designated TARGET GENE. PRO0297 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO0297, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0297 BINDING SITE, designated SEQ ID:16889, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45097] Another function of GAM3229 is therefore inhibition of PRO0297 (Accession NP_054800.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0297.

[45098] Presenilin 1 (alzheimer disease 3) (PSEN1, Accession NP_000012.1) is another GAM3229 target gene, herein designated TARGET GENE. PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by PSEN1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2, designated SEQ ID:20121 and SEQ ID:4484 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ

ID:221.

[45099] Another function of GAM3229 is therefore inhibition of Presenilin 1 (alzheimer disease 3) (PSEN1, Accession NP_000012.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSEN1.

[45100] PSK (Accession NP_057235.1) is another GAM3229 target gene, herein designated TARGET GENE. PSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSK BINDING SITE, designated SEQ ID:14317, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45101] Another function of GAM3229 is therefore inhibition of PSK (Accession NP_057235.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSK.

[45102] Proteasome (prosome, macropain) activator subunit 3 (pa28 gamma; ki) (PSME3, Accession NP_005780.2) is another GAM3229 target gene, herein designated TARGET

GENE. PSME3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSME3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSME3 BINDING SITE, designated SEQ ID:5202, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45103] Another function of GAM3229 is therefore inhibition of Proteasome (prosome, macropain) activator subunit 3 (pa28 gamma; ki) (PSME3, Accession NP_005780.2), a gene which is the activator subunit of the proteasome (prosome macropain). Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSME3.

[45104] The function of PSME3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM195.2.Proteasome (prosome, macropain) activator subunit 3 (pa28 gamma; ki) (PSME3, Accession NP_789839.1) is another GAM3229 target gene, herein designated TARGET GENE. PSME3 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSME3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSME3 BINDING SITE, designated SEQ ID:5202, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45105] Another function of GAM3229 is therefore inhibition of Proteasome (prosome, macropain) activator subunit 3 (pa28 gamma; ki) (PSME3, Accession NP_789839.1), a gene which is the activator subunit of the proteasome (prosome macropain). Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSME3.

[45106] The function of PSME3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM195.2.Phosphoserine phosphatase (PSPH, Accession NP_004568.1) is another GAM3229 target gene, herein designated TARGET GENE. PSPH BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PSPH, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSPH BINDING SITE, designated SEQ ID:9353, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45107] Another function of GAM3229 is therefore inhibition of Phosphoserine phosphatase (PSPH, Accession NP_004568.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSPH.

[45108] Prostaglandin e synthase (PTGES, Accession NP_004869.1) is another GAM3229 target gene, herein designated TARGET GENE. PTGES BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGES BINDING SITE, designated SEQ ID:11180, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45109] Another function of GAM3229 is therefore inhibition of

Prostaglandin e synthase (PTGES, Accession NP_004869.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGES.

[45110] Protein tyrosine phosphatase, non-receptor type 18 (brain-derived) (PTPN18, Accession NP_055184.2) is another GAM3229 target gene, herein designated TARGET GENE. PTPN18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTPN18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPN18 BINDING SITE, designated SEQ ID:10017, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45111] Another function of GAM3229 is therefore inhibition of Protein tyrosine phosphatase, non-receptor type 18 (brain-derived) (PTPN18, Accession NP_055184.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN18.

[45112] Protein tyrosine phosphatase, non-receptor type 21

(PTPN21, Accession NP_008970.1) is another GAM3229 target gene, herein designated TARGET GENE. PTPN21 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTPN21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPN21 BINDING SITE, designated SEQ ID:18866, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45113] Another function of GAM3229 is therefore inhibition of Protein tyrosine phosphatase, non-receptor type 21 (PTPN21, Accession NP_008970.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN21.

[45114] Poliovirus receptor (PVR, Accession NP_006496.2) is another GAM3229 target gene, herein designated TARGET GENE. PVR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PVR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of PVR BINDING SITE, designated SEQ ID:16119, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45115] Another function of GAM3229 is therefore inhibition of Poliovirus receptor (PVR, Accession NP_006496.2), a gene which is a poliovirus receptor and therefore may be associated with Poliomyelitis. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Poliomyelitis, and of other diseases and clinical conditions associated with PVR.

[45116] The function of PVR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.RA-GEF-2 (Accession NP_057424.1) is another GAM3229 target gene, herein designated TARGET GENE. RA-GEF-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RA-GEF-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RA-GEF-2 BINDING SITE, designated SEQ ID:685, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45117] Another function of GAM3229 is therefore inhibition of RA-GEF-2 (Accession NP_057424.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RA-GEF-2.

[45118] RAB11-FIP4 (Accession NP_116321.2) is another GAM3229 target gene, herein designated TARGET GENE. RAB11-FIP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB11-FIP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB11-FIP4 BINDING SITE, designated SEQ ID:4504, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45119] Another function of GAM3229 is therefore inhibition of RAB11-FIP4 (Accession NP_116321.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB11-FIP4.

[45120] Rab33b, member ras oncogene family (RAB33B, Accession NP_112586.1) is another GAM3229 target gene, herein

designated TARGET GENE. RAB33B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB33B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB33B BINDING SITE, designated SEQ ID:10964, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45121] Another function of GAM3229 is therefore inhibition of Rab33b, member ras oncogene family (RAB33B, Accession NP_112586.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB33B.

[45122] Retinoic acid induced 3 (RAI3, Accession NP_003970.1) is another GAM3229 target gene, herein designated TARGET GENE. RAI3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAI3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAI3 BINDING SITE, designated SEQ ID:2965, to the nucleotide sequence of GAM3229 RNA, herein des-

ignated GAM RNA, also designated SEQ ID:221.

[45123] Another function of GAM3229 is therefore inhibition of Retinoic acid induced 3 (RAI3, Accession NP_003970.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI3.

[45124] Retinoblastoma binding protein 9 (RBBP9, Accession NP_006597.2) is another GAM3229 target gene, herein designated TARGET GENE. RBBP9 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RBBP9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RBBP9 BINDING SITE, designated SEQ ID:14743, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45125] Another function of GAM3229 is therefore inhibition of Retinoblastoma binding protein 9 (RBBP9, Accession NP_006597.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP9.

[45126] RE2 (Accession NP_722561.1) is another GAM3229 target

gene, herein designated TARGET GENE. RE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by RE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RE2 BINDING SITE, designated SEQ ID:2783, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45127] Another function of GAM3229 is therefore inhibition of RE2 (Accession NP_722561.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RE2.

[45128] Rhesus blood group, d antigen (RHD, Accession NP_057309.2) is another GAM3229 target gene, herein designated TARGET GENE. RHD BINDING SITE1 and RHD BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by RHD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE1 and RHD BINDING SITE2, designated SEQ ID:6398 and SEQ ID:17898 respectively, to

the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45129] Another function of GAM3229 is therefore inhibition of Rhesus blood group, d antigen (RHD, Accession NP_057309.2), a gene which Major antigen of the RH system. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[45130] The function of RHD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Rhesus blood group, d antigen (RHD, Accession NP_057208.2) is another GAM3229 target gene, herein designated TARGET GENE. RHD BINDING SITE1 and RHD BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by RHD, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE1 and RHD BINDING SITE2, designated SEQ ID:6398 and SEQ ID:17898 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45131] Another function of GAM3229 is therefore inhibition of Rhesus blood group, d antigen (RHD, Accession NP_057208.2), a gene which Major antigen of the RH system. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD.

[45132] The function of RHD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.RHPN2 (Accession NP_149094.2) is another GAM3229 target gene, herein designated TARGET GENE. RHPN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RHPN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RHPN2 BINDING SITE, designated SEQ ID:14536, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45133] Another function of GAM3229 is therefore inhibition of RHPN2 (Accession NP_149094.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHPN2.

[45134] RI58 (Accession NP_036552.1) is another GAM3229 target gene, herein designated TARGET GENE. RI58 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RI58, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RI58 BINDING SITE, designated SEQ ID:10523, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45135] Another function of GAM3229 is therefore inhibition of RI58 (Accession NP_036552.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RI58.

[45136] RNF135 (Accession NP_115698.2) is another GAM3229 target gene, herein designated TARGET GENE. RNF135 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF135 BINDING SITE, designated SEQ ID:15831, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[45137] Another function of GAM3229 is therefore inhibition of RNF135 (Accession NP_115698.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF135.

[45138] RNF144 (Accession NP_055561.1) is another GAM3229 target gene, herein designated TARGET GENE. RNF144 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF144, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF144 BINDING SITE, designated SEQ ID:5448, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45139] Another function of GAM3229 is therefore inhibition of RNF144 (Accession NP_055561.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF144.

[45140] Ring finger protein 19 (RNF19, Accession NP_056250.2) is another GAM3229 target gene, herein designated TARGET

GENE. RNF19 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RNF19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF19 BINDING SITE, designated SEQ ID:15444, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45141] Another function of GAM3229 is therefore inhibition of Ring finger protein 19 (RNF19, Accession NP_056250.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF19.

[45142] Ring finger protein (c3hc4 type) 8 (RNF8, Accession NP_003949.1) is another GAM3229 target gene, herein designated TARGET GENE. RNF8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF8 BINDING SITE, designated SEQ ID:11343, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ

ID:221.

[45143] Another function of GAM3229 is therefore inhibition of Ring finger protein (c3hc4 type) 8 (RNF8, Accession NP_003949.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF8.

[45144] Retinitis pigmentosa 2 (x-linked recessive) (RP2, Accession NP_008846.1) is another GAM3229 target gene, herein designated TARGET GENE. RP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RP2 BINDING SITE, designated SEQ ID:15091, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45145] Another function of GAM3229 is therefore inhibition of Retinitis pigmentosa 2 (x-linked recessive) (RP2, Accession NP_008846.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RP2.

[45146] RP4-622L5 (Accession NP_061991.2) is another GAM3229

target gene, herein designated TARGET GENE. RP4-622L5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RP4-622L5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RP4-622L5 BINDING SITE, designated SEQ ID:6481, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45147] Another function of GAM3229 is therefore inhibition of RP4-622L5 (Accession NP_061991.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RP4-622L5.

[45148] Ribonucleotide reductase m2 b (tp53 inducible) (RRM2B, Accession XP_042096.1) is another GAM3229 target gene, herein designated TARGET GENE. RRM2B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RRM2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RRM2B BINDING SITE, designated SEQ ID:9272, to the nucleotide sequence

of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45149] Another function of GAM3229 is therefore inhibition of Ribonucleotide reductase m2 b (tp53 inducible) (RRM2B, Accession XP_042096.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RRM2B.

[45150] S100 calcium binding protein a1 (S100A1, Accession NP_006262.1) is another GAM3229 target gene, herein designated TARGET GENE. S100A1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by S100A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of S100A1 BINDING SITE, designated SEQ ID:7600, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45151] Another function of GAM3229 is therefore inhibition of S100 calcium binding protein a1 (S100A1, Accession NP_006262.1), a gene which weakly binds calcium but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. Ac-

cordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with S100A1.

[45152] The function of S100A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM724.1.Sterol-c4-methyl oxidase-like (SC4MOL, Accession NP_006736.1) is another GAM3229 target gene, herein designated TARGET GENE. SC4MOL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SC4MOL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SC4MOL BINDING SITE, designated SEQ ID:3278, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45153] Another function of GAM3229 is therefore inhibition of Sterol-c4-methyl oxidase-like (SC4MOL, Accession NP_006736.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SC4MOL.

[45154] SCAMP-4 (Accession NP_524558.1) is another GAM3229

target gene, herein designated TARGET GENE. SCAMP-4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCAMP-4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAMP-4 BINDING SITE, designated SEQ ID:15109, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45155] Another function of GAM3229 is therefore inhibition of SCAMP-4 (Accession NP_524558.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP-4.

[45156] Sex comb on midleg-like 2 (drosophila) (SCML2, Accession NP_006080.1) is another GAM3229 target gene, herein designated TARGET GENE. SCML2 BINDING SITE1 and SCML2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SCML2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCML2 BINDING SITE1 and SCML2 BINDING SITE2, desig-

nated SEQ ID:1648 and SEQ ID:12471 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45157] Another function of GAM3229 is therefore inhibition of Sex comb on midleg-like 2 (drosophila) (SCML2, Accession NP_006080.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCML2.

[45158] SCN3B (Accession NP_060870.1) is another GAM3229 target gene, herein designated TARGET GENE. SCN3B BINDING SITE1 through SCN3B BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by SCN3B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCN3B BINDING SITE1 through SCN3B BINDING SITE3, designated SEQ ID:12530, SEQ ID:19668 and SEQ ID:856 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45159] Another function of GAM3229 is therefore inhibition of SCN3B (Accession NP_060870.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with SCN3B.

[45160] Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1) is another GAM3229 target gene, herein designated TARGET GENE. SEDL BINDING SITE1 through SEDL BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by SEDL, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEDL BINDING SITE1 through SEDL BINDING SITE3, designated SEQ ID:15920, SEQ ID:6019 and SEQ ID:9526 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45161] Another function of GAM3229 is therefore inhibition of Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1), a gene which may play role in vesicular transport from endoplasmic reticulum to golgi. and therefore may be associated with Spondyloepiphyseal dysplasia. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Spondyloepiphyseal dysplasia, and of other diseases and clinical conditions associated with SEDL.

[45162] The function of SEDL and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Selenoprotein n, 1 (SEPN1, Accession NP_065184.1) is another GAM3229 target gene, herein designated TARGET GENE. SEPN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEPN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEPN1 BINDING SITE, designated SEQ ID:941, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45163] Another function of GAM3229 is therefore inhibition of Selenoprotein n, 1 (SEPN1, Accession NP_065184.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEPN1.

[45164] Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) is another GAM3229 target gene, herein designated TARGET GENE. SERF1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERF1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1A BINDING SITE, designated SEQ ID:4780, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45165] Another function of GAM3229 is therefore inhibition of Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1A.

[45166] Small edrk-rich factor 1b (centromeric) (SERF1B, Accession NP_075267.1) is another GAM3229 target gene, herein designated TARGET GENE. SERF1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERF1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1B BINDING SITE, designated SEQ ID:4780, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45167] Another function of GAM3229 is therefore inhibition of Small edrk-rich factor 1b (centromeric) (SERF1B, Accession

NP_075267.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1B.

[45168] Small edrk-rich factor 2 (SERF2, Accession NP_005761.2) is another GAM3229 target gene, herein designated TARGET GENE. SERF2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SERF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF2 BINDING SITE, designated SEQ ID:6225, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45169] Another function of GAM3229 is therefore inhibition of Small edrk-rich factor 2 (SERF2, Accession NP_005761.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF2.

[45170] Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 9 (SERPINB9, Accession NP_004146.1) is another GAM3229 target gene, herein designated TARGET GENE. SERPINB9 BINDING SITE1 and

SERPINB9 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SERPINB9, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERPINB9 BINDING SITE1 and SERPINB9 BINDING SITE2, designated SEQ ID:3013 and SEQ ID:10182 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45171] Another function of GAM3229 is therefore inhibition of Serine (or cysteine) proteinase inhibitor, clade b (ovalbumin), member 9 (SERPINB9, Accession NP_004146.1), a gene which may be a serpin serine protease inhibitor that interacts with granzyme B (GZMB). Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB9.

[45172] The function of SERPINB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM88.2.Short stature homeobox (SHOX, Accession NP_006874.1) is another GAM3229 target gene, herein designated TARGET GENE. SHOX BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SHOX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SHOX BINDING SITE, designated SEQ ID:10964, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45173] Another function of GAM3229 is therefore inhibition of Short stature homeobox (SHOX, Accession NP_006874.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHOX.

[45174] Sialic acid binding ig-like lectin 11 (SIGLEC11, Accession NP_443116.1) is another GAM3229 target gene, herein designated TARGET GENE. SIGLEC11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIGLEC11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIGLEC11 BINDING SITE, designated SEQ ID:11214, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA,

also designated SEQ ID:221.

[45175] Another function of GAM3229 is therefore inhibition of Sialic acid binding ig-like lectin 11 (SIGLEC11, Accession NP_443116.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIGLEC11.

[45176] Sialic acid binding ig-like lectin 5 (SIGLEC5, Accession NP_003821.1) is another GAM3229 target gene, herein designated TARGET GENE. SIGLEC5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIGLEC5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIGLEC5 BINDING SITE, designated SEQ ID:15567, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45177] Another function of GAM3229 is therefore inhibition of Sialic acid binding ig-like lectin 5 (SIGLEC5, Accession NP_003821.1), a gene which is a cell adhesion molecule for postnatal neural development. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIGLEC5.

[45178] The function of SIGLEC5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Sialic acid binding ig-like lectin 8 (SIGLEC8, Accession NP_055257.1) is another GAM3229 target gene, herein designated TARGET GENE. SIGLEC8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIGLEC8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIGLEC8 BINDING SITE, designated SEQ ID:6398, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45179] Another function of GAM3229 is therefore inhibition of Sialic acid binding ig-like lectin 8 (SIGLEC8, Accession NP_055257.1), a gene which is a cell adhesion molecule for postnatal neural development. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIGLEC8.

[45180] The function of SIGLEC8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM63.1.Src-like-adaptor 2 (SLA2, Accession NP_778252.1) is another GAM3229 target gene, herein designated TARGET GENE. SLA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLA2 BINDING SITE, designated SEQ ID:17394, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45181] Another function of GAM3229 is therefore inhibition of Src-like-adaptor 2 (SLA2, Accession NP_778252.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA2.

[45182] Src-like-adaptor 2 (SLA2, Accession NP_115590.1) is another GAM3229 target gene, herein designated TARGET GENE. SLA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SLA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of SLA2 BINDING SITE, designated SEQ ID:17394, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45183] Another function of GAM3229 is therefore inhibition of Src-like-adaptor 2 (SLA2, Accession NP_115590.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA2.

[45184] Solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8, Accession NP_078904.1) is another GAM3229 target gene, herein designated TARGET GENE. SLC12A8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC12A8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC12A8 BINDING SITE, designated SEQ ID:18490, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45185] Another function of GAM3229 is therefore inhibition of Solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8, Accession NP_078904.1) . Accord-

ingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC12A8.

[45186] Solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1, Accession NP_005064.1) is another GAM3229 target gene, herein designated TARGET GENE. SLC15A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC15A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC15A1 BINDING SITE, designated SEQ ID:940, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45187] Another function of GAM3229 is therefore inhibition of Solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1, Accession NP_005064.1), a gene which is a H(+)- coupled peptide transporter. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC15A1.

[45188] The function of SLC15A1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM30.1.Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) is another GAM3229 target gene, herein designated TARGET GENE. SLC16A6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC16A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC16A6 BINDING SITE, designated SEQ ID:3300, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45189] Another function of GAM3229 is therefore inhibition of Solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6, Accession NP_004685.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A6.

[45190] Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1, Accession NP_004718.1) is another GAM3229 target gene, herein designated TARGET GENE. SLC24A1 BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by SLC24A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC24A1 BINDING SITE, designated SEQ ID:1284, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45191] Another function of GAM3229 is therefore inhibition of Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (SLC24A1, Accession NP_004718.1), a gene which is a critical component of the visual transduction cascade, controlling the calcium concentration of outer segments during light and darkness. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC24A1.

[45192] The function of SLC24A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10, Accession NP_110404.1) is another GAM3229 target gene, herein

designated TARGET GENE. SLC2A10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC2A10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC2A10 BINDING SITE, designated SEQ ID:7814, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45193] Another function of GAM3229 is therefore inhibition of Solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10, Accession NP_110404.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC2A10.

[45194] SLC35E2 (Accession XP_049733.6) is another GAM3229 target gene, herein designated TARGET GENE. SLC35E2 BINDING SITE1 and SLC35E2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SLC35E2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC35E2 BINDING SITE1 and

SLC35E2 BINDING SITE2, designated SEQ ID:13880 and SEQ ID:16129 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45195] Another function of GAM3229 is therefore inhibition of SLC35E2 (Accession XP_049733.6) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35E2.

[45196] Solute carrier family 36 (proton/amino acid symporter), member 1 (SLC36A1, Accession NP_510968.1) is another GAM3229 target gene, herein designated TARGET GENE. SLC36A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC36A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC36A1 BINDING SITE, designated SEQ ID:989, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45197] Another function of GAM3229 is therefore inhibition of Solute carrier family 36 (proton/amino acid symporter), member 1 (SLC36A1, Accession NP_510968.1) . Accord-

ingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC36A1.

[45198] Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2) is another GAM3229 target gene, herein designated TARGET GENE. SLC39A1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC39A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC39A1 BINDING SITE, designated SEQ ID:17454, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45199] Another function of GAM3229 is therefore inhibition of Solute carrier family 39 (zinc transporter), member 1 (SLC39A1, Accession NP_055252.2), a gene which is a divalent (zinc/iron) metal ion transporter. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC39A1.

[45200] The function of SLC39A1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM175.1.Solute carrier family 5 (sodium-dependent vitamin transporter), member 6 (SLC5A6, Accession NP_066918.1) is another GAM3229 target gene, herein designated TARGET GENE. SLC5A6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC5A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC5A6 BINDING SITE, designated SEQ ID:11338, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45201] Another function of GAM3229 is therefore inhibition of Solute carrier family 5 (sodium-dependent vitamin transporter), member 6 (SLC5A6, Accession NP_066918.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC5A6.

[45202] Solute carrier family 6 (neurotransmitter transporter, betaine/gaba), member 12 (SLC6A12, Accession NP_003035.2) is another GAM3229 target gene, herein designated TARGET GENE. SLC6A12 BINDING SITE is a tar-

get binding site found in the 3` untranslated region of mRNA encoded by SLC6A12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC6A12 BINDING SITE, designated SEQ ID:9875, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45203] Another function of GAM3229 is therefore inhibition of Solute carrier family 6 (neurotransmitter transporter, betaine/gaba), member 12 (SLC6A12, Accession NP_003035.2), a gene which transports betaine and gaba. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A12.

[45204] The function of SLC6A12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1095.1.Solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5, Accession NP_003477.3) is another GAM3229 target gene, herein designated TARGET GENE. SLC7A5 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by SLC7A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC7A5 BINDING SITE, designated SEQ ID:15377, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45205] Another function of GAM3229 is therefore inhibition of Solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5, Accession NP_003477.3), a gene which mediates transport of large and small neutral amino acids. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC7A5.

[45206] The function of SLC7A5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM98.1.SLC9A8 (Accession XP_030524.2) is another GAM3229 target gene, herein designated TARGET GENE. SLC9A8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC9A8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of SLC9A8 BINDING SITE, designated SEQ ID:5218, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45207] Another function of GAM3229 is therefore inhibition of SLC9A8 (Accession XP_030524.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC9A8.

[45208] Swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 (SMARCF1, Accession NP_060920.4) is another GAM3229 target gene, herein designated TARGET GENE. SMARCF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SMARCF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMARCF1 BINDING SITE, designated SEQ ID:10764, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45209] Another function of GAM3229 is therefore inhibition of Swi/snf related, matrix associated, actin dependent regu-

lator of chromatin, subfamily f, member 1 (SMARCF1, Accession NP_060920.4) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMARCF1.

[45210] Swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 (SMARCF1, Accession NP_624361.1) is another GAM3229 target gene, herein designated TARGET GENE. SMARCF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SMARCF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMARCF1 BINDING SITE, designated SEQ ID:10764, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45211] Another function of GAM3229 is therefore inhibition of Swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 (SMARCF1, Accession NP_624361.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMARCF1.

[45212] Swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 (SMARCF1, Accession NP_006006.3) is another GAM3229 target gene, herein designated TARGET GENE. SMARCF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SMARCF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMARCF1 BINDING SITE, designated SEQ ID:10764, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45213] Another function of GAM3229 is therefore inhibition of Swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 (SMARCF1, Accession NP_006006.3) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMARCF1.

[45214] Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_003816.2) is another GAM3229 target gene, herein designated TARGET GENE. SNAP23 BINDING SITE is a target binding site found in the 3` untranslated region

of multiple transcripts of mRNA encoded by SNAP23, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP23 BINDING SITE, designated SEQ ID:15734, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45215] Another function of GAM3229 is therefore inhibition of Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_003816.2), a gene which is essential component of the high affinity receptor for the general membrane fusion machinery. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP23.

[45216] The function of SNAP23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_570710.1) is another GAM3229 target gene, herein designated TARGET GENE. SNAP23 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNAP23, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNAP23 BINDING SITE, designated SEQ ID:15734, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45217] Another function of GAM3229 is therefore inhibition of Synaptosomal-associated protein, 23kda (SNAP23, Accession NP_570710.1), a gene which is essential component of the high affinity receptor for the general membrane fusion machinery. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP23.

[45218] The function of SNAP23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.SNARK (Accession NP_112214.1) is another GAM3229 target gene, herein designated TARGET GENE. SNARK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNARK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of SNARK BINDING SITE, designated SEQ ID:9680, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45219] Another function of GAM3229 is therefore inhibition of SNARK (Accession NP_112214.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNARK.

[45220] Syntrophin, beta 2 (dystrophin-associated protein a1, 59kda, basic component 2) (SNTB2, Accession NP_006741.1) is another GAM3229 target gene, herein designated TARGET GENE. SNTB2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNTB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNTB2 BINDING SITE, designated SEQ ID:5203, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45221] Another function of GAM3229 is therefore inhibition of Syntrophin, beta 2 (dystrophin-associated protein a1, 59kda, basic component 2) (SNTB2, Accession NP_006741.1) . Accordingly, utilities of GAM3229 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with SNTB2.

[45222] Syntrophin, beta 2 (dystrophin-associated protein a1, 59kda, basic component 2) (SNTB2, Accession NP_570896.1) is another GAM3229 target gene, herein designated TARGET GENE. SNTB2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNTB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNTB2 BINDING SITE, designated SEQ ID:5203, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45223] Another function of GAM3229 is therefore inhibition of Syntrophin, beta 2 (dystrophin-associated protein a1, 59kda, basic component 2) (SNTB2, Accession NP_570896.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNTB2.

[45224] Sorting nexin 15 (SNX15, Accession NP_680086.1) is another GAM3229 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found

in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:17861, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45225] Another function of GAM3229 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NP_680086.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15.

[45226] Sorting nexin 15 (SNX15, Accession NP_037438.2) is another GAM3229 target gene, herein designated TARGET GENE. SNX15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:17861, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:221.

[45227] Another function of GAM3229 is therefore inhibition of Sorting nexin 15 (SNX15, Accession NP_037438.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15.

[45228] SNX22 (Accession NP_079074.1) is another GAM3229 target gene, herein designated TARGET GENE. SNX22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNX22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX22 BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45229] Another function of GAM3229 is therefore inhibition of SNX22 (Accession NP_079074.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX22.

[45230] SNX27 (Accession NP_112180.4) is another GAM3229 target gene, herein designated TARGET GENE. SNX27 BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by SNX27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX27 BINDING SITE, designated SEQ ID:4464, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45231] Another function of GAM3229 is therefore inhibition of SNX27 (Accession NP_112180.4) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX27.

[45232] Sp110 nuclear body protein (SP110, Accession NP_536349.1) is another GAM3229 target gene, herein designated TARGET GENE. SP110 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SP110, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SP110 BINDING SITE, designated SEQ ID:11431, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45233] Another function of GAM3229 is therefore inhibition of

Sp110 nuclear body protein (SP110, Accession NP_536349.1), a gene which is involved in transduction of interferon action. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SP110.

[45234] The function of SP110 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.2.Sp110 nuclear body protein (SP110, Accession NP_004500.2) is another GAM3229 target gene, herein designated TARGET GENE. SP110 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SP110, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SP110 BINDING SITE, designated SEQ ID:11431, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45235] Another function of GAM3229 is therefore inhibition of Sp110 nuclear body protein (SP110, Accession NP_004500.2), a gene which is involved in transduction of interferon action. Accordingly, utilities of GAM3229 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with SP110.

[45236] The function of SP110 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.2.SPCX (Accession NP_775260.1) is another GAM3229 target gene, herein designated TARGET GENE. SPCX BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SPCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPCX BINDING SITE, designated SEQ ID:6614, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45237] Another function of GAM3229 is therefore inhibition of SPCX (Accession NP_775260.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPCX.

[45238] Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1) is another GAM3229 target gene, herein designated TARGET GENE. SS18 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by SS18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SS18 BINDING SITE, designated SEQ ID:10286, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45239] Another function of GAM3229 is therefore inhibition of Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1), a gene which is a putative transcriptional activator. and therefore is associated with Human synovial sarcomas. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Human synovial sarcomas., and of other diseases and clinical conditions associated with SS18.

[45240] The function of SS18 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Taf11 rna polymerase ii, tata box binding protein (tbp)-associated factor, 28kda (TAF11, Accession NP_005634.1) is another GAM3229 target gene, herein designated TARGET GENE. TAF11 BINDING SITE1 and TAF11 BINDING SITE2 are target binding sites found in

untranslated regions of mRNA encoded by TAF11, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAF11 BINDING SITE1 and TAF11 BINDING SITE2, designated SEQ ID:16874 and SEQ ID:5021 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45241] Another function of GAM3229 is therefore inhibition of Taf11 rna polymerase ii, tata box binding protein (tbp)-associated factor, 28kda (TAF11, Accession NP_005634.1), a gene which plays a central role in mediating promoter responses to various activators and repressors. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAF11.

[45242] The function of TAF11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.T-cell acute lymphocytic leukemia 1 (TAL1, Accession NP_003180.1) is another GAM3229 target gene, herein designated TARGET GENE. TAL1 BINDING SITE1 and TAL1 BINDING SITE2 are target binding sites found in un-

translated regions of mRNA encoded by TAL1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAL1 BINDING SITE1 and TAL1 BINDING SITE2, designated SEQ ID:5904 and SEQ ID:3829 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45243] Another function of GAM3229 is therefore inhibition of T-cell acute lymphocytic leukemia 1 (TAL1, Accession NP_003180.1), a gene which may help control cell growth and differentiation. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAL1.

[45244] The function of TAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tap binding protein (tapasin) (TAPBP, Accession NP_003181.3) is another GAM3229 target gene, herein designated TARGET GENE. TAPBP BINDING SITE1 and TAPBP BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TAPBP, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TAPBP BINDING SITE1 and TAPBP BINDING SITE2, designated SEQ ID:9729 and SEQ ID:12850 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45245] Another function of GAM3229 is therefore inhibition of Tap binding protein (tapasin) (TAPBP, Accession NP_003181.3), a gene which is involved in MHC class I-restricted antigen processing. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAPBP.

[45246] The function of TAPBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Tea domain family member 3 (TEAD3, Accession NP_003205.1) is another GAM3229 target gene, herein designated TARGET GENE. TEAD3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TEAD3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of TEAD3 BINDING SITE, designated SEQ ID:11870, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45247] Another function of GAM3229 is therefore inhibition of Tea domain family member 3 (TEAD3, Accession NP_003205.1), a gene which binds to multiple functional elements of the human chorionic somatomammotropin- b gene enhancer. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEAD3.

[45248] The function of TEAD3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM497.1.Testis derived transcript (3 lim domains) (TES, Accession NP_690042.1) is another GAM3229 target gene, herein designated TARGET GENE. TES BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TES BINDING SITE, designated SEQ ID:16668, to the nu-

cleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45249] Another function of GAM3229 is therefore inhibition of Testis derived transcript (3 lim domains) (TES, Accession NP_690042.1), a gene which acts as a tumor suppressor and therefore may be associated with Ovarian carcinomas, breast cancer. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Ovarian carcinomas, breast cancer, and of other diseases and clinical conditions associated with TES.

[45250] The function of TES and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Testis derived transcript (3 lim domains) (TES, Accession NP_056456.1) is another GAM3229 target gene, herein designated TARGET GENE. TES BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TES BINDING SITE, designated SEQ ID:16668, to the nucleotide sequence of GAM3229 RNA, herein designated

GAM RNA, also designated SEQ ID:221.

[45251] Another function of GAM3229 is therefore inhibition of Testis derived transcript (3 lim domains) (TES, Accession NP_056456.1), a gene which acts as a tumor suppressor and therefore may be associated with Ovarian carcinomas, breast cancer. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Ovarian carcinomas, breast cancer, and of other diseases and clinical conditions associated with TES.

[45252] The function of TES and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Transforming growth factor, beta-induced, 68kda (TGFBI, Accession NP_000349.1) is another GAM3229 target gene, herein designated TARGET GENE. TGFBI BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGFBI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGFBI BINDING SITE, designated SEQ ID:15372, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45253] Another function of GAM3229 is therefore inhibition of Transforming growth factor, beta-induced, 68kda (TGFBI, Accession NP_000349.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFBI.

[45254] Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) is another GAM3229 target gene, herein designated TARGET GENE. TGIF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGIF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGIF2 BINDING SITE, designated SEQ ID:18631, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45255] Another function of GAM3229 is therefore inhibition of Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGIF2.

[45256] TIM50L (Accession XP_053074.2) is another GAM3229 target gene, herein designated TARGET GENE. TIM50L

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TIM50L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TIM50L BINDING SITE, designated SEQ ID:5198, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45257] Another function of GAM3229 is therefore inhibition of TIM50L (Accession XP_053074.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIM50L.

[45258] Tissue inhibitor of metalloproteinase 3 (sorsby fundus dystrophy, pseudoinflammatory) (TIMP3, Accession NP_000353.1) is another GAM3229 target gene, herein designated TARGET GENE. TIMP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TIMP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TIMP3 BINDING SITE, designated SEQ ID:10513, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ

ID:221.

[45259] Another function of GAM3229 is therefore inhibition of Tissue inhibitor of metalloproteinase 3 (sorsby fundus dystrophy, pseudoinflammatory) (TIMP3, Accession NP_000353.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIMP3.

[45260] Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_003833.3) is another GAM3229 target gene, herein designated TARGET GENE. TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF10B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2, designated SEQ ID:2703 and SEQ ID:2055 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45261] Another function of GAM3229 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_003833.3), a gene which forms

complex that induces apoptosis. and therefore may be associated with Squamous cell carcinoma . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Squamous cell carcinoma ., and of other diseases and clinical conditions associated with TNFRSF10B.

[45262] The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_671716.1) is another GAM3229 target gene, herein designated TARGET GENE. TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TNFRSF10B, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE1 and TNFRSF10B BINDING SITE2, designated SEQ ID:2055 and SEQ ID:2703 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45263] Another function of GAM3229 is therefore inhibition of

Tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B, Accession NP_671716.1), a gene which forms complex that induces apoptosis. and therefore may be associated with Squamous cell carcinoma . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Squamous cell carcinoma ., and of other diseases and clinical conditions associated with TNFRSF10B.

[45264] The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Tumor necrosis factor receptor superfamily, member 11a, activator of nfkb (TNFRSF11A, Accession NP_003830.1) is another GAM3229 target gene, herein designated TARGET GENE. TNFRSF11A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF11A BINDING SITE, designated SEQ ID:18341, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45265] Another function of GAM3229 is therefore inhibition of

Tumor necrosis factor receptor superfamily, member 11a, activator of nfkb (TNFRSF11A, Accession NP_003830.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF11A.

[45266] TP53I5 (Accession XP_290532.2) is another GAM3229 target gene, herein designated TARGET GENE. TP53I5 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TP53I5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TP53I5 BINDING SITE, designated SEQ ID:11115, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45267] Another function of GAM3229 is therefore inhibition of TP53I5 (Accession XP_290532.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53I5.

[45268] Thiopurine s-methyltransferase (TPMT, Accession NP_000358.1) is another GAM3229 target gene, herein designated TARGET GENE. TPMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by TPMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPMT BINDING SITE, designated SEQ ID:8393, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45269] Another function of GAM3229 is therefore inhibition of Thiopurine s-methyltransferase (TPMT, Accession NP_000358.1), a gene which catalyzes the s- methylation of thiopurine drugs such as 6- mercaptopurine. and therefore may be associated with Thiopurine s- methyl-transferase polymorphism. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Thiopurine s- methyltransferase polymorphism, and of other diseases and clinical conditions associated with TPMT.

[45270] The function of TPMT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Tryptase gamma 1 (TPSG1, Accession NP_036599.1) is another GAM3229 target gene, herein designated TARGET GENE. TPSG1 BINDING SITE is a target

binding site found in the 5` untranslated region of mRNA encoded by TPSG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TPSG1 BINDING SITE, designated SEQ ID:10281, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45271] Another function of GAM3229 is therefore inhibition of Tryptase gamma 1 (TPSG1, Accession NP_036599.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TPSG1.

[45272] TRAM2 (Accession NP_036420.1) is another GAM3229 target gene, herein designated TARGET GENE. TRAM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRAM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAM2 BINDING SITE, designated SEQ ID:14318, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45273] Another function of GAM3229 is therefore inhibition of TRAM2 (Accession NP_036420.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAM2.

[45274] Tripartite motif-containing 16 (TRIM16, Accession NP_006461.2) is another GAM3229 target gene, herein designated TARGET GENE. TRIM16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRIM16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM16 BINDING SITE, designated SEQ ID:14800, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45275] Another function of GAM3229 is therefore inhibition of Tripartite motif-containing 16 (TRIM16, Accession NP_006461.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM16.

[45276] Tripartite motif-containing 5 (TRIM5, Accession NP_149023.1) is another GAM3229 target gene, herein designated TARGET GENE. TRIM5 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TRIM5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM5 BINDING SITE, designated SEQ ID:11399, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45277] Another function of GAM3229 is therefore inhibition of Tripartite motif-containing 5 (TRIM5, Accession NP_149023.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM5.

[45278] Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542435.1) is another GAM3229 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ

ID:14539 and SEQ ID:3431 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45279] Another function of GAM3229 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542435.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[45280] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_061197.3) is another GAM3229 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:14539 and SEQ ID:3431 respec-

tively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45281] Another function of GAM3229 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_061197.3), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[45282] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1) is another GAM3229 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:14539 and SEQ ID:14539 respectively, to the nucleotide sequence of GAM3229 RNA,

herein designated GAM RNA, also designated SEQ ID:221.

[45283] Another function of GAM3229 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[45284] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1) is another GAM3229 target gene, herein designated TARGET GENE. TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TRPV1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 and TRPV1 BINDING SITE2, designated SEQ ID:3431 and SEQ ID:3431 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45285] Another function of GAM3229 is therefore inhibition of Transient receptor potential cation channel, subfamily v, member 1 (TRPV1, Accession NP_542436.1), a gene which functions as a receptor for capsaicin. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1.

[45286] The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.TU12B1-TY (Accession NP_057659.1) is another GAM3229 target gene, herein designated TARGET GENE. TU12B1-TY BINDING SITE1 through TU12B1-TY BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by TU12B1-TY, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TU12B1-TY BINDING SITE1 through TU12B1-TY BINDING SITE3, designated SEQ ID:1925, SEQ ID:3770 and SEQ ID:11645 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45287] Another function of GAM3229 is therefore inhibition of

TU12B1-TY (Accession NP_057659.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TU12B1-TY.

[45288] TUCAN (Accession NP_055774.1) is another GAM3229 target gene, herein designated TARGET GENE. TUCAN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TUCAN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUCAN BINDING SITE, designated SEQ ID:16766, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45289] Another function of GAM3229 is therefore inhibition of TUCAN (Accession NP_055774.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUCAN.

[45290] Tuftelin 1 (TUFT1, Accession NP_064512.1) is another GAM3229 target gene, herein designated TARGET GENE. TUFT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TUFT1, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUFT1 BINDING SITE, designated SEQ ID:5345, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45291] Another function of GAM3229 is therefore inhibition of Tuftelin 1 (TUFT1, Accession NP_064512.1), a gene which appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and capping. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUFT1.

[45292] The function of TUFT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.TUWD12 (Accession NP_758440.1) is another GAM3229 target gene, herein designated TARGET GENE. TUWD12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TUWD12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUWD12 BINDING SITE, designated

SEQ ID:9384, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45293] Another function of GAM3229 is therefore inhibition of TUWD12 (Accession NP_758440.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUWD12.

[45294] TXL-2 (Accession NP_835231.1) is another GAM3229 target gene, herein designated TARGET GENE. TXL-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TXL-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TXL-2 BINDING SITE, designated SEQ ID:15613, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45295] Another function of GAM3229 is therefore inhibition of TXL-2 (Accession NP_835231.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TXL-2.

[45296] UBF-fl (Accession NP_116217.1) is another GAM3229 tar-

get gene, herein designated TARGET GENE. UBF-fl BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBF-fl, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBF-fl BINDING SITE, designated SEQ ID:12691, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45297] Another function of GAM3229 is therefore inhibition of UBF-fl (Accession NP_116217.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBF-fl.

[45298] Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS, Accession NP_000364.1) is another GAM3229 target gene, herein designated TARGET GENE. UMPS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UMPS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UMPS BINDING SITE, designated SEQ ID:14691, to the nucleotide sequence of

GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45299] Another function of GAM3229 is therefore inhibition of Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS, Accession NP_000364.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UMPS.

[45300] Ubiquitin specific protease 22 (USP22, Accession XP_042698.2) is another GAM3229 target gene, herein designated TARGET GENE. USP22 BINDING SITE1 and USP22 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by USP22, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of USP22 BINDING SITE1 and USP22 BINDING SITE2, designated SEQ ID:14801 and SEQ ID:1601 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45301] Another function of GAM3229 is therefore inhibition of Ubiquitin specific protease 22 (USP22, Accession XP_042698.2) . Accordingly, utilities of GAM3229 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with USP22.

[45302] VDU1 (Accession NP_055832.2) is another GAM3229 target gene, herein designated TARGET GENE. VDU1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VDU1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VDU1 BINDING SITE, designated SEQ ID:10537, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45303] Another function of GAM3229 is therefore inhibition of VDU1 (Accession NP_055832.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VDU1.

[45304] Vent-like homeobox 2 (VENTX2, Accession NP_055283.1) is another GAM3229 target gene, herein designated TARGET GENE. VENTX2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VENTX2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of VENTX2 BINDING SITE, designated SEQ ID:19528, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45305] Another function of GAM3229 is therefore inhibition of Vent-like homeobox 2 (VENTX2, Accession NP_055283.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VENTX2.

[45306] Von hippel-lindau syndrome (VHL, Accession NP_000542.1) is another GAM3229 target gene, herein designated TARGET GENE. VHL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VHL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VHL BINDING SITE, designated SEQ ID:8629, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45307] Another function of GAM3229 is therefore inhibition of Von hippel-lindau syndrome (VHL, Accession NP_000542.1), a gene which may control rna stability

through the selective degradation of rna- bound proteins. and therefore is associated with Von hippel- lindau disease. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Von hippel- lindau disease, and of other diseases and clinical conditions associated with VHL.

[45308] The function of VHL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.VIK (Accession NP_612503.1) is another GAM3229 target gene, herein designated TARGET GENE. VIK BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by VIK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VIK BINDING SITE, designated SEQ ID:3535, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45309] Another function of GAM3229 is therefore inhibition of VIK (Accession NP_612503.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIK.

[45310] Vesicular membrane protein p24 (VMP, Accession NP_542454.2) is another GAM3229 target gene, herein designated TARGET GENE. VMP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VMP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VMP BINDING SITE, designated SEQ ID:5123, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45311] Another function of GAM3229 is therefore inhibition of Vesicular membrane protein p24 (VMP, Accession NP_542454.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VMP.

[45312] Vanin 1 (VNN1, Accession NP_004657.1) is another GAM3229 target gene, herein designated TARGET GENE. VNN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VNN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

VNN1 BINDING SITE, designated SEQ ID:16216, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45313] Another function of GAM3229 is therefore inhibition of Vanin 1 (VNN1, Accession NP_004657.1), a gene which may regulate steps in thymus homing and play a role in mammalian sexual development. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VNN1.

[45314] The function of VNN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.Vacuolar protein sorting 33a (yeast) (VPS33A, Accession NP_075067.2) is another GAM3229 target gene, herein designated TARGET GENE. VPS33A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VPS33A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VPS33A BINDING SITE, designated SEQ ID:12847, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45315] Another function of GAM3229 is therefore inhibition of Vacuolar protein sorting 33a (yeast) (VPS33A, Accession NP_075067.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS33A.

[45316] WBP3 (Accession NP_783863.2) is another GAM3229 target gene, herein designated TARGET GENE. WBP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WBP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBP3 BINDING SITE, designated SEQ ID:13231, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45317] Another function of GAM3229 is therefore inhibition of WBP3 (Accession NP_783863.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBP3.

[45318] Williams-beuren syndrome chromosome region 23 (WBSCR23, Accession NP_079318.1) is another GAM3229 target gene, herein designated TARGET GENE. WBSCR23 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by WBSCR23, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR23 BINDING SITE, designated SEQ ID:4757, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45319] Another function of GAM3229 is therefore inhibition of Williams-beuren syndrome chromosome region 23 (WBSCR23, Accession NP_079318.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR23.

[45320] WDFY3 (Accession NP_848700.1) is another GAM3229 target gene, herein designated TARGET GENE. WDFY3 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by WDFY3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WDFY3 BINDING SITE, designated SEQ ID:18416, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ

ID:221.

[45321] Another function of GAM3229 is therefore inhibition of WDFY3 (Accession NP_848700.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDFY3.

[45322] WFDC8 (Accession NP_852611.1) is another GAM3229 target gene, herein designated TARGET GENE. WFDC8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WFDC8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WFDC8 BINDING SITE, designated SEQ ID:15411, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45323] Another function of GAM3229 is therefore inhibition of WFDC8 (Accession NP_852611.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WFDC8.

[45324] Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_055734.1) is another GAM3229 target gene, herein designated TARGET GENE. WHSC1 BINDING SITE1

and WHSC1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by WHSC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE1 and WHSC1 BINDING SITE2, designated SEQ ID:18856 and SEQ ID:18856 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45325] Another function of GAM3229 is therefore inhibition of Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_055734.1), a gene which binds covalently to and repairs g/t mismatches. and therefore may be associated with Wolf- hirschhorn syndrome. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Wolf- hirschhorn syndrome, and of other diseases and clinical conditions associated with WHSC1.

[45326] The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_579878.1) is another GAM3229

target gene, herein designated TARGET GENE. WHSC1 BINDING SITE1 and WHSC1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by WHSC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE1 and WHSC1 BINDING SITE2, designated SEQ ID:18856 and SEQ ID:5144 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45327] Another function of GAM3229 is therefore inhibition of Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_579878.1), a gene which binds covalently to and repairs g/t mismatches. and therefore may be associated with Wolf- hirschhorn syndrome. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Wolf- hirschhorn syndrome, and of other diseases and clinical conditions associated with WHSC1.

[45328] The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Wolf-hirschhorn syndrome candidate 1

(WHSC1, Accession NP_579877.1) is another GAM3229 target gene, herein designated TARGET GENE. WHSC1 BINDING SITE1 and WHSC1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by WHSC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE1 and WHSC1 BINDING SITE2, designated SEQ ID:18856 and SEQ ID:18856 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45329] Another function of GAM3229 is therefore inhibition of Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_579877.1), a gene which binds covalently to and repairs g/t mismatches. and therefore may be associated with Wolf- hirschhorn syndrome. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Wolf- hirschhorn syndrome, and of other diseases and clinical conditions associated with WHSC1.

[45330] The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM30.1.Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_015627.1) is another GAM3229 target gene, herein designated TARGET GENE. WHSC1 BINDING SITE1 and WHSC1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by WHSC1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE1 and WHSC1 BINDING SITE2, designated SEQ ID:18856 and SEQ ID:18608 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45331] Another function of GAM3229 is therefore inhibition of Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_015627.1), a gene which binds covalently to and repairs g/t mismatches. and therefore may be associated with Wolf- hirschhorn syndrome. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of Wolf- hirschhorn syndrome, and of other diseases and clinical conditions associated with WHSC1.

[45332] The function of WHSC1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM30.1.X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1) is another GAM3229 target gene, herein designated TARGET GENE. XRCC2 BINDING SITE1 and XRCC2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by XRCC2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of XRCC2 BINDING SITE1 and XRCC2 BINDING SITE2, designated SEQ ID:14540 and SEQ ID:10425 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45333] Another function of GAM3229 is therefore inhibition of X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1), a gene which involves in the homologous recombination repair (hrr) pathway of double- stranded dna. Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XRCC2.

[45334] The function of XRCC2 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.ZAP (Accession NP_064504.2) is another GAM3229 target gene, herein designated TARGET GENE. ZAP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZAP BINDING SITE, designated SEQ ID:10075, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45335] Another function of GAM3229 is therefore inhibition of ZAP (Accession NP_064504.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAP.

[45336] ZFP42 (Accession NP_777560.1) is another GAM3229 target gene, herein designated TARGET GENE. ZFP42 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZFP42, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP42

BINDING SITE, designated SEQ ID:20009, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45337] Another function of GAM3229 is therefore inhibition of ZFP42 (Accession NP_777560.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP42.

[45338] Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_060667.1) is another GAM3229 target gene, herein designated TARGET GENE. ZFP64 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP64, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP64 BINDING SITE, designated SEQ ID:3840, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45339] Another function of GAM3229 is therefore inhibition of Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_060667.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP64.

[45340] Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_071371.2) is another GAM3229 target gene, herein designated TARGET GENE. ZFP64 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP64, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP64 BINDING SITE, designated SEQ ID:3840, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45341] Another function of GAM3229 is therefore inhibition of Zinc finger protein 64 homolog (mouse) (ZFP64, Accession NP_071371.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP64.

[45342] Zinc finger protein 95 homolog (mouse) (ZFP95, Accession NP_659570.1) is another GAM3229 target gene, herein designated TARGET GENE. ZFP95 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP95, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of ZFP95 BINDING SITE, designated SEQ ID:8365, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45343] Another function of GAM3229 is therefore inhibition of Zinc finger protein 95 homolog (mouse) (ZFP95, Accession NP_659570.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP95.

[45344] Zinc finger protein 95 homolog (mouse) (ZFP95, Accession NP_055384.1) is another GAM3229 target gene, herein designated TARGET GENE. ZFP95 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ZFP95, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP95 BINDING SITE, designated SEQ ID:8365, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45345] Another function of GAM3229 is therefore inhibition of Zinc finger protein 95 homolog (mouse) (ZFP95, Accession NP_055384.1) . Accordingly, utilities of GAM3229 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP95.

[45346] Zinc finger protein 138 (clone phz-32) (ZNF138, Accession XP_088081.1) is another GAM3229 target gene, herein designated TARGET GENE. ZNF138 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF138 BINDING SITE, designated SEQ ID:6482, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45347] Another function of GAM3229 is therefore inhibition of Zinc finger protein 138 (clone phz-32) (ZNF138, Accession XP_088081.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF138.

[45348] Zinc finger protein 214 (ZNF214, Accession NP_037381.1) is another GAM3229 target gene, herein designated TARGET GENE. ZNF214 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZNF214, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF214 BINDING SITE, designated SEQ ID:8097, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45349] Another function of GAM3229 is therefore inhibition of Zinc finger protein 214 (ZNF214, Accession NP_037381.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF214.

[45350] Zinc finger protein 264 (ZNF264, Accession NP_003408.1) is another GAM3229 target gene, herein designated TARGET GENE. ZNF264 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF264, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF264 BINDING SITE, designated SEQ ID:1422, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45351] Another function of GAM3229 is therefore inhibition of

Zinc finger protein 264 (ZNF264, Accession NP_003408.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF264.

[45352] Zinc finger protein 273 (ZNF273, Accession XP_088082.1) is another GAM3229 target gene, herein designated TARGET GENE. ZNF273 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF273, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF273 BINDING SITE, designated SEQ ID:16389, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45353] Another function of GAM3229 is therefore inhibition of Zinc finger protein 273 (ZNF273, Accession XP_088082.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF273.

[45354] Zinc finger protein 398 (ZNF398, Accession NP_065832.1) is another GAM3229 target gene, herein designated TARGET GENE. ZNF398 BINDING SITE is a target binding site

found in the 5` untranslated region of multiple transcripts of mRNA encoded by ZNF398, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF398 BINDING SITE, designated SEQ ID:16846, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45355] Another function of GAM3229 is therefore inhibition of Zinc finger protein 398 (ZNF398, Accession NP_065832.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF398.

[45356] ZNF430 (Accession NP_079465.1) is another GAM3229 target gene, herein designated TARGET GENE. ZNF430 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF430, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF430 BINDING SITE, designated SEQ ID:5502, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45357] Another function of GAM3229 is therefore inhibition of ZNF430 (Accession NP_079465.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF430.

[45358] ZNF431 (Accession XP_086098.2) is another GAM3229 target gene, herein designated TARGET GENE. ZNF431 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF431, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF431 BINDING SITE, designated SEQ ID:16935, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45359] Another function of GAM3229 is therefore inhibition of ZNF431 (Accession XP_086098.2) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF431.

[45360] ZNF440 (Accession NP_689570.1) is another GAM3229 target gene, herein designated TARGET GENE. ZNF440 BINDING SITE1 and ZNF440 BINDING SITE2 are target binding sites found in untranslated regions of mRNA en-

coded by ZNF440, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF440 BINDING SITE1 and ZNF440 BINDING SITE2, designated SEQ ID:13052 and SEQ ID:8337 respectively, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45361] Another function of GAM3229 is therefore inhibition of ZNF440 (Accession NP_689570.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF440.

[45362] ZNF450 (Accession NP_055612.1) is another GAM3229 target gene, herein designated TARGET GENE. ZNF450 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF450, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF450 BINDING SITE, designated SEQ ID:14177, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45363] Another function of GAM3229 is therefore inhibition of ZNF450 (Accession NP_055612.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF450.

[45364] Zinc finger protein 74 (cos52) (ZNF74, Accession NP_003417.1) is another GAM3229 target gene, herein designated TARGET GENE. ZNF74 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZNF74, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF74 BINDING SITE, designated SEQ ID:15580, to the nucleotide sequence of GAM3229 RNA, herein designated GAM RNA, also designated SEQ ID:221.

[45365] Another function of GAM3229 is therefore inhibition of Zinc finger protein 74 (cos52) (ZNF74, Accession NP_003417.1) . Accordingly, utilities of GAM3229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF74.

[45366]

[45367] Fig. 8 further provides a conceptual description of a novel

bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 3298 (GAM3298), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[45368] GAM3298 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM3298 was detected is described hereinabove with reference to Figs. 8-15.

[45369] GAM3298 gene, herein designated GAM GENE, and GAM3298 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[45370] GAM3298 gene encodes a GAM3298 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM3298 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3298 precursor RNA is designated SEQ ID:111, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:111 is located at position 131248914 relative to chromosome X.

[45371] GAM3298 precursor RNA folds onto itself, forming GAM3298 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[45372] GAM3298 precursor RNA folds onto itself, forming GAM3298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[45373] Nucleotide sequence of GAM3298 precursor RNA, designated SEQ-ID: 111, and a schematic representation of a predicted secondary folding of GAM3298 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[45374] An enzyme complex designated DICER COMPLEX, `dices` the GAM3298 folded precursor RNA into GAM3298 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM3298 RNA is designated SEQ ID:259, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[45375] GAM3298 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM3298 target RNA, herein designated GAM TARGET RNA. GAM3298 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[45376] GAM3298 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3298 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3298 RNA is an accurate or a partial inversed-reversed se-

quence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM3298 RNA may have a different number of target binding sites in untranslated regions of a GAM3298 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[45377] The complementary binding of GAM3298 RNA, herein designated GAM RNA, to target binding sites on GAM3298 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3298 target RNA into GAM3298 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[45378] It is appreciated that GAM3298 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM3298 target genes. The mRNA of each one of this

plurality of GAM3298 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3298 RNA, herein designated GAM RNA, and which when bound by GAM3298 RNA causes inhibition of translation of respective one or more GAM3298 target proteins.

[45379] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM3298 gene, herein designated GAM GENE, on one or more GAM3298 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[45380] It is appreciated that specific functions and accordingly

utilities of GAM3298 correlate with, and may be deduced from, the identity of the target genes which GAM3298 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[45381]

[45382]

[45383] 15E1.2 (Accession XP_290596.1) is a GAM3298 target gene, herein designated TARGET GENE. 15E1.2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by 15E1.2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of 15E1.2 BINDING SITE, designated SEQ ID:7468, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45384] A function of GAM3298 is therefore inhibition of 15E1.2 (Accession XP_290596.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 15E1.2.

[45385] Atp-binding cassette, sub-family c (cftr/mrp), member 13 (ABCC13, Accession NP_742021.1) is another GAM3298

target gene, herein designated TARGET GENE. ABCC13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABCC13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCC13 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45386] Another function of GAM3298 is therefore inhibition of Atp-binding cassette, sub-family c (cftr/mrp), member 13 (ABCC13, Accession NP_742021.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC13.

[45387] ACATE2 (Accession NP_036464.1) is another GAM3298 target gene, herein designated TARGET GENE. ACATE2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACATE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

ACATE2 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45388] Another function of GAM3298 is therefore inhibition of ACATE2 (Accession NP_036464.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACATE2.

[45389] Adenylate cyclase 1 (brain) (ADCY1, Accession NP_066939.1) is another GAM3298 target gene, herein designated TARGET GENE. ADCY1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADCY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY1 BINDING SITE, designated SEQ ID:14995, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45390] Another function of GAM3298 is therefore inhibition of Adenylate cyclase 1 (brain) (ADCY1, Accession NP_066939.1), a gene which a calmodulin- sensitive adenylyl cyclase. it may play a role in memory acquisition

and learning. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY1.

[45391] The function of ADCY1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.Adenylate cyclase 7 (ADCY7, Accession NP_001105.1) is another GAM3298 target gene, herein designated TARGET GENE. ADCY7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADCY7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY7 BINDING SITE, designated SEQ ID:17337, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45392] Another function of GAM3298 is therefore inhibition of Adenylate cyclase 7 (ADCY7, Accession NP_001105.1), a gene which this a membrane- bound, ca(2+)- inhibitable adenylyl cyclase. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY7.

[45393] The function of ADCY7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM75.1.Agmatine ureohydrolase (agmatinase) (AGMAT, Accession NP_079034.2) is another GAM3298 target gene, herein designated TARGET GENE. AGMAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AGMAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGMAT BINDING SITE, designated SEQ ID:16781, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45394] Another function of GAM3298 is therefore inhibition of Agmatine ureohydrolase (agmatinase) (AGMAT, Accession NP_079034.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGMAT.

[45395] Adenylate kinase 1 (AK1, Accession NP_000467.1) is another GAM3298 target gene, herein designated TARGET GENE. AK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AK1, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AK1 BINDING SITE, designated SEQ ID:816, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45396] Another function of GAM3298 is therefore inhibition of Adenylate kinase 1 (AK1, Accession NP_000467.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AK1.

[45397] Aldehyde dehydrogenase 3 family, member a2 (ALDH3A2, Accession NP_000373.1) is another GAM3298 target gene, herein designated TARGET GENE. ALDH3A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALDH3A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALDH3A2 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45398] Another function of GAM3298 is therefore inhibition of

Aldehyde dehydrogenase 3 family, member a2 (ALDH3A2, Accession NP_000373.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH3A2.

[45399] Aldehyde dehydrogenase 9 family, member a1 (ALDH9A1, Accession NP_000687.2) is another GAM3298 target gene, herein designated TARGET GENE. ALDH9A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALDH9A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALDH9A1 BINDING SITE, designated SEQ ID:3390, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45400] Another function of GAM3298 is therefore inhibition of Aldehyde dehydrogenase 9 family, member a1 (ALDH9A1, Accession NP_000687.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH9A1.

[45401] Ac-like transposable element (ALTE, Accession NP_004720.1) is another GAM3298 target gene, herein designated TARGET GENE. ALTE BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by ALTE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALTE BINDING SITE, designated SEQ ID:525, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45402] Another function of GAM3298 is therefore inhibition of Ac-like transposable element (ALTE, Accession NP_004720.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALTE.

[45403] ANAPC7 (Accession NP_057322.1) is another GAM3298 target gene, herein designated TARGET GENE. ANAPC7 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ANAPC7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANAPC7 BINDING SITE, designated SEQ ID:16150, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45404] Another function of GAM3298 is therefore inhibition of

ANAPC7 (Accession NP_057322.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANAPC7.

[45405] Apolipoprotein l, 1 (APOL1, Accession NP_663318.1) is another GAM3298 target gene, herein designated TARGET GENE. APOL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL1 BINDING SITE, designated SEQ ID:19832, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45406] Another function of GAM3298 is therefore inhibition of Apolipoprotein l, 1 (APOL1, Accession NP_663318.1), a gene which may participate in reverse cholesterol transport from peripheral cells to the liver. and therefore may be associated with Schizophrenia. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Schizophrenia, and of other diseases and clinical conditions associated with APOL1.

[45407] The function of APOL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Apolipoprotein l, 1 (APOL1, Accession NP_003652.2) is another GAM3298 target gene, herein designated TARGET GENE. APOL1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APOL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APOL1 BINDING SITE, designated SEQ ID:19832, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45408] Another function of GAM3298 is therefore inhibition of Apolipoprotein l, 1 (APOL1, Accession NP_003652.2), a gene which may participate in reverse cholesterol transport from peripheral cells to the liver. and therefore may be associated with Schizophrenia. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Schizophrenia, and of other diseases and clinical conditions associated with APOL1.

[45409] The function of APOL1 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1) is another GAM3298 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:15019, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45410] Another function of GAM3298 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[45411] The function of AQP6 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM51.1.Ankyrin repeat and socs box-containing 1 (ASB1, Accession NP_057198.1) is another GAM3298 target gene, herein designated TARGET GENE. ASB1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB1 BINDING SITE, designated SEQ ID:4892, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45412] Another function of GAM3298 is therefore inhibition of Ankyrin repeat and socs box-containing 1 (ASB1, Accession NP_057198.1), a gene which May mediate protein-protein interactions. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB1.

[45413] The function of ASB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Ankyrin repeat and socs box-containing 13 (ASB13, Accession NP_078977.2) is another GAM3298

target gene, herein designated TARGET GENE. ASB13 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASB13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB13 BINDING SITE, designated SEQ ID:17002, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45414] Another function of GAM3298 is therefore inhibition of Ankyrin repeat and socs box-containing 13 (ASB13, Accession NP_078977.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB13.

[45415] Ankyrin repeat and socs box-containing 9 (ASB9, Accession NP_076992.1) is another GAM3298 target gene, herein designated TARGET GENE. ASB9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASB9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB9 BINDING SITE, designated SEQ ID:4781, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45416] Another function of GAM3298 is therefore inhibition of Ankyrin repeat and socs box-containing 9 (ASB9, Accession NP_076992.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB9.

[45417] Activating transcription factor 5 (ATF5, Accession NP_036200.2) is another GAM3298 target gene, herein designated TARGET GENE. ATF5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATF5 BINDING SITE, designated SEQ ID:15319, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45418] Another function of GAM3298 is therefore inhibition of Activating transcription factor 5 (ATF5, Accession NP_036200.2), a gene which binds to cAMP- inducible promoters and is involved in gene transcription. Accordingly, utilities of GAM3298 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with ATF5.

[45419] The function of ATF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.1.Atpase, na+/k+ transporting, alpha 2 (+) polypeptide (ATP1A2, Accession NP_000693.1) is another GAM3298 target gene, herein designated TARGET GENE. ATP1A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP1A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP1A2 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45420] Another function of GAM3298 is therefore inhibition of Atpase, na+/k+ transporting, alpha 2 (+) polypeptide (ATP1A2, Accession NP_000693.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1A2.

[45421] Betaine-homocysteine methyltransferase 2 (BHMT2, Ac-

cession NP_060084.2) is another GAM3298 target gene, herein designated TARGET GENE. BHMT2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BHMT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BHMT2 BINDING SITE, designated SEQ ID:6371, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45422] Another function of GAM3298 is therefore inhibition of Betaine-homocysteine methyltransferase 2 (BHMT2, Accession NP_060084.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BHMT2.

[45423] 3'(2'), 5'-bisphosphate nucleotidase 1 (BPNT1, Accession NP_006076.2) is another GAM3298 target gene, herein designated TARGET GENE. BPNT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BPNT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

BPNT1 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45424] Another function of GAM3298 is therefore inhibition of 3'(2'), 5'-bisphosphate nucleotidase 1 (BPNT1, Accession NP_006076.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BPNT1.

[45425] 3'(2'), 5'-bisphosphate nucleotidase 1 (BPNT1, Accession XP_035738.1) is another GAM3298 target gene, herein designated TARGET GENE. BPNT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BPNT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BPNT1 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45426] Another function of GAM3298 is therefore inhibition of 3'(2'), 5'-bisphosphate nucleotidase 1 (BPNT1, Accession XP_035738.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with BPNT1.

[45427] Btb (poz) domain containing 5 (BTBD5, Accession NP_060128.1) is another GAM3298 target gene, herein designated TARGET GENE. BTBD5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTBD5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTBD5 BINDING SITE, designated SEQ ID:11724, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45428] Another function of GAM3298 is therefore inhibition of Btb (poz) domain containing 5 (BTBD5, Accession NP_060128.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTBD5.

[45429] Butyrophilin, subfamily 1, member a1 (BTN1A1, Accession NP_001723.1) is another GAM3298 target gene, herein designated TARGET GENE. BTN1A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTN1A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTN1A1 BINDING SITE, designated SEQ ID:6923, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45430] Another function of GAM3298 is therefore inhibition of Butyrophilin, subfamily 1, member a1 (BTN1A1, Accession NP_001723.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN1A1.

[45431] Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession NP_008979.2) is another GAM3298 target gene, herein designated TARGET GENE. BTN3A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTN3A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTN3A1 BINDING SITE, designated SEQ ID:2811, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45432] Another function of GAM3298 is therefore inhibition of Butyrophilin, subfamily 3, member a1 (BTN3A1, Accession

NP_008979.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN3A1.

[45433] Butyrophilin, subfamily 3, member a2 (BTN3A2, Accession NP_008978.1) is another GAM3298 target gene, herein designated TARGET GENE. BTN3A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTN3A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTN3A2 BINDING SITE, designated SEQ ID:16180, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45434] Another function of GAM3298 is therefore inhibition of Butyrophilin, subfamily 3, member a2 (BTN3A2, Accession NP_008978.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN3A2.

[45435] C14orf145 (Accession NP_689659.1) is another GAM3298 target gene, herein designated TARGET GENE. C14orf145 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf145, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf145 BINDING SITE, designated SEQ ID:11312, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45436] Another function of GAM3298 is therefore inhibition of C14orf145 (Accession NP_689659.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf145.

[45437] C14orf52 (Accession NP_660148.1) is another GAM3298 target gene, herein designated TARGET GENE. C14orf52 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C14orf52 BINDING SITE, designated SEQ ID:14163, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45438] Another function of GAM3298 is therefore inhibition of C14orf52 (Accession NP_660148.1) . Accordingly, utilities

of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf52.

[45439] Chromosome 1 open reading frame 34 (C1orf34, Accession XP_027172.1) is another GAM3298 target gene, herein designated TARGET GENE. C1orf34 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1orf34, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf34 BINDING SITE, designated SEQ ID:840, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45440] Another function of GAM3298 is therefore inhibition of Chromosome 1 open reading frame 34 (C1orf34, Accession XP_027172.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf34.

[45441] Chromosome 20 open reading frame 11 (C20orf11, Accession NP_060366.1) is another GAM3298 target gene, herein designated TARGET GENE. C20orf11 BINDING SITE is a target binding site found in the 3` untranslated re-

gion of mRNA encoded by C20orf11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf11 BINDING SITE, designated SEQ ID:19207, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45442] Another function of GAM3298 is therefore inhibition of Chromosome 20 open reading frame 11 (C20orf11, Accession NP_060366.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf11.

[45443] Chromosome 20 open reading frame 129 (C20orf129, Accession NP_112181.1) is another GAM3298 target gene, herein designated TARGET GENE. C20orf129 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf129, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf129 BINDING SITE, designated SEQ ID:7920, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45444] Another function of GAM3298 is therefore inhibition of Chromosome 20 open reading frame 129 (C20orf129, Accession NP_112181.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf129.

[45445] Chromosome 20 open reading frame 164 (C20orf164, Accession NP_542790.1) is another GAM3298 target gene, herein designated TARGET GENE. C20orf164 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf164, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf164 BINDING SITE, designated SEQ ID:9547, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45446] Another function of GAM3298 is therefore inhibition of Chromosome 20 open reading frame 164 (C20orf164, Accession NP_542790.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf164.

[45447] Chromosome 20 open reading frame 169 (C20orf169, Accession NP_291020.1) is another GAM3298 target gene,

herein designated TARGET GENE. C20orf169 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf169, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf169 BINDING SITE, designated SEQ ID:16567, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45448] Another function of GAM3298 is therefore inhibition of Chromosome 20 open reading frame 169 (C20orf169, Accession NP_291020.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf169.

[45449] C6orf96 (Accession NP_060379.1) is another GAM3298 target gene, herein designated TARGET GENE. C6orf96 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf96, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf96 BINDING SITE, designated SEQ ID:3433, to the nucleotide sequence of GAM3298 RNA, herein designated

GAM RNA, also designated SEQ ID:259.

[45450] Another function of GAM3298 is therefore inhibition of C6orf96 (Accession NP_060379.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf96.

[45451] Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_722452.1) is another GAM3298 target gene, herein designated TARGET GENE. CABYR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CABYR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CABYR BINDING SITE, designated SEQ ID:5933, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45452] Another function of GAM3298 is therefore inhibition of Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_722452.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with CABYR.

[45453] Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_036321.2) is another GAM3298 target gene, herein designated TARGET GENE. CABYR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CABYR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CABYR BINDING SITE, designated SEQ ID:5933, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45454] Another function of GAM3298 is therefore inhibition of Calcium-binding tyrosine-(y)-phosphorylation regulated (fibrousheathin 2) (CABYR, Accession NP_036321.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CABYR.

[45455] Calcium/calmodulin-dependent protein kinase (cam kinase) ii delta (CAMK2D, Accession NP_742125.1) is another GAM3298 target gene, herein designated TARGET GENE. CAMK2D BINDING SITE is a target binding site

found in the 3` untranslated region of multiple transcripts of mRNA encoded by CAMK2D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMK2D BINDING SITE, designated SEQ ID:879, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45456] Another function of GAM3298 is therefore inhibition of Calcium/calmodulin-dependent protein kinase (cam kinase) ii delta (CAMK2D, Accession NP_742125.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMK2D.

[45457] Calcium/calmodulin-dependent protein kinase (cam kinase) ii delta (CAMK2D, Accession NP_742126.1) is another GAM3298 target gene, herein designated TARGET GENE. CAMK2D BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CAMK2D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMK2D BIND-

ING SITE, designated SEQ ID:879, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45458] Another function of GAM3298 is therefore inhibition of Calcium/calmodulin-dependent protein kinase (cam kinase) ii delta (CAMK2D, Accession NP_742126.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMK2D.

[45459] Cd28 antigen (tp44) (CD28, Accession NP_006130.1) is another GAM3298 target gene, herein designated TARGET GENE. CD28 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD28, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD28 BINDING SITE, designated SEQ ID:6352, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45460] Another function of GAM3298 is therefore inhibition of Cd28 antigen (tp44) (CD28, Accession NP_006130.1), a gene which possibly involved in t- cell activation. Accordingly, utilities of GAM3298 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with CD28.

[45461] The function of CD28 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Cd68 antigen (CD68, Accession NP_001242.1) is another GAM3298 target gene, herein designated TARGET GENE. CD68 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD68, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD68 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45462] Another function of GAM3298 is therefore inhibition of Cd68 antigen (CD68, Accession NP_001242.1), a gene which is highly expressed by human monocytes and tissue macrophages. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD68.

[45463] The function of CD68 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.1.Congenital dyserythropoietic anemia, type i (CDAN1, Accession XP_085300.3) is another GAM3298 target gene, herein designated TARGET GENE. CDAN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDAN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDAN1 BINDING SITE, designated SEQ ID:12246, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45464] Another function of GAM3298 is therefore inhibition of Congenital dyserythropoietic anemia, type i (CDAN1, Accession XP_085300.3) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDAN1.

[45465] Cofilin 2 (muscle) (CFL2, Accession NP_068733.1) is another GAM3298 target gene, herein designated TARGET GENE. CFL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CFL2, corresponding to a target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CFL2 BINDING SITE, designated SEQ ID:16417, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45466] Another function of GAM3298 is therefore inhibition of Cofilin 2 (muscle) (CFL2, Accession NP_068733.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CFL2.

[45467] Claudin 15 (CLDN15, Accession NP_612438.1) is another GAM3298 target gene, herein designated TARGET GENE. CLDN15 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLDN15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLDN15 BINDING SITE, designated SEQ ID:16467, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45468] Another function of GAM3298 is therefore inhibition of Claudin 15 (CLDN15, Accession NP_612438.1) . Accord-

ingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLDN15.

[45469] Cyclin m3 (CNNM3, Accession NP_060093.2) is another GAM3298 target gene, herein designated TARGET GENE. CNNM3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CNNM3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNNM3 BINDING SITE, designated SEQ ID:1930, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45470] Another function of GAM3298 is therefore inhibition of Cyclin m3 (CNNM3, Accession NP_060093.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNNM3.

[45471] Coatomer protein complex, subunit alpha (COPA, Accession NP_004362.1) is another GAM3298 target gene, herein designated TARGET GENE. COPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by COPA, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COPA BINDING SITE, designated SEQ ID:815, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45472] Another function of GAM3298 is therefore inhibition of Coatomer protein complex, subunit alpha (COPA, Accession NP_004362.1), a gene which is invovled protein transport between the endoplasmic reticulum (ER) and Golgi compartments. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COPA.

[45473] The function of COPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.CRN (Accession NP_006578.2) is another GAM3298 target gene, herein designated TARGET GENE. CRN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

CRN BINDING SITE, designated SEQ ID:5868, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45474] Another function of GAM3298 is therefore inhibition of CRN (Accession NP_006578.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRN.

[45475] CRTAM (Accession NP_062550.1) is another GAM3298 target gene, herein designated TARGET GENE. CRTAM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRTAM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRTAM BINDING SITE, designated SEQ ID:840, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45476] Another function of GAM3298 is therefore inhibition of CRTAM (Accession NP_062550.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRTAM.

[45477] CT120 (Accession NP_079068.1) is another GAM3298 target gene, herein designated TARGET GENE. CT120 BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CT120, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CT120 BINDING SITE, designated SEQ ID:13728, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45478] Another function of GAM3298 is therefore inhibition of CT120 (Accession NP_079068.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CT120.

[45479] CYCS (Accession NP_061820.1) is another GAM3298 target gene, herein designated TARGET GENE. CYCS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYCS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYCS BINDING SITE, designated SEQ ID:5995, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45480] Another function of GAM3298 is therefore inhibition of

CYCS (Accession NP_061820.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYCS.

[45481] Dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST, Accession NP_005207.2) is another GAM3298 target gene, herein designated TARGET GENE. DDOST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DDOST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDOST BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45482] Another function of GAM3298 is therefore inhibition of Dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST, Accession NP_005207.2), a gene which transfers high- mannose oligosaccharides to nascent polypeptides. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDOST.

[45483] The function of DDOST and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM347.2.DDX51 (Accession NP_778236.1) is another GAM3298 target gene, herein designated TARGET GENE. DDX51 BINDING SITE1 and DDX51 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DDX51, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX51 BINDING SITE1 and DDX51 BINDING SITE2, designated SEQ ID:5949 and SEQ ID:6665 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45484] Another function of GAM3298 is therefore inhibition of DDX51 (Accession NP_778236.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX51.

[45485] DDX54 (Accession NP_076977.2) is another GAM3298 target gene, herein designated TARGET GENE. DDX54 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DDX54, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of DDX54 BINDING SITE, designated SEQ ID:8510, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45486] Another function of GAM3298 is therefore inhibition of DDX54 (Accession NP_076977.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX54.

[45487] Dead/h (asp-glu-ala-asp/his) box polypeptide 9 (rna helicase a, nuclear dna helicase ii; leukophysin) (DDX9, Accession NP_085077.1) is another GAM3298 target gene, herein designated TARGET GENE. DDX9 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by DDX9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX9 BINDING SITE, designated SEQ ID:12897, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45488] Another function of GAM3298 is therefore inhibition of Dead/h (asp-glu-ala-asp/his) box polypeptide 9 (rna helicase a, nuclear dna helicase ii; leukophysin) (DDX9, Ac-

cession NP_085077.1), a gene which plays an important role in transcription, RNA processing, translation, and RNA replication. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX9.

[45489] The function of DDX9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.DKFZp434E1119 (Accession XP_210937.1) is another GAM3298 target gene, herein designated TARGET GENE. DKFZp434E1119 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434E1119, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434E1119 BINDING SITE, designated SEQ ID:13379, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45490] Another function of GAM3298 is therefore inhibition of DKFZp434E1119 (Accession XP_210937.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZp434E1119.

[45491] DKFZP586C1324 (Accession XP_045876.1) is another GAM3298 target gene, herein designated TARGET GENE. DKFZP586C1324 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586C1324, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586C1324 BINDING SITE, designated SEQ ID:13787, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45492] Another function of GAM3298 is therefore inhibition of DKFZP586C1324 (Accession XP_045876.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586C1324.

[45493] DKFZp761G058 (Accession NP_689755.2) is another GAM3298 target gene, herein designated TARGET GENE. DKFZp761G058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761G058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761G058 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45494] Another function of GAM3298 is therefore inhibition of DKFZp761G058 (Accession NP_689755.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761G058.

[45495] DKFZP761G1913 (Accession NP_113662.1) is another GAM3298 target gene, herein designated TARGET GENE. DKFZP761G1913 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP761G1913, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP761G1913 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45496] Another function of GAM3298 is therefore inhibition of DKFZP761G1913 (Accession NP_113662.1) . Accordingly,

utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761G1913.

[45497] DKFZp761K1423 (Accession NP_060892.1) is another GAM3298 target gene, herein designated TARGET GENE. DKFZp761K1423 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761K1423, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761K1423 BINDING SITE, designated SEQ ID:13788, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45498] Another function of GAM3298 is therefore inhibition of DKFZp761K1423 (Accession NP_060892.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761K1423.

[45499] Endothelial differentiation, sphingolipid g-protein-coupled receptor, 3 (EDG3, Accession NP_005217.1) is another GAM3298 target gene, herein designated TARGET GENE. EDG3 BINDING SITE is a target binding site

found in the 5` untranslated region of mRNA encoded by EDG3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDG3 BINDING SITE, designated SEQ ID:6456, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45500] Another function of GAM3298 is therefore inhibition of Endothelial differentiation, sphingolipid g-protein-coupled receptor, 3 (EDG3, Accession NP_005217.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDG3.

[45501] Eukaryotic translation initiation factor 2c, 1 (EIF2C1, Accession NP_036331.1) is another GAM3298 target gene, herein designated TARGET GENE. EIF2C1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EIF2C1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF2C1 BINDING SITE, designated SEQ ID:17274, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA,

also designated SEQ ID:259.

[45502] Another function of GAM3298 is therefore inhibition of Eukaryotic translation initiation factor 2c, 1 (EIF2C1, Accession NP_036331.1), a gene which plays an important role in the eukaryotic peptide chain initiation process. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2C1.

[45503] The function of EIF2C1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Erythrocyte membrane protein band 4.1 like 4b (EPB41L4B, Accession NP_061987.2) is another GAM3298 target gene, herein designated TARGET GENE. EPB41L4B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EPB41L4B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EPB41L4B BINDING SITE, designated SEQ ID:5651, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45504] Another function of GAM3298 is therefore inhibition of Erythrocyte membrane protein band 4.1 like 4b (EPB41L4B, Accession NP_061987.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPB41L4B.

[45505] ERAP140 (Accession XP_059748.2) is another GAM3298 target gene, herein designated TARGET GENE. ERAP140 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ERAP140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ERAP140 BINDING SITE, designated SEQ ID:7576, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45506] Another function of GAM3298 is therefore inhibition of ERAP140 (Accession XP_059748.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERAP140.

[45507] V-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) (ERBB3, Accession NP_001973.1) is another

GAM3298 target gene, herein designated TARGET GENE. ERBB3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ERBB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ERBB3 BINDING SITE, designated SEQ ID:6353, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45508] Another function of GAM3298 is therefore inhibition of V-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) (ERBB3, Accession NP_001973.1), a gene which binds and is activated by neuregulins and ntak. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERBB3.

[45509] The function of ERBB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.ET (Accession NP_077287.1) is another GAM3298 target gene, herein designated TARGET GENE. ET BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ET, correspond-

ing to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ET BINDING SITE, designated SEQ ID:1920, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45510] Another function of GAM3298 is therefore inhibition of ET (Accession NP_077287.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ET.

[45511] Epithelial v-like antigen 1 (EVA1, Accession NP_005788.1) is another GAM3298 target gene, herein designated TARGET GENE. EVA1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EVA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EVA1 BINDING SITE, designated SEQ ID:11961, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45512] Another function of GAM3298 is therefore inhibition of Epithelial v-like antigen 1 (EVA1, Accession NP_005788.1)

. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVA1.

[45513] Coagulation factor ii (thrombin) receptor-like 3 (F2RL3, Accession NP_003941.1) is another GAM3298 target gene, herein designated TARGET GENE. F2RL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F2RL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F2RL3 BINDING SITE, designated SEQ ID:12961, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45514] Another function of GAM3298 is therefore inhibition of Coagulation factor ii (thrombin) receptor-like 3 (F2RL3, Accession NP_003941.1), a gene which Protease- activated receptor 4; G protein- coupled receptor that increases phosphoinositide hydrolysis. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2RL3.

[45515] The function of F2RL3 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM72.1.Fanconi anemia, complementation group d2 (FANCD2, Accession NP_149075.2) is another GAM3298 target gene, herein designated TARGET GENE. FANCD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCD2 BINDING SITE, designated SEQ ID:9757, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45516] Another function of GAM3298 is therefore inhibition of Fanconi anemia, complementation group d2 (FANCD2, Accession NP_149075.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCD2.

[45517] FBLP-1 (Accession XP_290943.1) is another GAM3298 target gene, herein designated TARGET GENE. FBLP-1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBLP-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBLP-1 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45518] Another function of GAM3298 is therefore inhibition of FBLP-1 (Accession XP_290943.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBLP-1.

[45519] F-box only protein 27 (FBXO27, Accession NP_849142.1) is another GAM3298 target gene, herein designated TARGET GENE. FBXO27 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXO27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXO27 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45520] Another function of GAM3298 is therefore inhibition of F-box only protein 27 (FBXO27, Accession NP_849142.1) . Accordingly, utilities of GAM3298 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with FBXO27.

[45521] F-box only protein 27 (FBXO27, Accession XP_059045.1) is another GAM3298 target gene, herein designated TARGET GENE. FBXO27 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXO27, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXO27 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45522] Another function of GAM3298 is therefore inhibition of F-box only protein 27 (FBXO27, Accession XP_059045.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO27.

[45523] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075263.1) is another GAM3298 target gene, herein designated TARGET

GENE. FGFR2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45524] Another function of GAM3298 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075263.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[45525] Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075262.1) is another GAM3298 target gene, herein designated TARGET GENE. FGFR2 BINDING SITE is a target binding site found

in the 3` untranslated region of multiple transcripts of mRNA encoded by FGFR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45526] Another function of GAM3298 is therefore inhibition of Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2, Accession NP_075262.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2.

[45527] Fk506 binding protein 14, 22 kda (FKBP14, Accession NP_060416.1) is another GAM3298 target gene, herein designated TARGET GENE. FKBP14 BINDING SITE1 and FKBP14 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FKBP14, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FKBP14 BINDING SITE1 and FKBP14 BINDING SITE2, designated SEQ ID:3706 and SEQ ID:17308 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45528] Another function of GAM3298 is therefore inhibition of Fk506 binding protein 14, 22 kda (FKBP14, Accession NP_060416.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKBP14.

[45529] FKSG17 (Accession NP_114420.1) is another GAM3298 target gene, herein designated TARGET GENE. FKSG17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FKSG17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FKSG17 BINDING SITE, designated SEQ ID:18744, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45530] Another function of GAM3298 is therefore inhibition of FKSG17 (Accession NP_114420.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with FKSG17.

[45531] FLJ10058 (Accession NP_060455.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ10058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10058 BINDING SITE, designated SEQ ID:841, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45532] Another function of GAM3298 is therefore inhibition of FLJ10058 (Accession NP_060455.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10058.

[45533] FLJ10665 (Accession NP_060643.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ10665 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10665, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ10665 BINDING SITE, designated SEQ ID:3983, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45534] Another function of GAM3298 is therefore inhibition of FLJ10665 (Accession NP_060643.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10665.

[45535] FLJ10853 (Accession NP_060716.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ10853 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10853, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10853 BINDING SITE, designated SEQ ID:16806, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45536] Another function of GAM3298 is therefore inhibition of FLJ10853 (Accession NP_060716.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10853.

[45537] FLJ11011 (Accession NP_060769.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ11011 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11011, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11011 BINDING SITE, designated SEQ ID:1510, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45538] Another function of GAM3298 is therefore inhibition of FLJ11011 (Accession NP_060769.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11011.

[45539] FLJ11259 (Accession NP_060840.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ11259 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11259, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11259 BINDING SITE, designated SEQ ID:6479, to the

nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45540] Another function of GAM3298 is therefore inhibition of FLJ11259 (Accession NP_060840.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11259.

[45541] FLJ11267 (Accession NP_062553.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ11267 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11267, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11267 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45542] Another function of GAM3298 is therefore inhibition of FLJ11267 (Accession NP_062553.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11267.

[45543] FLJ11996 (Accession NP_079252.1) is another GAM3298

target gene, herein designated TARGET GENE. FLJ11996 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11996, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11996 BINDING SITE, designated SEQ ID:17309, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45544] Another function of GAM3298 is therefore inhibition of FLJ11996 (Accession NP_079252.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11996.

[45545] FLJ12132 (Accession NP_079256.2) is another GAM3298 target gene, herein designated TARGET GENE. FLJ12132 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12132 BINDING SITE, designated SEQ ID:18184, to the nucleotide sequence of GAM3298 RNA, herein designated

GAM RNA, also designated SEQ ID:259.

[45546] Another function of GAM3298 is therefore inhibition of FLJ12132 (Accession NP_079256.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12132.

[45547] FLJ12270 (Accession XP_290704.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ12270 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12270, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12270 BINDING SITE, designated SEQ ID:19970, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45548] Another function of GAM3298 is therefore inhibition of FLJ12270 (Accession XP_290704.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12270.

[45549] FLJ12595 (Accession NP_079270.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ12595

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12595, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12595 BINDING SITE, designated SEQ ID:2951, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45550] Another function of GAM3298 is therefore inhibition of FLJ12595 (Accession NP_079270.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12595.

[45551] FLJ13114 (Accession NP_078817.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ13114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13114 BINDING SITE, designated SEQ ID:14687, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45552] Another function of GAM3298 is therefore inhibition of FLJ13114 (Accession NP_078817.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13114.

[45553] FLJ13456 (Accession XP_038291.5) is another GAM3298 target gene, herein designated TARGET GENE. FLJ13456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13456 BINDING SITE, designated SEQ ID:20122, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45554] Another function of GAM3298 is therefore inhibition of FLJ13456 (Accession XP_038291.5) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13456.

[45555] FLJ13621 (Accession NP_079285.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ13621 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ13621, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13621 BINDING SITE, designated SEQ ID:16777, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45556] Another function of GAM3298 is therefore inhibition of FLJ13621 (Accession NP_079285.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13621.

[45557] FLJ14082 (Accession NP_079300.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ14082 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14082, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14082 BINDING SITE, designated SEQ ID:13784, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45558] Another function of GAM3298 is therefore inhibition of

FLJ14082 (Accession NP_079300.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14082.

[45559] FLJ14107 (Accession NP_079302.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ14107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14107 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45560] Another function of GAM3298 is therefore inhibition of FLJ14107 (Accession NP_079302.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14107.

[45561] FLJ14399 (Accession NP_116169.2) is another GAM3298 target gene, herein designated TARGET GENE. FLJ14399 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14399, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14399 BINDING SITE, designated SEQ ID:7464, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45562] Another function of GAM3298 is therefore inhibition of FLJ14399 (Accession NP_116169.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14399.

[45563] FLJ14642 (Accession NP_116207.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ14642 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14642, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14642 BINDING SITE, designated SEQ ID:816, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45564] Another function of GAM3298 is therefore inhibition of FLJ14642 (Accession NP_116207.1) . Accordingly, utilities

of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14642.

[45565] FLJ14888 (Accession NP_116245.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ14888 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14888, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14888 BINDING SITE, designated SEQ ID:17382, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45566] Another function of GAM3298 is therefore inhibition of FLJ14888 (Accession NP_116245.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14888.

[45567] FLJ20059 (Accession NP_060114.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ20059 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20059, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20059 BINDING SITE, designated SEQ ID:841, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45568] Another function of GAM3298 is therefore inhibition of FLJ20059 (Accession NP_060114.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20059.

[45569] FLJ20359 (Accession NP_060251.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ20359 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20359, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20359 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45570] Another function of GAM3298 is therefore inhibition of FLJ20359 (Accession NP_060251.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20359.

[45571] FLJ20452 (Accession NP_060298.2) is another GAM3298 target gene, herein designated TARGET GENE. FLJ20452 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20452, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20452 BINDING SITE, designated SEQ ID:16046, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45572] Another function of GAM3298 is therefore inhibition of FLJ20452 (Accession NP_060298.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20452.

[45573] FLJ20464 (Accession NP_060304.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ20464 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20464, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ20464 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45574] Another function of GAM3298 is therefore inhibition of FLJ20464 (Accession NP_060304.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20464.

[45575] FLJ20582 (Accession XP_090970.4) is another GAM3298 target gene, herein designated TARGET GENE. FLJ20582 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20582, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20582 BINDING SITE, designated SEQ ID:5838, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45576] Another function of GAM3298 is therefore inhibition of FLJ20582 (Accession XP_090970.4) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20582.

[45577] FLJ20700 (Accession NP_060402.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ20700 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20700, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20700 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45578] Another function of GAM3298 is therefore inhibition of FLJ20700 (Accession NP_060402.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20700.

[45579] FLJ21144 (Accession NP_073611.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ21144 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21144, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ21144 BINDING SITE, designated SEQ ID:20084, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45580] Another function of GAM3298 is therefore inhibition of FLJ21144 (Accession NP_073611.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21144.

[45581] FLJ21369 (Accession NP_079078.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ21369 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21369, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21369 BINDING SITE, designated SEQ ID:18903, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45582] Another function of GAM3298 is therefore inhibition of FLJ21369 (Accession NP_079078.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21369.

[45583] FLJ21673 (Accession NP_112160.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ21673 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21673, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21673 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45584] Another function of GAM3298 is therefore inhibition of FLJ21673 (Accession NP_112160.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21673.

[45585] FLJ21870 (Accession NP_075392.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ21870 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21870, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21870 BINDING SITE, designated SEQ ID:3706, to the

nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45586] Another function of GAM3298 is therefore inhibition of FLJ21870 (Accession NP_075392.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21870.

[45587] FLJ23042 (Accession NP_079433.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ23042 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23042, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23042 BINDING SITE, designated SEQ ID:6627, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45588] Another function of GAM3298 is therefore inhibition of FLJ23042 (Accession NP_079433.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23042.

[45589] FLJ23129 (Accession NP_079039.1) is another GAM3298

target gene, herein designated TARGET GENE. FLJ23129 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23129, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23129 BINDING SITE, designated SEQ ID:730, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45590] Another function of GAM3298 is therefore inhibition of FLJ23129 (Accession NP_079039.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23129.

[45591] FLJ23235 (Accession NP_079219.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ23235 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23235, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23235 BINDING SITE, designated SEQ ID:14990, to the nucleotide sequence of GAM3298 RNA, herein designated

GAM RNA, also designated SEQ ID:259.

[45592] Another function of GAM3298 is therefore inhibition of FLJ23235 (Accession NP_079219.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23235.

[45593] FLJ23360 (Accession NP_075564.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ23360 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23360, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23360 BINDING SITE, designated SEQ ID:17938, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45594] Another function of GAM3298 is therefore inhibition of FLJ23360 (Accession NP_075564.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23360.

[45595] FLJ23447 (Accession NP_079101.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ23447

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23447, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23447 BINDING SITE, designated SEQ ID:8160, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45596] Another function of GAM3298 is therefore inhibition of FLJ23447 (Accession NP_079101.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23447.

[45597] FLJ23499 (Accession NP_073598.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ23499 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23499, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23499 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45598] Another function of GAM3298 is therefore inhibition of FLJ23499 (Accession NP_073598.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23499.

[45599] FLJ23499 (Accession NP_073598.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ23499 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23499, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23499 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45600] Another function of GAM3298 is therefore inhibition of FLJ23499 (Accession NP_073598.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23499.

[45601] FLJ23751 (Accession NP_689495.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ23751 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ23751, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23751 BINDING SITE, designated SEQ ID:5102, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45602] Another function of GAM3298 is therefore inhibition of FLJ23751 (Accession NP_689495.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23751.

[45603] FLJ23834 (Accession NP_689963.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ23834 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23834 BINDING SITE, designated SEQ ID:8593, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45604] Another function of GAM3298 is therefore inhibition of

FLJ23834 (Accession NP_689963.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23834.

[45605] FLJ25179 (Accession NP_653271.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ25179 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25179, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25179 BINDING SITE, designated SEQ ID:8989, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45606] Another function of GAM3298 is therefore inhibition of FLJ25179 (Accession NP_653271.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25179.

[45607] FLJ30317 (Accession NP_742148.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ30317 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30317, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30317 BINDING SITE, designated SEQ ID:14675, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45608] Another function of GAM3298 is therefore inhibition of FLJ30317 (Accession NP_742148.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30317.

[45609] FLJ30899 (Accession NP_689943.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ30899 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30899 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45610] Another function of GAM3298 is therefore inhibition of FLJ30899 (Accession NP_689943.1) . Accordingly, utilities

of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30899.

[45611] FLJ31208 (Accession NP_694568.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ31208 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31208, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31208 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45612] Another function of GAM3298 is therefore inhibition of FLJ31208 (Accession NP_694568.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31208.

[45613] FLJ31434 (Accession NP_689709.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ31434 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31434, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31434 BINDING SITE, designated SEQ ID:7468, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45614] Another function of GAM3298 is therefore inhibition of FLJ31434 (Accession NP_689709.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31434.

[45615] FLJ31659 (Accession NP_694572.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ31659 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31659, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31659 BINDING SITE, designated SEQ ID:18701, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45616] Another function of GAM3298 is therefore inhibition of FLJ31659 (Accession NP_694572.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ31659.

[45617] FLJ31842 (Accession NP_689700.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ31842 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31842 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45618] Another function of GAM3298 is therefore inhibition of FLJ31842 (Accession NP_689700.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31842.

[45619] FLJ31882 (Accession NP_689673.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ31882 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31882, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ31882 BINDING SITE, designated SEQ ID:9354, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45620] Another function of GAM3298 is therefore inhibition of FLJ31882 (Accession NP_689673.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31882.

[45621] FLJ32029 (Accession NP_775853.2) is another GAM3298 target gene, herein designated TARGET GENE. FLJ32029 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32029, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32029 BINDING SITE, designated SEQ ID:840, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45622] Another function of GAM3298 is therefore inhibition of FLJ32029 (Accession NP_775853.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ32029.

[45623] FLJ32833 (Accession NP_689701.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ32833 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32833, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32833 BINDING SITE, designated SEQ ID:16532, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45624] Another function of GAM3298 is therefore inhibition of FLJ32833 (Accession NP_689701.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32833.

[45625] FLJ33167 (Accession NP_689896.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ33167 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ33167 BINDING SITE, designated SEQ ID:10382, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45626] Another function of GAM3298 is therefore inhibition of FLJ33167 (Accession NP_689896.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33167.

[45627] FLJ33505 (Accession NP_689530.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ33505 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33505, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33505 BINDING SITE, designated SEQ ID:17309, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45628] Another function of GAM3298 is therefore inhibition of FLJ33505 (Accession NP_689530.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33505.

[45629] FLJ34917 (Accession NP_694995.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ34917 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ34917, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34917 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45630] Another function of GAM3298 is therefore inhibition of FLJ34917 (Accession NP_694995.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34917.

[45631] FLJ37228 (Accession NP_787113.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ37228 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37228, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37228 BINDING SITE, designated SEQ ID:3706, to the

nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45632] Another function of GAM3298 is therefore inhibition of FLJ37228 (Accession NP_787113.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37228.

[45633] FLJ38690 (Accession NP_848608.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ38690 BINDING SITE1 and FLJ38690 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38690, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38690 BINDING SITE1 and FLJ38690 BINDING SITE2, designated SEQ ID:3706 and SEQ ID:7398 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45634] Another function of GAM3298 is therefore inhibition of FLJ38690 (Accession NP_848608.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ38690.

[45635] FLJ38991 (Accession NP_776188.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ38991 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38991, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38991 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45636] Another function of GAM3298 is therefore inhibition of FLJ38991 (Accession NP_776188.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38991.

[45637] FLJ39005 (Accession NP_848616.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ39005 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39005, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ39005 BINDING SITE, designated SEQ ID:16046, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45638] Another function of GAM3298 is therefore inhibition of FLJ39005 (Accession NP_848616.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39005.

[45639] FLJ90165 (Accession NP_699169.1) is another GAM3298 target gene, herein designated TARGET GENE. FLJ90165 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ90165, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ90165 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45640] Another function of GAM3298 is therefore inhibition of FLJ90165 (Accession NP_699169.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ90165.

[45641] FRSB (Accession NP_005678.2) is another GAM3298 target gene, herein designated TARGET GENE. FRSB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FRSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FRSB BINDING SITE, designated SEQ ID:840, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45642] Another function of GAM3298 is therefore inhibition of FRSB (Accession NP_005678.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FRSB.

[45643] Udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 7 (galnac-t7) (GALNT7, Accession NP_473451.2) is another GAM3298 target gene, herein designated TARGET GENE. GALNT7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GALNT7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of GALNT7 BINDING SITE, designated SEQ ID:6665, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45644] Another function of GAM3298 is therefore inhibition of Udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 7 (galnac-t7) (GALNT7, Accession NP_473451.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNT7.

[45645] GBP4 (Accession NP_443173.2) is another GAM3298 target gene, herein designated TARGET GENE. GBP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GBP4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GBP4 BINDING SITE, designated SEQ ID:7240, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45646] Another function of GAM3298 is therefore inhibition of GBP4 (Accession NP_443173.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GBP4.

[45647] GK001 (Accession NP_064583.1) is another GAM3298 target gene, herein designated TARGET GENE. GK001 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GK001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GK001 BINDING SITE, designated SEQ ID:11534, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45648] Another function of GAM3298 is therefore inhibition of GK001 (Accession NP_064583.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GK001.

[45649] Glyoxalase i (GLO1, Accession NP_006699.1) is another GAM3298 target gene, herein designated TARGET GENE. GLO1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GLO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GLO1 BINDING SITE, designated SEQ ID:4209, to the nucleotide sequence of GAM3298 RNA, herein designated

GAM RNA, also designated SEQ ID:259.

[45650] Another function of GAM3298 is therefore inhibition of Glyoxalase i (GLO1, Accession NP_006699.1), a gene which converts methylglyoxal and glutathione to S- lactoylglutathione. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLO1.

[45651] The function of GLO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1550.1.G protein-coupled receptor 6 (GPR6, Accession NP_005275.1) is another GAM3298 target gene, herein designated TARGET GENE. GPR6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR6 BINDING SITE, designated SEQ ID:4712, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45652] Another function of GAM3298 is therefore inhibition of G protein-coupled receptor 6 (GPR6, Accession

NP_005275.1), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR6.

[45653] The function of GPR6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM203.2.G protein-coupled receptor kinase 7 (GPRK7, Accession NP_631948.1) is another GAM3298 target gene, herein designated TARGET GENE. GPRK7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPRK7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPRK7 BINDING SITE, designated SEQ ID:12104, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45654] Another function of GAM3298 is therefore inhibition of G protein-coupled receptor kinase 7 (GPRK7, Accession NP_631948.1), a gene which regulates the G protein-coupled receptors. Accordingly, utilities of GAM3298 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with GPRK7.

[45655] The function of GPRK7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.GRIPE (Accession XP_170749.4) is another GAM3298 target gene, herein designated TARGET GENE. GRIPE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GRIPE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRIPE BINDING SITE, designated SEQ ID:2629, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45656] Another function of GAM3298 is therefore inhibition of GRIPE (Accession XP_170749.4) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIPE.

[45657] Gtp binding protein 5 (putative) (GTPBP5, Accession NP_056481.1) is another GAM3298 target gene, herein designated TARGET GENE. GTPBP5 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by GTPBP5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTPBP5 BINDING SITE, designated SEQ ID:17309, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45658] Another function of GAM3298 is therefore inhibition of Gtp binding protein 5 (putative) (GTPBP5, Accession NP_056481.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTPBP5.

[45659] H2a histone family, member j (H2AFJ, Accession NP_060737.1) is another GAM3298 target gene, herein designated TARGET GENE. H2AFJ BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H2AFJ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H2AFJ BINDING SITE, designated SEQ ID:11330, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45660] Another function of GAM3298 is therefore inhibition of H2a histone family, member j (H2AFJ, Accession NP_060737.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H2AFJ.

[45661] HIG2 (Accession NP_037464.1) is another GAM3298 target gene, herein designated TARGET GENE. HIG2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HIG2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIG2 BINDING SITE, designated SEQ ID:840, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45662] Another function of GAM3298 is therefore inhibition of HIG2 (Accession NP_037464.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIG2.

[45663] Histocompatibility (minor) 13 (HM13, Accession NP_848697.1) is another GAM3298 target gene, herein designated TARGET GENE. HM13 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by HM13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HM13 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45664] Another function of GAM3298 is therefore inhibition of Histocompatibility (minor) 13 (HM13, Accession NP_848697.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HM13.

[45665] HSPC043 (Accession NP_067041.1) is another GAM3298 target gene, herein designated TARGET GENE. HSPC043 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSPC043, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPC043 BINDING SITE, designated SEQ ID:16780, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45666] Another function of GAM3298 is therefore inhibition of

HSPC043 (Accession NP_067041.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC043.

[45667] Interferon-induced protein with tetratricopeptide repeats 4 (IFIT4, Accession NP_001540.2) is another GAM3298 target gene, herein designated TARGET GENE. IFIT4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IFIT4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IFIT4 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45668] Another function of GAM3298 is therefore inhibition of Interferon-induced protein with tetratricopeptide repeats 4 (IFIT4, Accession NP_001540.2), a gene which is an interferon- induced protein. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IFIT4.

[45669] The function of IFIT4 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM347.1.Interleukin 12 receptor, beta 2 (IL12RB2, Accession NP_001550.1) is another GAM3298 target gene, herein designated TARGET GENE. IL12RB2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL12RB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL12RB2 BINDING SITE, designated SEQ ID:5498, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45670] Another function of GAM3298 is therefore inhibition of Interleukin 12 receptor, beta 2 (IL12RB2, Accession NP_001550.1), a gene which is involved in il- 12 transduction. binds to il- 12 with a low affinity. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL12RB2.

[45671] The function of IL12RB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM374.1.IL23R (Accession NP_653302.2) is another

GAM3298 target gene, herein designated TARGET GENE. IL23R BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL23R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL23R BINDING SITE, designated SEQ ID:15196, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45672] Another function of GAM3298 is therefore inhibition of IL23R (Accession NP_653302.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL23R.

[45673] Inositol polyphosphate-5-phosphatase, 75kda (INPP5B, Accession XP_300739.1) is another GAM3298 target gene, herein designated TARGET GENE. INPP5B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INPP5B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INPP5B BINDING SITE, designated SEQ ID:19238, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA,

also designated SEQ ID:259.

[45674] Another function of GAM3298 is therefore inhibition of Inositol polyphosphate-5-phosphatase, 75kda (INPP5B, Accession XP_300739.1), a gene which hydrolyzes the calcium- mobilizing second messenger ins(1,4,5)p3. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INPP5B.

[45675] The function of INPP5B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.1.Interleukin-1 receptor-associated kinase 4 (IRAK4, Accession NP_057207.1) is another GAM3298 target gene, herein designated TARGET GENE. IRAK4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IRAK4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRAK4 BINDING SITE, designated SEQ ID:16303, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45676] Another function of GAM3298 is therefore inhibition of

Interleukin-1 receptor-associated kinase 4 (IRAK4, Accession NP_057207.1), a gene which may function as an IRAK1 kinase, triggering a cascade of phosphorylation events. and therefore may be associated with Renal tumors. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Renal tumors, and of other diseases and clinical conditions associated with IRAK4.

[45677] The function of IRAK4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Il2-inducible t-cell kinase (ITK, Accession NP_005537.3) is another GAM3298 target gene, herein designated TARGET GENE. ITK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ITK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITK BINDING SITE, designated SEQ ID:19655, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45678] Another function of GAM3298 is therefore inhibition of Il2-inducible t-cell kinase (ITK, Accession NP_005537.3),

a gene which plays a role in t cell proliferation and differentiation. and therefore may be associated with Myelodysplastic syndrome. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Myelodysplastic syndrome, and of other diseases and clinical conditions associated with ITK.

[45679] The function of ITK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.Potassium voltage-gated channel, shaker-related subfamily, member 7 (KCNA7, Accession NP_114092.2) is another GAM3298 target gene, herein designated TARGET GENE. KCNA7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KCNA7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNA7 BINDING SITE, designated SEQ ID:11198, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45680] Another function of GAM3298 is therefore inhibition of Potassium voltage-gated channel, shaker-related subfam-

ily, member 7 (KCNA7, Accession NP_114092.2), a gene which allows nerve cells to efficiently repolarize following an action potential. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNA7.

[45681] The function of KCNA7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.KIAA0356 (Accession XP_038655.4) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0356 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0356 BINDING SITE, designated SEQ ID:11293, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45682] Another function of GAM3298 is therefore inhibition of KIAA0356 (Accession XP_038655.4) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0356.

[45683] KIAA0391 (Accession NP_055487.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0391 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0391, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0391 BINDING SITE, designated SEQ ID:18795, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45684] Another function of GAM3298 is therefore inhibition of KIAA0391 (Accession NP_055487.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0391.

[45685] KIAA0408 (Accession NP_055517.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0408 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA0408 BINDING SITE, designated SEQ ID:7576, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45686] Another function of GAM3298 is therefore inhibition of KIAA0408 (Accession NP_055517.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0408.

[45687] KIAA0446 (Accession XP_044155.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0446 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0446, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0446 BINDING SITE, designated SEQ ID:1087, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45688] Another function of GAM3298 is therefore inhibition of KIAA0446 (Accession XP_044155.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0446.

[45689] KIAA0514 (Accession NP_055511.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0514 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0514, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0514 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45690] Another function of GAM3298 is therefore inhibition of KIAA0514 (Accession NP_055511.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0514.

[45691] KIAA0628 (Accession NP_055604.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0628 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0628, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0628 BINDING SITE, designated SEQ ID:5410, to the

nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45692] Another function of GAM3298 is therefore inhibition of KIAA0628 (Accession NP_055604.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0628.

[45693] KIAA0831 (Accession NP_055739.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0831 BINDING SITE1 and KIAA0831 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0831, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0831 BINDING SITE1 and KIAA0831 BINDING SITE2, designated SEQ ID:840 and SEQ ID:19561 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45694] Another function of GAM3298 is therefore inhibition of KIAA0831 (Accession NP_055739.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0831.

[45695] KIAA0872 (Accession NP_055755.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0872 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0872, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0872 BINDING SITE, designated SEQ ID:10203, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45696] Another function of GAM3298 is therefore inhibition of KIAA0872 (Accession NP_055755.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0872.

[45697] KIAA0889 (Accession NP_056192.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0889 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA0889, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of KIAA0889 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45698] Another function of GAM3298 is therefore inhibition of KIAA0889 (Accession NP_056192.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0889.

[45699] KIAA0913 (Accession XP_044347.3) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0913 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0913, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0913 BINDING SITE, designated SEQ ID:12246, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45700] Another function of GAM3298 is therefore inhibition of KIAA0913 (Accession XP_044347.3) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0913.

[45701] KIAA0953 (Accession XP_039733.2) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0953 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0953, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0953 BINDING SITE, designated SEQ ID:6353, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45702] Another function of GAM3298 is therefore inhibition of KIAA0953 (Accession XP_039733.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0953.

[45703] KIAA0982 (Accession NP_054742.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0982 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0982, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA0982 BINDING SITE, designated SEQ ID:4347, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45704] Another function of GAM3298 is therefore inhibition of KIAA0982 (Accession NP_054742.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0982.

[45705] KIAA0992 (Accession NP_057165.2) is another GAM3298 target gene, herein designated TARGET GENE. KIAA0992 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0992, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0992 BINDING SITE, designated SEQ ID:16161, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45706] Another function of GAM3298 is therefore inhibition of KIAA0992 (Accession NP_057165.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0992.

[45707] KIAA1194 (Accession NP_056270.2) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1194 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1194 BINDING SITE, designated SEQ ID:12999, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45708] Another function of GAM3298 is therefore inhibition of KIAA1194 (Accession NP_056270.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1194.

[45709] KIAA1377 (Accession XP_040708.2) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1377 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1377, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1377 BINDING SITE, designated SEQ ID:9122, to the

nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45710] Another function of GAM3298 is therefore inhibition of KIAA1377 (Accession XP_040708.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1377.

[45711] KIAA1456 (Accession XP_040100.3) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1456 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45712] Another function of GAM3298 is therefore inhibition of KIAA1456 (Accession XP_040100.3) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1456.

[45713] KIAA1559 (Accession XP_054472.2) is another GAM3298

target gene, herein designated TARGET GENE. KIAA1559 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1559, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1559 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45714] Another function of GAM3298 is therefore inhibition of KIAA1559 (Accession XP_054472.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1559.

[45715] KIAA1595 (Accession XP_045520.5) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1595 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1595, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1595 BINDING SITE, designated SEQ ID:11215, to the nucleotide sequence of GAM3298 RNA, herein designated

GAM RNA, also designated SEQ ID:259.

[45716] Another function of GAM3298 is therefore inhibition of KIAA1595 (Accession XP_045520.5) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1595.

[45717] KIAA1630 (Accession NP_061176.2) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1630 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1630, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1630 BINDING SITE, designated SEQ ID:8338, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45718] Another function of GAM3298 is therefore inhibition of KIAA1630 (Accession NP_061176.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1630.

[45719] KIAA1724 (Accession XP_040280.2) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1724

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1724, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1724 BINDING SITE, designated SEQ ID:20160, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45720] Another function of GAM3298 is therefore inhibition of KIAA1724 (Accession XP_040280.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1724.

[45721] KIAA1727 (Accession XP_034262.4) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1727 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1727, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1727 BINDING SITE, designated SEQ ID:10851, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45722] Another function of GAM3298 is therefore inhibition of KIAA1727 (Accession XP_034262.4) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1727.

[45723] KIAA1735 (Accession XP_290496.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1735 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1735 BINDING SITE, designated SEQ ID:6665, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45724] Another function of GAM3298 is therefore inhibition of KIAA1735 (Accession XP_290496.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1735.

[45725] KIAA1771 (Accession XP_086404.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1771 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1771, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1771 BINDING SITE, designated SEQ ID:7993, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45726] Another function of GAM3298 is therefore inhibition of KIAA1771 (Accession XP_086404.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1771.

[45727] KIAA1871 (Accession XP_290737.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1871 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1871, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1871 BINDING SITE, designated SEQ ID:18994, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45728] Another function of GAM3298 is therefore inhibition of

KIAA1871 (Accession XP_290737.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1871.

[45729] KIAA1950 (Accession XP_166532.1) is another GAM3298 target gene, herein designated TARGET GENE. KIAA1950 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1950, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1950 BINDING SITE, designated SEQ ID:6327, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45730] Another function of GAM3298 is therefore inhibition of KIAA1950 (Accession XP_166532.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1950.

[45731] KIF11 (Accession NP_004514.2) is another GAM3298 target gene, herein designated TARGET GENE. KIF11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIF11, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIF11 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45732] Another function of GAM3298 is therefore inhibition of KIF11 (Accession NP_004514.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF11.

[45733] Kinesin family member 3b (KIF3B, Accession NP_004789.1) is another GAM3298 target gene, herein designated TARGET GENE. KIF3B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIF3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIF3B BINDING SITE, designated SEQ ID:14234, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45734] Another function of GAM3298 is therefore inhibition of Kinesin family member 3b (KIF3B, Accession

NP_004789.1), a gene which is a microtubule- based anterograde translocator for membranous organelles. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF3B.

[45735] The function of KIF3B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Karyopherin (importin) beta 3 (KPNB3, Accession NP_002262.3) is another GAM3298 target gene, herein designated TARGET GENE. KPNB3 BINDING SITE1 and KPNB3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KPNB3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KPNB3 BINDING SITE1 and KPNB3 BINDING SITE2, designated SEQ ID:7119 and SEQ ID:18083 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45736] Another function of GAM3298 is therefore inhibition of Karyopherin (importin) beta 3 (KPNB3, Accession NP_002262.3) . Accordingly, utilities of GAM3298 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with KPNB3.

[45737] Kringle containing transmembrane protein 1 (KREMEN1, Accession NP_114434.3) is another GAM3298 target gene, herein designated TARGET GENE. KREMEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KREMEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KREMEN1 BINDING SITE, designated SEQ ID:841, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45738] Another function of GAM3298 is therefore inhibition of Kringle containing transmembrane protein 1 (KREMEN1, Accession NP_114434.3) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KREMEN1.

[45739] Link-GEFII (Accession NP_057423.1) is another GAM3298 target gene, herein designated TARGET GENE. Link-GEFII BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Link-GEFII, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Link-GEFII BINDING SITE, designated SEQ ID:15182, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45740] Another function of GAM3298 is therefore inhibition of Link-GEFII (Accession NP_057423.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Link-GEFII.

[45741] LOC115129 (Accession XP_055292.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC115129 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC115129, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115129 BINDING SITE, designated SEQ ID:8061, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45742] Another function of GAM3298 is therefore inhibition of LOC115129 (Accession XP_055292.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115129.

[45743] LOC116143 (Accession NP_612467.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC116143 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC116143, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC116143 BINDING SITE, designated SEQ ID:7468, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45744] Another function of GAM3298 is therefore inhibition of LOC116143 (Accession NP_612467.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116143.

[45745] LOC116228 (Accession XP_300752.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC116228 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC116228, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC116228 BINDING SITE, designated SEQ ID:815, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45746] Another function of GAM3298 is therefore inhibition of LOC116228 (Accession XP_300752.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116228.

[45747] LOC124411 (Accession XP_058804.4) is another GAM3298 target gene, herein designated TARGET GENE. LOC124411 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC124411, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC124411 BINDING SITE, designated SEQ ID:9305, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45748] Another function of GAM3298 is therefore inhibition of LOC124411 (Accession XP_058804.4) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124411.

[45749] LOC130574 (Accession XP_059451.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC130574 BINDING SITE1 and LOC130574 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC130574, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130574 BINDING SITE1 and LOC130574 BINDING SITE2, designated SEQ ID:5219 and SEQ ID:10337 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45750] Another function of GAM3298 is therefore inhibition of LOC130574 (Accession XP_059451.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130574.

[45751] LOC132724 (Accession XP_068002.4) is another

GAM3298 target gene, herein designated TARGET GENE. LOC132724 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC132724, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC132724 BINDING SITE, designated SEQ ID:8048, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45752] Another function of GAM3298 is therefore inhibition of LOC132724 (Accession XP_068002.4) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132724.

[45753] LOC134147 (Accession NP_620164.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC134147 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC134147, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC134147 BINDING SITE, desig-

nated SEQ ID:11885, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45754] Another function of GAM3298 is therefore inhibition of LOC134147 (Accession NP_620164.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC134147.

[45755] LOC142779 (Accession XP_084337.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC142779 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC142779, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC142779 BINDING SITE, designated SEQ ID:9354, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45756] Another function of GAM3298 is therefore inhibition of LOC142779 (Accession XP_084337.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC142779.

[45757] LOC143458 (Accession NP_777562.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC143458 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC143458, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143458 BINDING SITE, designated SEQ ID:19260, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45758] Another function of GAM3298 is therefore inhibition of LOC143458 (Accession NP_777562.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143458.

[45759] LOC144817 (Accession XP_084972.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC144817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144817 BINDING SITE, designated SEQ ID:7468, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45760] Another function of GAM3298 is therefore inhibition of LOC144817 (Accession XP_084972.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144817.

[45761] LOC144845 (Accession NP_612483.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC144845 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144845, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144845 BINDING SITE, designated SEQ ID:7468, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45762] Another function of GAM3298 is therefore inhibition of LOC144845 (Accession NP_612483.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144845.

[45763] LOC145231 (Accession XP_096740.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC145231 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145231, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145231 BINDING SITE, designated SEQ ID:16046, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45764] Another function of GAM3298 is therefore inhibition of LOC145231 (Accession XP_096740.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145231.

[45765] LOC145663 (Accession XP_096829.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC145663 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC145663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145663 BINDING SITE, designated SEQ ID:6352, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45766] Another function of GAM3298 is therefore inhibition of LOC145663 (Accession XP_096829.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145663.

[45767] LOC145757 (Accession XP_085227.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC145757 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145757, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145757 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45768] Another function of GAM3298 is therefore inhibition of LOC145757 (Accession XP_085227.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145757.

[45769] LOC145824 (Accession XP_085247.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC145824 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145824, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145824 BINDING SITE, designated SEQ ID:14990, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45770] Another function of GAM3298 is therefore inhibition of LOC145824 (Accession XP_085247.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145824.

[45771] LOC146013 (Accession XP_096919.1) is another GAM3298 target gene, herein designated TARGET GENE.

LOC146013 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146013, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146013 BINDING SITE, designated SEQ ID:8603, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45772] Another function of GAM3298 is therefore inhibition of LOC146013 (Accession XP_096919.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146013.

[45773] LOC146958 (Accession XP_097142.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC146958 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146958, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146958 BINDING SITE, designated SEQ ID:11424, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45774] Another function of GAM3298 is therefore inhibition of LOC146958 (Accession XP_097142.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146958.

[45775] LOC147841 (Accession XP_085924.2) is another GAM3298 target gene, herein designated TARGET GENE. LOC147841 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147841, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147841 BINDING SITE, designated SEQ ID:16695, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45776] Another function of GAM3298 is therefore inhibition of LOC147841 (Accession XP_085924.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147841.

[45777] LOC149464 (Accession XP_097645.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC149464 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149464, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149464 BINDING SITE, designated SEQ ID:7723, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45778] Another function of GAM3298 is therefore inhibition of LOC149464 (Accession XP_097645.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149464.

[45779] LOC149910 (Accession XP_086699.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC149910 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149910, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC149910 BINDING SITE, designated SEQ ID:3001, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45780] Another function of GAM3298 is therefore inhibition of LOC149910 (Accession XP_086699.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149910.

[45781] LOC150225 (Accession XP_097870.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC150225 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150225, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150225 BINDING SITE, designated SEQ ID:10727, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45782] Another function of GAM3298 is therefore inhibition of LOC150225 (Accession XP_097870.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC150225.

[45783] LOC150287 (Accession XP_086889.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC150287 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150287, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150287 BINDING SITE, designated SEQ ID:3702, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45784] Another function of GAM3298 is therefore inhibition of LOC150287 (Accession XP_086889.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150287.

[45785] LOC150299 (Accession XP_097869.2) is another GAM3298 target gene, herein designated TARGET GENE. LOC150299 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150299, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150299 BINDING SITE, designated SEQ ID:12013, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45786] Another function of GAM3298 is therefore inhibition of LOC150299 (Accession XP_097869.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150299.

[45787] LOC150630 (Accession XP_097931.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC150630 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150630, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150630 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45788] Another function of GAM3298 is therefore inhibition of

LOC150630 (Accession XP_097931.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150630.

[45789] LOC151068 (Accession XP_098000.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC151068 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151068, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151068 BINDING SITE, designated SEQ ID:12510, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45790] Another function of GAM3298 is therefore inhibition of LOC151068 (Accession XP_098000.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151068.

[45791] LOC151438 (Accession XP_098060.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC151438 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC151438, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151438 BINDING SITE, designated SEQ ID:6221, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45792] Another function of GAM3298 is therefore inhibition of LOC151438 (Accession XP_098060.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151438.

[45793] LOC153338 (Accession XP_098361.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC153338 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153338, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153338 BINDING SITE, designated SEQ ID:16145, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:259.

[45794] Another function of GAM3298 is therefore inhibition of LOC153338 (Accession XP_098361.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153338.

[45795] LOC153561 (Accession XP_087708.6) is another GAM3298 target gene, herein designated TARGET GENE. LOC153561 BINDING SITE1 and LOC153561 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC153561, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153561 BINDING SITE1 and LOC153561 BINDING SITE2, designated SEQ ID:4776 and SEQ ID:3706 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45796] Another function of GAM3298 is therefore inhibition of LOC153561 (Accession XP_087708.6) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153561.

[45797] LOC153682 (Accession XP_098414.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC153682 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153682, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153682 BINDING SITE, designated SEQ ID:8989, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45798] Another function of GAM3298 is therefore inhibition of LOC153682 (Accession XP_098414.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153682.

[45799] LOC153727 (Accession XP_098422.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC153727 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153727, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC153727 BINDING SITE, designated SEQ ID:6353, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45800] Another function of GAM3298 is therefore inhibition of LOC153727 (Accession XP_098422.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153727.

[45801] LOC155006 (Accession XP_088117.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC155006 BINDING SITE1 and LOC155006 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC155006, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC155006 BINDING SITE1 and LOC155006 BINDING SITE2, designated SEQ ID:12246 and SEQ ID:3706 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45802] Another function of GAM3298 is therefore inhibition of LOC155006 (Accession XP_088117.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155006.

[45803] LOC157531 (Accession XP_212210.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC157531 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC157531, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157531 BINDING SITE, designated SEQ ID:15279, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45804] Another function of GAM3298 is therefore inhibition of LOC157531 (Accession XP_212210.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157531.

[45805] LOC158434 (Accession XP_098939.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC158434 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC158434, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158434 BINDING SITE, designated SEQ ID:8220, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45806] Another function of GAM3298 is therefore inhibition of LOC158434 (Accession XP_098939.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158434.

[45807] LOC159036 (Accession XP_099018.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC159036 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC159036, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC159036 BINDING SITE, designated SEQ ID:816, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45808] Another function of GAM3298 is therefore inhibition of LOC159036 (Accession XP_099018.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159036.

[45809] LOC163259 (Accession XP_088769.6) is another GAM3298 target gene, herein designated TARGET GENE. LOC163259 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC163259, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163259 BINDING SITE, designated SEQ ID:7144, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45810] Another function of GAM3298 is therefore inhibition of LOC163259 (Accession XP_088769.6) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163259.

[45811] LOC165324 (Accession XP_092518.1) is another GAM3298 target gene, herein designated TARGET GENE.

LOC165324 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC165324, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC165324 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45812] Another function of GAM3298 is therefore inhibition of LOC165324 (Accession XP_092518.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC165324.

[45813] LOC166522 (Accession XP_093920.5) is another GAM3298 target gene, herein designated TARGET GENE. LOC166522 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC166522, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC166522 BINDING SITE, designated SEQ ID:16780, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45814] Another function of GAM3298 is therefore inhibition of LOC166522 (Accession XP_093920.5) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC166522.

[45815] LOC196540 (Accession XP_116933.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC196540 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC196540, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196540 BINDING SITE, designated SEQ ID:2952, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45816] Another function of GAM3298 is therefore inhibition of LOC196540 (Accession XP_116933.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196540.

[45817] LOC199733 (Accession XP_117123.2) is another GAM3298 target gene, herein designated TARGET GENE. LOC199733 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC199733, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199733 BINDING SITE, designated SEQ ID:7468, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45818] Another function of GAM3298 is therefore inhibition of LOC199733 (Accession XP_117123.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199733.

[45819] LOC200008 (Accession XP_114089.3) is another GAM3298 target gene, herein designated TARGET GENE. LOC200008 BINDING SITE1 and LOC200008 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC200008, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC200008 BINDING SITE1 and LOC200008 BINDING SITE2, designated SEQ ID:6353 and SEQ ID:3706 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45820] Another function of GAM3298 is therefore inhibition of LOC200008 (Accession XP_114089.3) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200008.

[45821] LOC201475 (Accession XP_113967.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC201475 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201475 BINDING SITE, designated SEQ ID:9894, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45822] Another function of GAM3298 is therefore inhibition of LOC201475 (Accession XP_113967.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201475.

[45823] LOC201810 (Accession XP_114383.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC201810 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201810, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201810 BINDING SITE, designated SEQ ID:840, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45824] Another function of GAM3298 is therefore inhibition of LOC201810 (Accession XP_114383.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201810.

[45825] LOC202134 (Accession XP_117365.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC202134 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC202134, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202134 BINDING SITE, designated SEQ ID:19238, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45826] Another function of GAM3298 is therefore inhibition of LOC202134 (Accession XP_117365.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202134.

[45827] LOC220739 (Accession XP_167548.3) is another GAM3298 target gene, herein designated TARGET GENE. LOC220739 BINDING SITE1 and LOC220739 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC220739, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220739 BINDING SITE1 and LOC220739 BINDING SITE2, designated SEQ ID:16984 and SEQ ID:5839 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated

GAM RNA, also designated SEQ ID:259.

[45828] Another function of GAM3298 is therefore inhibition of LOC220739 (Accession XP_167548.3) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220739.

[45829] LOC221035 (Accession XP_167640.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC221035 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221035, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221035 BINDING SITE, designated SEQ ID:18581, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45830] Another function of GAM3298 is therefore inhibition of LOC221035 (Accession XP_167640.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221035.

[45831] LOC221601 (Accession XP_168071.1) is another

GAM3298 target gene, herein designated TARGET GENE. LOC221601 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221601, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221601 BINDING SITE, designated SEQ ID:10387, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45832] Another function of GAM3298 is therefore inhibition of LOC221601 (Accession XP_168071.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221601.

[45833] LOC221931 (Accession XP_168348.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC221931 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221931, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221931 BINDING SITE, desig-

nated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45834] Another function of GAM3298 is therefore inhibition of LOC221931 (Accession XP_168348.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221931.

[45835] LOC221954 (Accession XP_168349.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC221954 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC221954, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221954 BINDING SITE, designated SEQ ID:15872, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45836] Another function of GAM3298 is therefore inhibition of LOC221954 (Accession XP_168349.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC221954.

[45837] LOC222060 (Accession XP_168427.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC222060 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222060, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222060 BINDING SITE, designated SEQ ID:14995, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45838] Another function of GAM3298 is therefore inhibition of LOC222060 (Accession XP_168427.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222060.

[45839] LOC222160 (Accession XP_168431.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC222160 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222160, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222160 BINDING SITE, designated SEQ ID:8175, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45840] Another function of GAM3298 is therefore inhibition of LOC222160 (Accession XP_168431.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222160.

[45841] LOC253782 (Accession XP_171023.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC253782 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC253782, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253782 BINDING SITE, designated SEQ ID:10198, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45842] Another function of GAM3298 is therefore inhibition of LOC253782 (Accession XP_171023.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253782.

[45843] LOC255185 (Accession XP_170826.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC255185 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC255185, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255185 BINDING SITE, designated SEQ ID:6353, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45844] Another function of GAM3298 is therefore inhibition of LOC255185 (Accession XP_170826.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255185.

[45845] LOC282915 (Accession XP_212579.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC282915 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC282915, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282915 BINDING SITE, designated SEQ ID:19337, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45846] Another function of GAM3298 is therefore inhibition of LOC282915 (Accession XP_212579.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282915.

[45847] LOC282951 (Accession XP_212627.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC282951 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282951, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282951 BINDING SITE, designated SEQ ID:19337, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45848] Another function of GAM3298 is therefore inhibition of LOC282951 (Accession XP_212627.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282951.

[45849] LOC282973 (Accession XP_208463.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC282973 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282973, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282973 BINDING SITE, designated SEQ ID:7468, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45850] Another function of GAM3298 is therefore inhibition of LOC282973 (Accession XP_208463.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282973.

[45851] LOC283005 (Accession XP_208481.1) is another GAM3298 target gene, herein designated TARGET GENE.

LOC283005 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283005, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283005 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45852] Another function of GAM3298 is therefore inhibition of LOC283005 (Accession XP_208481.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283005.

[45853] LOC283061 (Accession XP_210875.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC283061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283061 BINDING SITE, designated SEQ ID:841, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45854] Another function of GAM3298 is therefore inhibition of LOC283061 (Accession XP_210875.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283061.

[45855] LOC283199 (Accession XP_210929.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC283199 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283199, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283199 BINDING SITE, designated SEQ ID:14868, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45856] Another function of GAM3298 is therefore inhibition of LOC283199 (Accession XP_210929.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283199.

[45857] LOC283230 (Accession XP_210945.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC283230 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283230, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283230 BINDING SITE, designated SEQ ID:7329, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45858] Another function of GAM3298 is therefore inhibition of LOC283230 (Accession XP_210945.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283230.

[45859] LOC283289 (Accession XP_210960.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC283289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC283289 BINDING SITE, designated SEQ ID:19239, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45860] Another function of GAM3298 is therefore inhibition of LOC283289 (Accession XP_210960.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283289.

[45861] LOC283460 (Accession XP_208682.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC283460 BINDING SITE1 and LOC283460 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283460, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283460 BINDING SITE1 and LOC283460 BINDING SITE2, designated SEQ ID:3706 and SEQ ID:7398 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45862] Another function of GAM3298 is therefore inhibition of LOC283460 (Accession XP_208682.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283460.

[45863] LOC283475 (Accession XP_211056.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC283475 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283475 BINDING SITE, designated SEQ ID:8626, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45864] Another function of GAM3298 is therefore inhibition of LOC283475 (Accession XP_211056.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283475.

[45865] LOC283508 (Accession XP_211070.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC283508 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC283508, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283508 BINDING SITE, designated SEQ ID:8580, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45866] Another function of GAM3298 is therefore inhibition of LOC283508 (Accession XP_211070.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283508.

[45867] LOC283672 (Accession XP_211152.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC283672 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283672, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283672 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45868] Another function of GAM3298 is therefore inhibition of LOC283672 (Accession XP_211152.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283672.

[45869] LOC283690 (Accession XP_211167.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC283690 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283690, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283690 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45870] Another function of GAM3298 is therefore inhibition of LOC283690 (Accession XP_211167.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283690.

[45871] LOC283693 (Accession XP_208788.1) is another GAM3298 target gene, herein designated TARGET GENE.

LOC283693 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283693, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283693 BINDING SITE, designated SEQ ID:16061, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45872] Another function of GAM3298 is therefore inhibition of LOC283693 (Accession XP_208788.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283693.

[45873] LOC283760 (Accession XP_208826.2) is another GAM3298 target gene, herein designated TARGET GENE. LOC283760 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283760, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283760 BINDING SITE, designated SEQ ID:11927, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45874] Another function of GAM3298 is therefore inhibition of LOC283760 (Accession XP_208826.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283760.

[45875] LOC283891 (Accession XP_208889.2) is another GAM3298 target gene, herein designated TARGET GENE. LOC283891 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283891, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283891 BINDING SITE, designated SEQ ID:5840, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45876] Another function of GAM3298 is therefore inhibition of LOC283891 (Accession XP_208889.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283891.

[45877] LOC283924 (Accession XP_208906.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC283924 BINDING SITE1 and LOC283924 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283924, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283924 BINDING SITE1 and LOC283924 BINDING SITE2, designated SEQ ID:3706 and SEQ ID:6479 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45878] Another function of GAM3298 is therefore inhibition of LOC283924 (Accession XP_208906.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283924.

[45879] LOC283985 (Accession NP_835229.1) is another

GAM3298 target gene, herein designated TARGET GENE. LOC283985 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC283985, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283985 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45880] Another function of GAM3298 is therefore inhibition of LOC283985 (Accession NP_835229.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283985.

[45881] LOC283985 (Accession XP_208951.2) is another GAM3298 target gene, herein designated TARGET GENE. LOC283985 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC283985, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283985

BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45882] Another function of GAM3298 is therefore inhibition of LOC283985 (Accession XP_208951.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283985.

[45883] LOC284014 (Accession XP_211300.2) is another GAM3298 target gene, herein designated TARGET GENE. LOC284014 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284014, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284014 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45884] Another function of GAM3298 is therefore inhibition of LOC284014 (Accession XP_211300.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284014.

[45885] LOC284024 (Accession XP_208970.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284024 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45886] Another function of GAM3298 is therefore inhibition of LOC284024 (Accession XP_208970.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284024.

[45887] LOC284161 (Accession XP_209047.2) is another GAM3298 target gene, herein designated TARGET GENE. LOC284161 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284161, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284161 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45888] Another function of GAM3298 is therefore inhibition of LOC284161 (Accession XP_209047.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284161.

[45889] LOC284313 (Accession XP_209116.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284313 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284313, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284313 BINDING SITE, designated SEQ ID:16046, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45890] Another function of GAM3298 is therefore inhibition of LOC284313 (Accession XP_209116.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284313.

[45891] LOC284371 (Accession XP_209155.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284371 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45892] Another function of GAM3298 is therefore inhibition of LOC284371 (Accession XP_209155.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284371.

[45893] LOC284417 (Accession XP_209187.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284417 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC284417, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284417 BINDING SITE, designated SEQ ID:6665, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45894] Another function of GAM3298 is therefore inhibition of LOC284417 (Accession XP_209187.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284417.

[45895] LOC284461 (Accession XP_211476.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284461 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284461, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284461 BINDING SITE, designated SEQ ID:17236, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45896] Another function of GAM3298 is therefore inhibition of LOC284461 (Accession XP_211476.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284461.

[45897] LOC284475 (Accession XP_211478.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284475 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284475 BINDING SITE, designated SEQ ID:8335, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45898] Another function of GAM3298 is therefore inhibition of LOC284475 (Accession XP_211478.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284475.

[45899] LOC284486 (Accession XP_209231.1) is another GAM3298 target gene, herein designated TARGET GENE.

LOC284486 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284486, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284486 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45900] Another function of GAM3298 is therefore inhibition of LOC284486 (Accession XP_209231.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284486.

[45901] LOC284542 (Accession XP_209254.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284542 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284542, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284542 BINDING SITE, designated SEQ ID:12376, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45902] Another function of GAM3298 is therefore inhibition of LOC284542 (Accession XP_209254.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284542.

[45903] LOC284552 (Accession XP_211516.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284552 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284552, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284552 BINDING SITE, designated SEQ ID:1017, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45904] Another function of GAM3298 is therefore inhibition of LOC284552 (Accession XP_211516.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284552.

[45905] LOC284639 (Accession XP_211567.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284639 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284639, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284639 BINDING SITE, designated SEQ ID:3703, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45906] Another function of GAM3298 is therefore inhibition of LOC284639 (Accession XP_211567.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284639.

[45907] LOC284647 (Accession XP_211569.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284647 BINDING SITE1 and LOC284647 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284647, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC284647 BINDING SITE1 and LOC284647 BINDING SITE2, designated SEQ ID:10343 and SEQ ID:15701 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45908] Another function of GAM3298 is therefore inhibition of LOC284647 (Accession XP_211569.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284647.

[45909] LOC284665 (Accession XP_211581.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284665 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284665, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284665 BINDING SITE, designated SEQ ID:7468, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45910] Another function of GAM3298 is therefore inhibition of LOC284665 (Accession XP_211581.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284665.

[45911] LOC284707 (Accession XP_211598.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284707 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284707, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284707 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45912] Another function of GAM3298 is therefore inhibition of LOC284707 (Accession XP_211598.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284707.

[45913] LOC284739 (Accession XP_211609.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284739 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC284739, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284739 BINDING SITE, designated SEQ ID:18406, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45914] Another function of GAM3298 is therefore inhibition of LOC284739 (Accession XP_211609.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284739.

[45915] LOC284857 (Accession XP_211671.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284857 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284857, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284857 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45916] Another function of GAM3298 is therefore inhibition of LOC284857 (Accession XP_211671.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284857.

[45917] LOC284858 (Accession XP_209386.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284858 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284858, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284858 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45918] Another function of GAM3298 is therefore inhibition of LOC284858 (Accession XP_209386.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284858.

[45919] LOC284911 (Accession XP_211684.1) is another GAM3298 target gene, herein designated TARGET GENE.

LOC284911 BINDING SITE1 and LOC284911 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284911, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284911 BINDING SITE1 and LOC284911 BINDING SITE2, designated SEQ ID:3706 and SEQ ID:12485 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45920] Another function of GAM3298 is therefore inhibition of LOC284911 (Accession XP_211684.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284911.

[45921] LOC284912 (Accession XP_209413.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284912 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284912, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284912 BINDING SITE, desig-

nated SEQ ID:5498, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45922] Another function of GAM3298 is therefore inhibition of LOC284912 (Accession XP_209413.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284912.

[45923] LOC284972 (Accession XP_211712.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284972 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284972 BINDING SITE, designated SEQ ID:13200, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45924] Another function of GAM3298 is therefore inhibition of LOC284972 (Accession XP_211712.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284972.

[45925] LOC284995 (Accession XP_211729.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284995 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284995, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284995 BINDING SITE, designated SEQ ID:17671, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45926] Another function of GAM3298 is therefore inhibition of LOC284995 (Accession XP_211729.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284995.

[45927] LOC284998 (Accession XP_211726.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC284998 BINDING SITE1 and LOC284998 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284998, corresponding to target binding sites such as BINDING SITE I, BINDING SITE

II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284998 BINDING SITE1 and LOC284998 BINDING SITE2, designated SEQ ID:14399 and SEQ ID:13613 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45928] Another function of GAM3298 is therefore inhibition of LOC284998 (Accession XP_211726.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284998.

[45929] LOC285001 (Accession XP_211730.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285001 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285001 BINDING SITE, designated SEQ ID:16577, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45930] Another function of GAM3298 is therefore inhibition of

LOC285001 (Accession XP_211730.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285001.

[45931] LOC285052 (Accession XP_211751.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285052 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45932] Another function of GAM3298 is therefore inhibition of LOC285052 (Accession XP_211751.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285052.

[45933] LOC285082 (Accession XP_211759.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285082 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC285082, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285082 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45934] Another function of GAM3298 is therefore inhibition of LOC285082 (Accession XP_211759.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285082.

[45935] LOC285376 (Accession XP_211864.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285376 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285376, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285376 BINDING SITE, designated SEQ ID:4250, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:259.

[45936] Another function of GAM3298 is therefore inhibition of LOC285376 (Accession XP_211864.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285376.

[45937] LOC285378 (Accession XP_211859.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285378 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285378, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285378 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45938] Another function of GAM3298 is therefore inhibition of LOC285378 (Accession XP_211859.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285378.

[45939] LOC285379 (Accession XP_211868.1) is another

GAM3298 target gene, herein designated TARGET GENE. LOC285379 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285379, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285379 BINDING SITE, designated SEQ ID:12631, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45940] Another function of GAM3298 is therefore inhibition of LOC285379 (Accession XP_211868.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285379.

[45941] LOC285398 (Accession XP_209593.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285398 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285398, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285398 BINDING SITE, desig-

nated SEQ ID:18417, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45942] Another function of GAM3298 is therefore inhibition of LOC285398 (Accession XP_209593.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285398.

[45943] LOC285400 (Accession XP_209596.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285400 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285400 BINDING SITE, designated SEQ ID:19239, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45944] Another function of GAM3298 is therefore inhibition of LOC285400 (Accession XP_209596.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285400.

[45945] LOC285540 (Accession XP_209654.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285540 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285540, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285540 BINDING SITE, designated SEQ ID:4958, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45946] Another function of GAM3298 is therefore inhibition of LOC285540 (Accession XP_209654.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285540.

[45947] LOC285676 (Accession XP_209718.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285676 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285676, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285676 BINDING SITE, designated SEQ ID:2225, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45948] Another function of GAM3298 is therefore inhibition of LOC285676 (Accession XP_209718.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285676.

[45949] LOC285719 (Accession XP_211990.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285719 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285719 BINDING SITE, designated SEQ ID:840, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45950] Another function of GAM3298 is therefore inhibition of LOC285719 (Accession XP_211990.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285719.

[45951] LOC285722 (Accession XP_211997.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285722 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285722, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285722 BINDING SITE, designated SEQ ID:14868, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45952] Another function of GAM3298 is therefore inhibition of LOC285722 (Accession XP_211997.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285722.

[45953] LOC285747 (Accession XP_209742.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285747 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC285747, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285747 BINDING SITE, designated SEQ ID:17940, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45954] Another function of GAM3298 is therefore inhibition of LOC285747 (Accession XP_209742.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285747.

[45955] LOC285749 (Accession XP_212010.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285749 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285749, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285749 BINDING SITE, designated SEQ ID:10387, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45956] Another function of GAM3298 is therefore inhibition of LOC285749 (Accession XP_212010.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285749.

[45957] LOC285758 (Accession XP_212012.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285758 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285758, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285758 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45958] Another function of GAM3298 is therefore inhibition of LOC285758 (Accession XP_212012.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285758.

[45959] LOC285833 (Accession XP_209790.1) is another GAM3298 target gene, herein designated TARGET GENE.

LOC285833 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285833, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285833 BINDING SITE, designated SEQ ID:19337, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45960] Another function of GAM3298 is therefore inhibition of LOC285833 (Accession XP_209790.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285833.

[45961] LOC285854 (Accession XP_209770.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285854 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285854, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285854 BINDING SITE, designated SEQ ID:5474, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45962] Another function of GAM3298 is therefore inhibition of LOC285854 (Accession XP_209770.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285854.

[45963] LOC285859 (Accession XP_209775.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285859 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285859, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285859 BINDING SITE, designated SEQ ID:17309, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45964] Another function of GAM3298 is therefore inhibition of LOC285859 (Accession XP_209775.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285859.

[45965] LOC285869 (Accession XP_212058.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285869 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285869, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285869 BINDING SITE, designated SEQ ID:18034, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45966] Another function of GAM3298 is therefore inhibition of LOC285869 (Accession XP_212058.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285869.

[45967] LOC285912 (Accession XP_212078.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285912 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285912, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC285912 BINDING SITE, designated SEQ ID:816, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45968] Another function of GAM3298 is therefore inhibition of LOC285912 (Accession XP_212078.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285912.

[45969] LOC285920 (Accession XP_212091.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285920 BINDING SITE1 and LOC285920 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC285920, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285920 BINDING SITE1 and LOC285920 BINDING SITE2, designated SEQ ID:15927 and SEQ ID:3706 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45970] Another function of GAM3298 is therefore inhibition of LOC285920 (Accession XP_212091.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285920.

[45971] LOC285926 (Accession XP_208368.2) is another GAM3298 target gene, herein designated TARGET GENE. LOC285926 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285926, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285926 BINDING SITE, designated SEQ ID:11962, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45972] Another function of GAM3298 is therefore inhibition of LOC285926 (Accession XP_208368.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285926.

[45973] LOC285928 (Accession XP_212087.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285928 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC285928, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285928 BINDING SITE, designated SEQ ID:16949, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45974] Another function of GAM3298 is therefore inhibition of LOC285928 (Accession XP_212087.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285928.

[45975] LOC285953 (Accession XP_209820.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285953 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285953, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285953 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45976] Another function of GAM3298 is therefore inhibition of LOC285953 (Accession XP_209820.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285953.

[45977] LOC285960 (Accession XP_212088.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC285960 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285960, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285960 BINDING SITE, designated SEQ ID:14995, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45978] Another function of GAM3298 is therefore inhibition of LOC285960 (Accession XP_212088.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285960.

[45979] LOC286129 (Accession XP_209910.2) is another GAM3298 target gene, herein designated TARGET GENE.

LOC286129 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286129, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286129 BINDING SITE, designated SEQ ID:7202, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45980] Another function of GAM3298 is therefore inhibition of LOC286129 (Accession XP_209910.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286129.

[45981] LOC286166 (Accession XP_209925.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC286166 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286166 BINDING SITE, designated SEQ ID:7939, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45982] Another function of GAM3298 is therefore inhibition of LOC286166 (Accession XP_209925.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286166.

[45983] LOC286184 (Accession XP_212216.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC286184 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286184, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286184 BINDING SITE, designated SEQ ID:3702, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45984] Another function of GAM3298 is therefore inhibition of LOC286184 (Accession XP_212216.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286184.

[45985] LOC286186 (Accession XP_212219.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC286186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286186 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45986] Another function of GAM3298 is therefore inhibition of LOC286186 (Accession XP_212219.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286186.

[45987] LOC286197 (Accession XP_209940.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC286197 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286197, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC286197 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45988] Another function of GAM3298 is therefore inhibition of LOC286197 (Accession XP_209940.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286197.

[45989] LOC286222 (Accession XP_209955.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC286222 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286222, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286222 BINDING SITE, designated SEQ ID:14873, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45990] Another function of GAM3298 is therefore inhibition of LOC286222 (Accession XP_209955.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC286222.

[45991] LOC286337 (Accession XP_212274.3) is another GAM3298 target gene, herein designated TARGET GENE. LOC286337 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286337, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286337 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45992] Another function of GAM3298 is therefore inhibition of LOC286337 (Accession XP_212274.3) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286337.

[45993] LOC286374 (Accession XP_212293.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC286374 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286374, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286374 BINDING SITE, designated SEQ ID:10184, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45994] Another function of GAM3298 is therefore inhibition of LOC286374 (Accession XP_212293.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286374.

[45995] LOC286470 (Accession XP_212325.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC286470 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286470, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286470 BINDING SITE, designated SEQ ID:7468, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45996] Another function of GAM3298 is therefore inhibition of

LOC286470 (Accession XP_212325.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286470.

[45997] LOC338549 (Accession XP_294651.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC338549 BINDING SITE1 and LOC338549 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC338549, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338549 BINDING SITE1 and LOC338549 BINDING SITE2, designated SEQ ID:8366 and SEQ ID:5498 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[45998] Another function of GAM3298 is therefore inhibition of LOC338549 (Accession XP_294651.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338549.

[45999] LOC338594 (Accession XP_294660.1) is another GAM3298 target gene, herein designated TARGET GENE.

LOC338594 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338594, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338594 BINDING SITE, designated SEQ ID:5843, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46000] Another function of GAM3298 is therefore inhibition of LOC338594 (Accession XP_294660.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338594.

[46001] LOC338963 (Accession XP_294757.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC338963 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338963, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338963 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46002] Another function of GAM3298 is therefore inhibition of LOC338963 (Accession XP_294757.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338963.

[46003] LOC339290 (Accession XP_294901.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC339290 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339290, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339290 BINDING SITE, designated SEQ ID:13707, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46004] Another function of GAM3298 is therefore inhibition of LOC339290 (Accession XP_294901.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339290.

[46005] LOC339373 (Accession XP_294921.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC339373 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339373, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339373 BINDING SITE, designated SEQ ID:815, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46006] Another function of GAM3298 is therefore inhibition of LOC339373 (Accession XP_294921.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339373.

[46007] LOC339413 (Accession XP_294936.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC339413 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339413, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC339413 BINDING SITE, designated SEQ ID:19562, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46008] Another function of GAM3298 is therefore inhibition of LOC339413 (Accession XP_294936.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339413.

[46009] LOC339761 (Accession XP_291005.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC339761 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339761, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339761 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46010] Another function of GAM3298 is therefore inhibition of LOC339761 (Accession XP_291005.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC339761.

[46011] LOC339841 (Accession XP_291038.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC339841 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339841, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339841 BINDING SITE, designated SEQ ID:7576, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46012] Another function of GAM3298 is therefore inhibition of LOC339841 (Accession XP_291038.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339841.

[46013] LOC340038 (Accession XP_291125.2) is another GAM3298 target gene, herein designated TARGET GENE. LOC340038 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340038, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340038 BINDING SITE, designated SEQ ID:19238, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46014] Another function of GAM3298 is therefore inhibition of LOC340038 (Accession XP_291125.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340038.

[46015] LOC340087 (Accession XP_295153.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC340087 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340087, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340087 BINDING SITE, designated SEQ ID:16347, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46016] Another function of GAM3298 is therefore inhibition of

LOC340087 (Accession XP_295153.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340087.

[46017] LOC340184 (Accession XP_295183.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC340184 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340184, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340184 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46018] Another function of GAM3298 is therefore inhibition of LOC340184 (Accession XP_295183.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340184.

[46019] LOC340208 (Accession XP_295187.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC340208 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC340208, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340208 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46020] Another function of GAM3298 is therefore inhibition of LOC340208 (Accession XP_295187.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340208.

[46021] LOC340269 (Accession XP_295199.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC340269 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340269, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340269 BINDING SITE, designated SEQ ID:16625, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:259.

[46022] Another function of GAM3298 is therefore inhibition of LOC340269 (Accession XP_295199.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340269.

[46023] LOC340320 (Accession XP_295211.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC340320 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340320, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340320 BINDING SITE, designated SEQ ID:4826, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46024] Another function of GAM3298 is therefore inhibition of LOC340320 (Accession XP_295211.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340320.

[46025] LOC340362 (Accession XP_295225.1) is another

GAM3298 target gene, herein designated TARGET GENE. LOC340362 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340362, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340362 BINDING SITE, designated SEQ ID:8160, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46026] Another function of GAM3298 is therefore inhibition of LOC340362 (Accession XP_295225.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340362.

[46027] LOC340394 (Accession XP_295235.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC340394 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340394, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340394 BINDING SITE, desig-

nated SEQ ID:15241, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46028] Another function of GAM3298 is therefore inhibition of LOC340394 (Accession XP_295235.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340394.

[46029] LOC340547 (Accession XP_291331.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC340547 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340547, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340547 BINDING SITE, designated SEQ ID:1347, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46030] Another function of GAM3298 is therefore inhibition of LOC340547 (Accession XP_291331.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC340547.

[46031] LOC343434 (Accession XP_295562.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC343434 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC343434, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC343434 BINDING SITE, designated SEQ ID:5570, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46032] Another function of GAM3298 is therefore inhibition of LOC343434 (Accession XP_295562.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC343434.

[46033] LOC346232 (Accession XP_294131.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC346232 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC346232, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC346232 BINDING SITE, designated SEQ ID:18321, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46034] Another function of GAM3298 is therefore inhibition of LOC346232 (Accession XP_294131.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC346232.

[46035] LOC348102 (Accession XP_302651.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC348102 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348102, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348102 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46036] Another function of GAM3298 is therefore inhibition of LOC348102 (Accession XP_302651.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348102.

[46037] LOC348442 (Accession XP_057659.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC348442 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348442 BINDING SITE, designated SEQ ID:815, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46038] Another function of GAM3298 is therefore inhibition of LOC348442 (Accession XP_057659.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348442.

[46039] LOC348456 (Accession XP_302761.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC348456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC348456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348456 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46040] Another function of GAM3298 is therefore inhibition of LOC348456 (Accession XP_302761.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348456.

[46041] LOC348527 (Accession XP_300779.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC348527 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348527, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348527 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46042] Another function of GAM3298 is therefore inhibition of LOC348527 (Accession XP_300779.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348527.

[46043] LOC348738 (Accession XP_300826.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC348738 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348738, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348738 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46044] Another function of GAM3298 is therefore inhibition of LOC348738 (Accession XP_300826.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348738.

[46045] LOC349063 (Accession XP_302949.1) is another GAM3298 target gene, herein designated TARGET GENE.

LOC349063 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349063, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349063 BINDING SITE, designated SEQ ID:18034, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46046] Another function of GAM3298 is therefore inhibition of LOC349063 (Accession XP_302949.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349063.

[46047] LOC349092 (Accession XP_302959.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC349092 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349092, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349092 BINDING SITE, designated SEQ ID:16691, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46048] Another function of GAM3298 is therefore inhibition of LOC349092 (Accession XP_302959.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349092.

[46049] LOC349169 (Accession XP_302978.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC349169 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349169, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349169 BINDING SITE, designated SEQ ID:17395, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46050] Another function of GAM3298 is therefore inhibition of LOC349169 (Accession XP_302978.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349169.

[46051] LOC349170 (Accession XP_300969.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC349170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349170 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46052] Another function of GAM3298 is therefore inhibition of LOC349170 (Accession XP_300969.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349170.

[46053] LOC349282 (Accession XP_301008.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC349282 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC349282 BINDING SITE, designated SEQ ID:19238, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46054] Another function of GAM3298 is therefore inhibition of LOC349282 (Accession XP_301008.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349282.

[46055] LOC349313 (Accession XP_301024.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC349313 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349313, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349313 BINDING SITE, designated SEQ ID:19238, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46056] Another function of GAM3298 is therefore inhibition of LOC349313 (Accession XP_301024.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC349313.

[46057] LOC349323 (Accession XP_301029.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC349323 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349323 BINDING SITE, designated SEQ ID:18956, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46058] Another function of GAM3298 is therefore inhibition of LOC349323 (Accession XP_301029.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349323.

[46059] LOC51333 (Accession NP_057727.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC51333 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC51333, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51333 BINDING SITE, designated SEQ ID:17893, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46060] Another function of GAM3298 is therefore inhibition of LOC51333 (Accession NP_057727.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51333.

[46061] LOC51759 (Accession NP_057566.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC51759 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC51759, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC51759 BINDING SITE, designated SEQ ID:4777, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46062] Another function of GAM3298 is therefore inhibition of LOC51759 (Accession NP_057566.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51759.

[46063] LOC85865 (Accession NP_149098.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC85865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC85865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC85865 BINDING SITE, designated SEQ ID:6826, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46064] Another function of GAM3298 is therefore inhibition of LOC85865 (Accession NP_149098.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC85865.

[46065] LOC91056 (Accession NP_612377.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC91056 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC91056, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91056 BINDING SITE, designated SEQ ID:12246, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46066] Another function of GAM3298 is therefore inhibition of LOC91056 (Accession NP_612377.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91056.

[46067] LOC91565 (Accession XP_039231.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC91565 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91565, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91565 BINDING SITE, designated SEQ ID:6049, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46068] Another function of GAM3298 is therefore inhibition of LOC91565 (Accession XP_039231.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91565.

[46069] LOC93613 (Accession XP_052568.1) is another GAM3298 target gene, herein designated TARGET GENE. LOC93613 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC93613, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC93613 BINDING SITE, designated SEQ ID:10184, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46070] Another function of GAM3298 is therefore inhibition of LOC93613 (Accession XP_052568.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93613.

[46071] LPHN3 (Accession NP_056051.1) is another GAM3298 target gene, herein designated TARGET GENE. LPHN3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LPHN3, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LPHN3 BINDING SITE, designated SEQ ID:3875, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46072] Another function of GAM3298 is therefore inhibition of LPHN3 (Accession NP_056051.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPHN3.

[46073] Mitogen-activated protein kinase kinase kinase 8 (MAP3K8, Accession NP_005195.2) is another GAM3298 target gene, herein designated TARGET GENE. MAP3K8 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MAP3K8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAP3K8 BINDING SITE, designated SEQ ID:11824, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46074] Another function of GAM3298 is therefore inhibition of Mitogen-activated protein kinase kinase kinase 8 (MAP3K8, Accession NP_005195.2), a gene which is able

to activate nf- kappa- b 1 by stimulating proteasome-mediated p. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K8.

[46075] The function of MAP3K8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Matrin 3 (MATR3, Accession NP_061322.2) is another GAM3298 target gene, herein designated TARGET GENE. MATR3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MATR3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MATR3 BINDING SITE, designated SEQ ID:19562, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46076] Another function of GAM3298 is therefore inhibition of Matrin 3 (MATR3, Accession NP_061322.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MATR3.

[46077] MAWBP (Accession NP_071412.1) is another GAM3298 target gene, herein designated TARGET GENE. MAWBP BINDING SITE1 and MAWBP BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by MAWBP, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAWBP BINDING SITE1 and MAWBP BINDING SITE2, designated SEQ ID:4940 and SEQ ID:15240 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46078] Another function of GAM3298 is therefore inhibition of MAWBP (Accession NP_071412.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAWBP.

[46079] Methionyl aminopeptidase 1 (METAP1, Accession NP_055958.1) is another GAM3298 target gene, herein designated TARGET GENE. METAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by METAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of METAP1 BINDING SITE, designated SEQ ID:12453, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46080] Another function of GAM3298 is therefore inhibition of Methionyl aminopeptidase 1 (METAP1, Accession NP_055958.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with METAP1.

[46081] Mannosyl (beta-1,4-)-glycoprotein beta-1,4-n-acetylglucosaminyltransferase (MGAT3, Accession NP_835470.1) is another GAM3298 target gene, herein designated TARGET GENE. MGAT3 BINDING SITE1 and MGAT3 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by MGAT3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGAT3 BINDING SITE1 and MGAT3 BINDING SITE2, designated SEQ ID:16776 and SEQ ID:16780 respectively, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46082] Another function of GAM3298 is therefore inhibition of Mannosyl (beta-1,4-)-glycoprotein beta-1,4-n-acetylglucosaminyltransferase (MGAT3, Accession NP_835470.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAT3.

[46083] MGC10765 (Accession NP_077321.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC10765 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10765, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10765 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46084] Another function of GAM3298 is therefore inhibition of MGC10765 (Accession NP_077321.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10765.

[46085] MGC10771 (Accession NP_078782.2) is another GAM3298 target gene, herein designated TARGET GENE. MGC10771

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC10771, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10771 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46086] Another function of GAM3298 is therefore inhibition of MGC10771 (Accession NP_078782.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10771.

[46087] MGC10814 (Accession NP_116060.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC10814 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC10814, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC10814 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46088] Another function of GAM3298 is therefore inhibition of MGC10814 (Accession NP_116060.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10814.

[46089] MGC13053 (Accession NP_116099.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC13053 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC13053, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13053 BINDING SITE, designated SEQ ID:11709, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46090] Another function of GAM3298 is therefore inhibition of MGC13053 (Accession NP_116099.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13053.

[46091] MGC16703 (Accession NP_659479.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC16703 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by MGC16703, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC16703 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46092] Another function of GAM3298 is therefore inhibition of MGC16703 (Accession NP_659479.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16703.

[46093] MGC17791 (Accession NP_689575.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC17791 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC17791, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC17791 BINDING SITE, designated SEQ ID:15278, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46094] Another function of GAM3298 is therefore inhibition of

MGC17791 (Accession NP_689575.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC17791.

[46095] MGC17986 (Accession NP_705836.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC17986 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC17986, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC17986 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46096] Another function of GAM3298 is therefore inhibition of MGC17986 (Accession NP_705836.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC17986.

[46097] MGC2396 (Accession NP_443084.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC2396 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC2396, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2396 BINDING SITE, designated SEQ ID:6794, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46098] Another function of GAM3298 is therefore inhibition of MGC2396 (Accession NP_443084.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2396.

[46099] MGC29937 (Accession NP_653198.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC29937 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC29937, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC29937 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46100] Another function of GAM3298 is therefore inhibition of MGC29937 (Accession NP_653198.1) . Accordingly, utili-

ties of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29937.

[46101] MGC30052 (Accession NP_653322.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC30052 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC30052, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC30052 BINDING SITE, designated SEQ ID:6970, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46102] Another function of GAM3298 is therefore inhibition of MGC30052 (Accession NP_653322.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC30052.

[46103] MGC3195 (Accession NP_114111.2) is another GAM3298 target gene, herein designated TARGET GENE. MGC3195 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3195, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3195 BINDING SITE, designated SEQ ID:7576, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46104] Another function of GAM3298 is therefore inhibition of MGC3195 (Accession NP_114111.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3195.

[46105] MGC3207 (Accession NP_115661.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC3207 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3207, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3207 BINDING SITE, designated SEQ ID:6665, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46106] Another function of GAM3298 is therefore inhibition of MGC3207 (Accession NP_115661.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MGC3207.

[46107] MGC34034 (Accession NP_694956.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC34034 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC34034, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34034 BINDING SITE, designated SEQ ID:17939, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46108] Another function of GAM3298 is therefore inhibition of MGC34034 (Accession NP_694956.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34034.

[46109] MGC50836 (Accession XP_171060.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC50836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC50836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC50836 BINDING SITE, designated SEQ ID:17939, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46110] Another function of GAM3298 is therefore inhibition of MGC50836 (Accession XP_171060.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC50836.

[46111] MGC5384 (Accession NP_112234.1) is another GAM3298 target gene, herein designated TARGET GENE. MGC5384 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC5384, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC5384 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46112] Another function of GAM3298 is therefore inhibition of MGC5384 (Accession NP_112234.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC5384.

[46113] Mhc class i polypeptide-related sequence a (MICA, Accession NP_000238.1) is another GAM3298 target gene, herein designated TARGET GENE. MICA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MICA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MICA BINDING SITE, designated SEQ ID:15857, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46114] Another function of GAM3298 is therefore inhibition of Mhc class i polypeptide-related sequence a (MICA, Accession NP_000238.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MICA.

[46115] MONDOA (Accession NP_055753.1) is another GAM3298 target gene, herein designated TARGET GENE. MONDOA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MONDOA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MONDOA BINDING SITE, designated SEQ ID:16680, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46116] Another function of GAM3298 is therefore inhibition of MONDOA (Accession NP_055753.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MONDOA.

[46117] MPRG (Accession NP_060175.2) is another GAM3298 target gene, herein designated TARGET GENE. MPRG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPRG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPRG BINDING SITE, designated SEQ ID:17939, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46118] Another function of GAM3298 is therefore inhibition of MPRG (Accession NP_060175.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPRG.

[46119] Mre11 meiotic recombination 11 homolog a (s. cerevisiae) (MRE11A, Accession NP_005582.1) is another GAM3298 target gene, herein designated TARGET GENE. MRE11A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRE11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRE11A BINDING SITE, designated SEQ ID:9057, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46120] Another function of GAM3298 is therefore inhibition of Mre11 meiotic recombination 11 homolog a (s. cerevisiae) (MRE11A, Accession NP_005582.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRE11A.

[46121] Mre11 meiotic recombination 11 homolog a (s. cerevisiae) (MRE11A, Accession NP_005581.2) is another GAM3298 target gene, herein designated TARGET GENE. MRE11A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded

by MRE11A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRE11A BINDING SITE, designated SEQ ID:9057, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46122] Another function of GAM3298 is therefore inhibition of Mre11 meiotic recombination 11 homolog a (s. cerevisiae) (MRE11A, Accession NP_005581.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRE11A.

[46123] Mitochondrial ribosomal protein s18b (MRPS18B, Accession NP_054765.1) is another GAM3298 target gene, herein designated TARGET GENE. MRPS18B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MRPS18B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPS18B BINDING SITE, designated SEQ ID:5843, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA,

also designated SEQ ID:259.

[46124] Another function of GAM3298 is therefore inhibition of Mitochondrial ribosomal protein s18b (MRPS18B, Accession NP_054765.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS18B.

[46125] Muts homolog 3 (e. coli) (MSH3, Accession NP_002430.1) is another GAM3298 target gene, herein designated TARGET GENE. MSH3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MSH3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MSH3 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46126] Another function of GAM3298 is therefore inhibition of Muts homolog 3 (e. coli) (MSH3, Accession NP_002430.1), a gene which belongs to the dna mismatch repair muts family. and therefore may be associated with Hereditary nonpolyposis colorectal cancer. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Hereditary nonpolyposis colorectal cancer, and of other

diseases and clinical conditions associated with MSH3.

[46127] The function of MSH3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.1.Major vault protein (MVP, Accession NP_059447.2) is another GAM3298 target gene, herein designated TARGET GENE. MVP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MVP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MVP BINDING SITE, designated SEQ ID:6247, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46128] Another function of GAM3298 is therefore inhibition of Major vault protein (MVP, Accession NP_059447.2), a gene which may be involved in nucleo- cytoplasmic transport. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MVP.

[46129] The function of MVP and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM1674.1.NBR2 (Accession NP_005812.1) is another GAM3298 target gene, herein designated TARGET GENE. NBR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NBR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NBR2 BINDING SITE, designated SEQ ID:17309, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46130] Another function of GAM3298 is therefore inhibition of NBR2 (Accession NP_005812.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NBR2.

[46131] Nuclear receptor coactivator 3 (NCOA3, Accession NP_006525.1) is another GAM3298 target gene, herein designated TARGET GENE. NCOA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NCOA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCOA3 BINDING SITE, desig-

nated SEQ ID:13706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46132] Another function of GAM3298 is therefore inhibition of Nuclear receptor coactivator 3 (NCOA3, Accession NP_006525.1), a gene which directly binds nuclear receptors and stimulates the transcriptional activities in hormone- dependent fashion. and therefore may be associated with Steroid- dependent cancers. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Steroid- dependent cancers., and of other diseases and clinical conditions associated with NCOA3.

[46133] The function of NCOA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM385.2.NDP52 (Accession NP_005822.1) is another GAM3298 target gene, herein designated TARGET GENE. NDP52 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDP52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDP52 BINDING SITE, designated SEQ ID:2868, to the

nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46134] Another function of GAM3298 is therefore inhibition of NDP52 (Accession NP_005822.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDP52.

[46135] Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) is another GAM3298 target gene, herein designated TARGET GENE. NDUFC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDUFC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NDUFC2 BINDING SITE, designated SEQ ID:12246, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46136] Another function of GAM3298 is therefore inhibition of Nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kda (NDUFC2, Accession NP_004540.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with NDUFC2.

[46137] Neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L, Accession NP_056092.2) is another GAM3298 target gene, herein designated TARGET GENE. NEDD4L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NEDD4L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEDD4L BINDING SITE, designated SEQ ID:12224, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46138] Another function of GAM3298 is therefore inhibition of Neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L, Accession NP_056092.2), a gene which may play a role in the regulation of epithelial sodium channel function. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEDD4L.

[46139] The function of NEDD4L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM499.2.Nuclear factor of activated t-cells 5, tonicity-responsive (NFAT5, Accession NP_775322.1) is another GAM3298 target gene, herein designated TARGET GENE. NFAT5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NFAT5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NFAT5 BINDING SITE, designated SEQ ID:12246, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46140] Another function of GAM3298 is therefore inhibition of Nuclear factor of activated t-cells 5, tonicity-responsive (NFAT5, Accession NP_775322.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFAT5.

[46141] Natural killer-tumor recognition sequence (NKTR, Accession NP_005376.2) is another GAM3298 target gene, herein designated TARGET GENE. NKTR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NKTR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NKTR BINDING SITE, designated SEQ ID:14143, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46142] Another function of GAM3298 is therefore inhibition of Natural killer-tumor recognition sequence (NKTR, Accession NP_005376.2), a gene which is involved in the function of nk cells. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NKTR.

[46143] The function of NKTR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM467.2.NMA (Accession NP_036474.1) is another GAM3298 target gene, herein designated TARGET GENE. NMA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NMA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NMA BINDING SITE, designated SEQ ID:12002, to the nucleotide sequence of GAM3298 RNA, herein designated

GAM RNA, also designated SEQ ID:259.

[46144] Another function of GAM3298 is therefore inhibition of NMA (Accession NP_036474.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NMA.

[46145] ODAG (Accession NP_066990.2) is another GAM3298 target gene, herein designated TARGET GENE. ODAG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ODAG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ODAG BINDING SITE, designated SEQ ID:13789, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46146] Another function of GAM3298 is therefore inhibition of ODAG (Accession NP_066990.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ODAG.

[46147] Optineurin (OPTN, Accession NP_068815.2) is another GAM3298 target gene, herein designated TARGET GENE. OPTN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OPTN, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OPTN BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46148] Another function of GAM3298 is therefore inhibition of Optineurin (OPTN, Accession NP_068815.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OPTN.

[46149] Platelet-activating factor acetylhydrolase 2, 40kda (PAFAH2, Accession NP_000428.2) is another GAM3298 target gene, herein designated TARGET GENE. PAFAH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PAFAH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PAFAH2 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46150] Another function of GAM3298 is therefore inhibition of

Platelet-activating factor acetylhydrolase 2, 40kda (PAFAH2, Accession NP_000428.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAFAH2.

[46151] PBXIP1 (Accession NP_065385.2) is another GAM3298 target gene, herein designated TARGET GENE. PBXIP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PBXIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PBXIP1 BINDING SITE, designated SEQ ID:19722, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46152] Another function of GAM3298 is therefore inhibition of PBXIP1 (Accession NP_065385.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PBXIP1.

[46153] Protocadherin 11 y-linked (PCDH11Y, Accession NP_116753.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDH11Y BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by PCDH11Y, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDH11Y BINDING SITE, designated SEQ ID:815, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46154] Another function of GAM3298 is therefore inhibition of Protocadherin 11 y-linked (PCDH11Y, Accession NP_116753.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11Y.

[46155] Protocadherin 11 y-linked (PCDH11Y, Accession NP_116754.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDH11Y BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDH11Y, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDH11Y BINDING SITE, designated SEQ ID:815, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46156] Another function of GAM3298 is therefore inhibition of Protocadherin 11 y-linked (PCDH11Y, Accession NP_116754.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11Y.

[46157] Protocadherin alpha 1 (PCDHA1, Accession NP_113599.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA1 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46158] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 1 (PCDHA1, Accession NP_113599.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA1.

[46159] Protocadherin alpha 1 (PCDHA1, Accession NP_061723.1) is another GAM3298 target gene, herein designated TAR-

GET GENE. PCDHA1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA1 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46160] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 1 (PCDHA1, Accession NP_061723.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA1.

[46161] Protocadherin alpha 10 (PCDHA10, Accession NP_061724.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA10 BINDING SITE, designated SEQ ID:12657, to

the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46162] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 10 (PCDHA10, Accession NP_061724.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA10.

[46163] Protocadherin alpha 10 (PCDHA10, Accession NP_114066.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA10 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA10 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46164] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 10 (PCDHA10, Accession NP_114066.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA10.

[46165] Protocadherin alpha 11 (PCDHA11, Accession NP_061725.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA11 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46166] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 11 (PCDHA11, Accession NP_061725.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA11.

[46167] Protocadherin alpha 12 (PCDHA12, Accession NP_061726.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 il-

lustrates the complementarity of the nucleotide sequences of PCDHA12 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46168] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 12 (PCDHA12, Accession NP_061726.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA12.

[46169] Protocadherin alpha 13 (PCDHA13, Accession NP_061727.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA13 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46170] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 13 (PCDHA13, Accession NP_061727.1) . Accordingly, utilities of GAM3298 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA13.

[46171] Protocadherin alpha 2 (PCDHA2, Accession NP_061728.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA2 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46172] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 2 (PCDHA2, Accession NP_061728.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA2.

[46173] Protocadherin alpha 3 (PCDHA3, Accession NP_061729.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHA3, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA3 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46174] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 3 (PCDHA3, Accession NP_061729.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA3.

[46175] Protocadherin alpha 4 (PCDHA4, Accession NP_061730.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA4 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46176] Another function of GAM3298 is therefore inhibition of

Protocadherin alpha 4 (PCDHA4, Accession NP_061730.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA4.

[46177] Protocadherin alpha 5 (PCDHA5, Accession NP_061731.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHA5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA5 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46178] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 5 (PCDHA5, Accession NP_061731.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA5.

[46179] Protocadherin alpha 6 (PCDHA6, Accession NP_061732.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA6 BINDING SITE is a target binding site

found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA6 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46180] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 6 (PCDHA6, Accession NP_061732.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA6.

[46181] Protocadherin alpha 6 (PCDHA6, Accession NP_114037.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA6 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA,

also designated SEQ ID:259.

[46182] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 6 (PCDHA6, Accession NP_114037.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA6.

[46183] Protocadherin alpha 7 (PCDHA7, Accession NP_061733.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHA7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA7 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46184] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 7 (PCDHA7, Accession NP_061733.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA7.

[46185] Protocadherin alpha 8 (PCDHA8, Accession NP_061734.1)

is another GAM3298 target gene, herein designated TARGET GENE. PCDHA8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHA8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA8 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46186] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 8 (PCDHA8, Accession NP_061734.1). Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA8.

[46187] Protocadherin alpha 9 (PCDHA9, Accession NP_114063.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHA9 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHA9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHA9 BIND-

ING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46188] Another function of GAM3298 is therefore inhibition of Protocadherin alpha 9 (PCDHA9, Accession NP_114063.1), a gene which is a calcium- dependent cell- adhesion protein. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA9.

[46189] The function of PCDHA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Protocadherin alpha subfamily c, 1 (PCDHAC1, Accession NP_061721.2) is another GAM3298 target gene, herein designated TARGET GENE. PCDHAC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PCDHAC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHAC1 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ

ID:259.

[46190] Another function of GAM3298 is therefore inhibition of Protocadherin alpha subfamily c, 1 (PCDHAC1, Accession NP_061721.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHAC1.

[46191] Protocadherin alpha subfamily c, 2 (PCDHAC2, Accession NP_061722.1) is another GAM3298 target gene, herein designated TARGET GENE. PCDHAC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHAC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHAC2 BINDING SITE, designated SEQ ID:12657, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46192] Another function of GAM3298 is therefore inhibition of Protocadherin alpha subfamily c, 2 (PCDHAC2, Accession NP_061722.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHAC2.

[46193] PEX26 (Accession NP_060399.1) is another GAM3298 tar-

get gene, herein designated TARGET GENE. PEX26 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PEX26, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PEX26 BINDING SITE, designated SEQ ID:16060, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46194] Another function of GAM3298 is therefore inhibition of PEX26 (Accession NP_060399.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEX26.

[46195] Phosphatidylinositol glycan, class m (PIGM, Accession NP_660150.1) is another GAM3298 target gene, herein designated TARGET GENE. PIGM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIGM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIGM BINDING SITE, designated SEQ ID:1310, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ

ID:259.

[46196] Another function of GAM3298 is therefore inhibition of Phosphatidylinositol glycan, class m (PIGM, Accession NP_660150.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGM.

[46197] PIGO (Accession NP_116023.2) is another GAM3298 target gene, herein designated TARGET GENE. PIGO BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PIGO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIGO BINDING SITE, designated SEQ ID:19803, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46198] Another function of GAM3298 is therefore inhibition of PIGO (Accession NP_116023.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGO.

[46199] PIGO (Accession NP_690577.1) is another GAM3298 target gene, herein designated TARGET GENE. PIGO BINDING SITE is a target binding site found in the 3` untranslated re-

gion of multiple transcripts of mRNA encoded by PIGO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIGO BINDING SITE, designated SEQ ID:19803, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46200] Another function of GAM3298 is therefore inhibition of PIGO (Accession NP_690577.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGO.

[46201] Phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta) (PIK3R2, Accession NP_005018.1) is another GAM3298 target gene, herein designated TARGET GENE. PIK3R2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIK3R2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIK3R2 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46202] Another function of GAM3298 is therefore inhibition of Phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta) (PIK3R2, Accession NP_005018.1), a gene which acts as an adapter and is regulatory subunit (p85 beta) of phosphatidylinositol 3- kinase. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3R2.

[46203] The function of PIK3R2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM439.1.Polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1, Accession NP_619639.2) is another GAM3298 target gene, herein designated TARGET GENE. PKHD1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PKHD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PKHD1 BINDING SITE, designated SEQ ID:12090, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46204] Another function of GAM3298 is therefore inhibition of Polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1, Accession NP_619639.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKHD1.

[46205] Placenta-specific 1 (PLAC1, Accession NP_068568.1) is another GAM3298 target gene, herein designated TARGET GENE. PLAC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLAC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PLAC1 BINDING SITE, designated SEQ ID:1845, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46206] Another function of GAM3298 is therefore inhibition of Placenta-specific 1 (PLAC1, Accession NP_068568.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAC1.

[46207] PNPLA1 (Accession NP_775947.1) is another GAM3298 target gene, herein designated TARGET GENE. PNPLA1

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PNPLA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PNPLA1 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46208] Another function of GAM3298 is therefore inhibition of PNPLA1 (Accession NP_775947.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNPLA1.

[46209] Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) is another GAM3298 target gene, herein designated TARGET GENE. POFUT1 BINDING SITE1 and POFUT1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by POFUT1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POFUT1 BINDING SITE1 and POFUT1 BINDING SITE2, designated SEQ ID:8174 and SEQ ID:6456 respectively, to the nucleotide sequence of

GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46210] Another function of GAM3298 is therefore inhibition of Protein o-fucosyltransferase 1 (POFUT1, Accession NP_056167.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POFUT1.

[46211] Polymerase (dna directed), eta (POLH, Accession NP_006493.1) is another GAM3298 target gene, herein designated TARGET GENE. POLH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLH BINDING SITE, designated SEQ ID:11747, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46212] Another function of GAM3298 is therefore inhibition of Polymerase (dna directed), eta (POLH, Accession NP_006493.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLH.

[46213] PORIMIN (Accession NP_443164.1) is another GAM3298 target gene, herein designated TARGET GENE. PORIMIN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PORIMIN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PORIMIN BINDING SITE, designated SEQ ID:5738, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46214] Another function of GAM3298 is therefore inhibition of PORIMIN (Accession NP_443164.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PORIMIN.

[46215] Pyrophosphatase (inorganic) (PP, Accession NP_066952.1) is another GAM3298 target gene, herein designated TARGET GENE. PP BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP BINDING SITE, designated SEQ ID:5885, to

the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46216] Another function of GAM3298 is therefore inhibition of Pyrophosphatase (inorganic) (PP, Accession NP_066952.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP.

[46217] Protein phosphatase 1, regulatory (inhibitor) subunit 3b (PPP1R3B, Accession NP_078883.1) is another GAM3298 target gene, herein designated TARGET GENE. PPP1R3B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPP1R3B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R3B BINDING SITE, designated SEQ ID:19238, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46218] Another function of GAM3298 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 3b (PPP1R3B, Accession NP_078883.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

PPP1R3B.

[46219] Protein phosphatase 6, catalytic subunit (PPP6C, Accession NP_002712.1) is another GAM3298 target gene, herein designated TARGET GENE. PPP6C BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PPP6C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP6C BINDING SITE, designated SEQ ID:17178, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46220] Another function of GAM3298 is therefore inhibition of Protein phosphatase 6, catalytic subunit (PPP6C, Accession NP_002712.1), a gene which is the catalytic subunit of protein phosphatase 6 which may function in cell cycle regulation. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP6C.

[46221] The function of PPP6C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM287.2.Protein kinase, y-linked (PRKY, Accession

NP_002751.1) is another GAM3298 target gene, herein designated TARGET GENE. PRKY BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRKY, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKY BINDING SITE, designated SEQ ID:9486, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46222] Another function of GAM3298 is therefore inhibition of Protein kinase, y-linked (PRKY, Accession NP_002751.1), a gene which is a putative protein kinase. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKY.

[46223] The function of PRKY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.PRO0478 (Accession NP_054848.1) is another GAM3298 target gene, herein designated TARGET GENE. PRO0478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

PRO0478, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO0478 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46224] Another function of GAM3298 is therefore inhibition of PRO0478 (Accession NP_054848.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0478.

[46225] PRO1496 (Accession NP_061073.1) is another GAM3298 target gene, herein designated TARGET GENE. PRO1496 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO1496, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO1496 BINDING SITE, designated SEQ ID:16693, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46226] Another function of GAM3298 is therefore inhibition of

PRO1496 (Accession NP_061073.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1496.

[46227] PRO1853 (Accession NP_061077.1) is another GAM3298 target gene, herein designated TARGET GENE. PRO1853 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PRO1853, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO1853 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46228] Another function of GAM3298 is therefore inhibition of PRO1853 (Accession NP_061077.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1853.

[46229] PRO2859 (Accession NP_061013.1) is another GAM3298 target gene, herein designated TARGET GENE. PRO2859 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by PRO2859, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO2859 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46230] Another function of GAM3298 is therefore inhibition of PRO2859 (Accession NP_061013.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2859.

[46231] PRO2949 (Accession NP_061014.1) is another GAM3298 target gene, herein designated TARGET GENE. PRO2949 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO2949, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO2949 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46232] Another function of GAM3298 is therefore inhibition of

PRO2949 (Accession NP_061014.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2949.

[46233] Presenilin 1 (alzheimer disease 3) (PSEN1, Accession NP_015557.1) is another GAM3298 target gene, herein designated TARGET GENE. PSEN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSEN1 BINDING SITE, designated SEQ ID:8810, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46234] Another function of GAM3298 is therefore inhibition of Presenilin 1 (alzheimer disease 3) (PSEN1, Accession NP_015557.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSEN1.

[46235] Presenilin 1 (alzheimer disease 3) (PSEN1, Accession NP_000012.1) is another GAM3298 target gene, herein designated TARGET GENE. PSEN1 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PSEN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSEN1 BINDING SITE, designated SEQ ID:8810, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46236] Another function of GAM3298 is therefore inhibition of Presenilin 1 (alzheimer disease 3) (PSEN1, Accession NP_000012.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSEN1.

[46237] PSK (Accession NP_057235.1) is another GAM3298 target gene, herein designated TARGET GENE. PSK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSK BINDING SITE, designated SEQ ID:17787, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46238] Another function of GAM3298 is therefore inhibition of PSK (Accession NP_057235.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSK.

[46239] Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1) is another GAM3298 target gene, herein designated TARGET GENE. PTGIS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGIS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGIS BINDING SITE, designated SEQ ID:4543, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46240] Another function of GAM3298 is therefore inhibition of Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1), a gene which catalyzes the isomerization of prostaglandin h2 to prostacyclin (= prostaglandin i2). Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGIS.

[46241] The function of PTGIS and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Ptk6 protein tyrosine kinase 6 (PTK6, Accession NP_005966.1) is another GAM3298 target gene, herein designated TARGET GENE. PTK6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTK6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTK6 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46242] Another function of GAM3298 is therefore inhibition of Ptk6 protein tyrosine kinase 6 (PTK6, Accession NP_005966.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTK6.

[46243] Rab4b, member ras oncogene family (RAB4B, Accession NP_057238.2) is another GAM3298 target gene, herein designated TARGET GENE. RAB4B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RAB4B, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB4B BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46244] Another function of GAM3298 is therefore inhibition of Rab4b, member ras oncogene family (RAB4B, Accession NP_057238.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB4B.

[46245] RABEX5 (Accession NP_055319.1) is another GAM3298 target gene, herein designated TARGET GENE. RABEX5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RABEX5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RABEX5 BINDING SITE, designated SEQ ID:6850, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46246] Another function of GAM3298 is therefore inhibition of RABEX5 (Accession NP_055319.1) . Accordingly, utilities of

GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABEX5.

[46247] Rad51 homolog (reca homolog, e. coli) (s. cerevisiae) (RAD51, Accession NP_002866.2) is another GAM3298 target gene, herein designated TARGET GENE. RAD51 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAD51, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD51 BINDING SITE, designated SEQ ID:16562, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46248] Another function of GAM3298 is therefore inhibition of Rad51 homolog (reca homolog, e. coli) (s. cerevisiae) (RAD51, Accession NP_002866.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD51.

[46249] Rad51 homolog (reca homolog, e. coli) (s. cerevisiae) (RAD51, Accession NP_597994.1) is another GAM3298 target gene, herein designated TARGET GENE. RAD51 BINDING SITE is a target binding site found in the 3` un-

translated region of multiple transcripts of mRNA encoded by RAD51, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD51 BINDING SITE, designated SEQ ID:16562, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46250] Another function of GAM3298 is therefore inhibition of Rad51 homolog (reca homolog, e. coli) (s. cerevisiae) (RAD51, Accession NP_597994.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD51.

[46251] RDHL (Accession NP_005762.2) is another GAM3298 target gene, herein designated TARGET GENE. RDHL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RDHL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RDHL BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46252] Another function of GAM3298 is therefore inhibition of RDHL (Accession NP_005762.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RDHL.

[46253] Recq protein-like 5 (RECQL5, Accession NP_004250.1) is another GAM3298 target gene, herein designated TARGET GENE. RECQL5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RECQL5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RECQL5 BINDING SITE, designated SEQ ID:2405, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46254] Another function of GAM3298 is therefore inhibition of Recq protein-like 5 (RECQL5, Accession NP_004250.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RECQL5.

[46255] SCR59 (Accession NP_075559.1) is another GAM3298 target gene, herein designated TARGET GENE. SCR59 BINDING SITE is a target binding site found in the 3` untrans-

lated region of mRNA encoded by SCR59, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCR59 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46256] Another function of GAM3298 is therefore inhibition of SCR59 (Accession NP_075559.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCR59.

[46257] Secreted and transmembrane 1 (SECTM1, Accession NP_002995.1) is another GAM3298 target gene, herein designated TARGET GENE. SECTM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SECTM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SECTM1 BINDING SITE, designated SEQ ID:18249, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46258] Another function of GAM3298 is therefore inhibition of

Secreted and transmembrane 1 (SECTM1, Accession NP_002995.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SECTM1.

[46259] Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) is another GAM3298 target gene, herein designated TARGET GENE. SERF1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERF1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1A BINDING SITE, designated SEQ ID:4210, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46260] Another function of GAM3298 is therefore inhibition of Small edrk-rich factor 1a (telomeric) (SERF1A, Accession NP_068802.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1A.

[46261] Small edrk-rich factor 1b (centromeric) (SERF1B, Accession NP_075267.1) is another GAM3298 target gene, herein designated TARGET GENE. SERF1B BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by SERF1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERF1B BINDING SITE, designated SEQ ID:4210, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46262] Another function of GAM3298 is therefore inhibition of Small edrk-rich factor 1b (centromeric) (SERF1B, Accession NP_075267.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1B.

[46263] Solute carrier family 17 (anion/sugar transporter), member 5 (SLC17A5, Accession NP_036566.1) is another GAM3298 target gene, herein designated TARGET GENE. SLC17A5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC17A5 BINDING SITE, designated SEQ ID:3707, to the nucleotide sequence of GAM3298 RNA,

herein designated GAM RNA, also designated SEQ ID:259.

[46264] Another function of GAM3298 is therefore inhibition of Solute carrier family 17 (anion/sugar transporter), member 5 (SLC17A5, Accession NP_036566.1), a gene which is a member of a family of anion/cation symporters and therefore may be associated with Salla disease ; infantile sialic acid storage disorder. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Salla disease ; infantile sialic acid storage disorder, and of other diseases and clinical conditions associated with SLC17A5.

[46265] The function of SLC17A5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.2.Solute carrier family 26, member 4 (SLC26A4, Accession NP_000432.1) is another GAM3298 target gene, herein designated TARGET GENE. SLC26A4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC26A4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC26A4 BINDING SITE, designated SEQ ID:3706, to the

nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46266] Another function of GAM3298 is therefore inhibition of Solute carrier family 26, member 4 (SLC26A4, Accession NP_000432.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC26A4.

[46267] Solute carrier family 31 (copper transporters), member 1 (SLC31A1, Accession NP_001850.1) is another GAM3298 target gene, herein designated TARGET GENE. SLC31A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC31A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC31A1 BINDING SITE, designated SEQ ID:912, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46268] Another function of GAM3298 is therefore inhibition of Solute carrier family 31 (copper transporters), member 1 (SLC31A1, Accession NP_001850.1), a gene which is involved in high- affinity copper uptake. Accordingly, utilities of GAM3298 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with SLC31A1.

[46269] The function of SLC31A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM257.1.SLC35E1 (Accession NP_079157.2) is another GAM3298 target gene, herein designated TARGET GENE. SLC35E1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC35E1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC35E1 BINDING SITE, designated SEQ ID:6353, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46270] Another function of GAM3298 is therefore inhibition of SLC35E1 (Accession NP_079157.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35E1.

[46271] Swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 (SMARCD2, Ac-

cession NP_003068.2) is another GAM3298 target gene, herein designated TARGET GENE. SMARCD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SMARCD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMARCD2 BINDING SITE, designated SEQ ID:6099, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46272] Another function of GAM3298 is therefore inhibition of Swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 (SMARCD2, Accession NP_003068.2), a gene which is involved in chromatin remodeling. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMARCD2.

[46273] The function of SMARCD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM537.1.Syntaphilin (SNPH, Accession NP_055538.1) is another GAM3298 target gene, herein designated TARGET GENE. SNPH BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by SNPH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNPH BINDING SITE, designated SEQ ID:4989, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46274] Another function of GAM3298 is therefore inhibition of Syntaphilin (SNPH, Accession NP_055538.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNPH.

[46275] Sorting nexin 11 (SNX11, Accession NP_037455.2) is another GAM3298 target gene, herein designated TARGET GENE. SNX11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX11 BINDING SITE, designated SEQ ID:19139, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46276] Another function of GAM3298 is therefore inhibition of Sorting nexin 11 (SNX11, Accession NP_037455.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX11.

[46277] Sorting nexin 11 (SNX11, Accession NP_689450.1) is another GAM3298 target gene, herein designated TARGET GENE. SNX11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX11 BINDING SITE, designated SEQ ID:19139, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46278] Another function of GAM3298 is therefore inhibition of Sorting nexin 11 (SNX11, Accession NP_689450.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX11.

[46279] SNX22 (Accession NP_079074.1) is another GAM3298 target gene, herein designated TARGET GENE. SNX22 BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SNX22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX22 BINDING SITE, designated SEQ ID:8175, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46280] Another function of GAM3298 is therefore inhibition of SNX22 (Accession NP_079074.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX22.

[46281] SNX25 (Accession NP_114159.1) is another GAM3298 target gene, herein designated TARGET GENE. SNX25 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SNX25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX25 BINDING SITE, designated SEQ ID:11908, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46282] Another function of GAM3298 is therefore inhibition of

SNX25 (Accession NP_114159.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX25.

[46283] Serine palmitoyltransferase, long chain base subunit 1 (SPTLC1, Accession NP_847894.1) is another GAM3298 target gene, herein designated TARGET GENE. SPTLC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SPTLC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPTLC1 BINDING SITE, designated SEQ ID:478, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46284] Another function of GAM3298 is therefore inhibition of Serine palmitoyltransferase, long chain base subunit 1 (SPTLC1, Accession NP_847894.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPTLC1.

[46285] Staufen, rna binding protein (drosophila) (STAU, Accession NP_059347.1) is another GAM3298 target gene, herein designated TARGET GENE. STAU BINDING SITE is a target

binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by STAU, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STAU BINDING SITE, designated SEQ ID:17501, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46286] Another function of GAM3298 is therefore inhibition of Staufen, rna binding protein (drosophila) (STAU, Accession NP_059347.1), a gene which may play a role in specific positioning of mrnas at given sites in the cell and in stimulating their translation at the site. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAU.

[46287] The function of STAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM37.1.Synaptojanin 2 binding protein (SYNJ2BP, Accession NP_060843.1) is another GAM3298 target gene, herein designated TARGET GENE. SYNJ2BP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SYNJ2BP, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SYNJ2BP BINDING SITE, designated SEQ ID:666, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46288] Another function of GAM3298 is therefore inhibition of Synaptojanin 2 binding protein (SYNJ2BP, Accession NP_060843.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYNJ2BP.

[46289] TEM7 (Accession NP_065138.2) is another GAM3298 target gene, herein designated TARGET GENE. TEM7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TEM7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TEM7 BINDING SITE, designated SEQ ID:14878, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46290] Another function of GAM3298 is therefore inhibition of TEM7 (Accession NP_065138.2), a gene which involves in

angiogenesis and therefore may be associated with Colorectal cancer. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Colorectal cancer, and of other diseases and clinical conditions associated with TEM7.

[46291] The function of TEM7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Testis expressed sequence 15 (TEX15, Accession NP_112561.1) is another GAM3298 target gene, herein designated TARGET GENE. TEX15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TEX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TEX15 BINDING SITE, designated SEQ ID:18387, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46292] Another function of GAM3298 is therefore inhibition of Testis expressed sequence 15 (TEX15, Accession NP_112561.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with TEX15.

[46293] TMG4 (Accession NP_076986.1) is another GAM3298 target gene, herein designated TARGET GENE. TMG4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TMG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMG4 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46294] Another function of GAM3298 is therefore inhibition of TMG4 (Accession NP_076986.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMG4.

[46295] Tumor necrosis factor receptor superfamily, member 10a (TNFRSF10A, Accession NP_003835.2) is another GAM3298 target gene, herein designated TARGET GENE. TNFRSF10A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF10A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of TNFRSF10A BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46296] Another function of GAM3298 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10a (TNFRSF10A, Accession NP_003835.2), a gene which is a member of the tumor necrosis factor receptor superfamily; involved in apoptosis; contains a cytoplasmic death domain. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF10A.

[46297] The function of TNFRSF10A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM236.1.Tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain (TNFRSF10D, Accession NP_003831.2) is another GAM3298 target gene, herein designated TARGET GENE. TNFRSF10D BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF10D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF10D BINDING SITE, designated SEQ ID:20093, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46298] Another function of GAM3298 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain (TNFRSF10D, Accession NP_003831.2), a gene which activates NF- kappaB and inhibits TRAIL- induced apoptosis. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF10D.

[46299] The function of TNFRSF10D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM236.1.TOPK (Accession NP_060962.2) is another GAM3298 target gene, herein designated TARGET GENE. TOPK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TOPK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of TOPK BINDING SITE, designated SEQ ID:4288, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46300] Another function of GAM3298 is therefore inhibition of TOPK (Accession NP_060962.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOPK.

[46301] Tripartite motif-containing 8 (TRIM8, Accession NP_112174.1) is another GAM3298 target gene, herein designated TARGET GENE. TRIM8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRIM8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM8 BINDING SITE, designated SEQ ID:16708, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46302] Another function of GAM3298 is therefore inhibition of Tripartite motif-containing 8 (TRIM8, Accession NP_112174.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM8.

[46303] Transient receptor potential cation channel, subfamily m, member 1 (TRPM1, Accession NP_002411.2) is another GAM3298 target gene, herein designated TARGET GENE. TRPM1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPM1 BINDING SITE, designated SEQ ID:840, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46304] Another function of GAM3298 is therefore inhibition of Transient receptor potential cation channel, subfamily m, member 1 (TRPM1, Accession NP_002411.2), a gene which is suggested to mediate calcium entry. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPM1.

[46305] The function of TRPM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) is another GAM3298 target gene, herein

designated TARGET GENE. TXNL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TXNL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TXNL2 BINDING SITE, designated SEQ ID:16694, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46306] Another function of GAM3298 is therefore inhibition of Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TXNL2.

[46307] Uroplakin 1b (UPK1B, Accession NP_008883.1) is another GAM3298 target gene, herein designated TARGET GENE. UPK1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UPK1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UPK1B BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated

GAM RNA, also designated SEQ ID:259.

[46308] Another function of GAM3298 is therefore inhibition of Uroplakin 1b (UPK1B, Accession NP_008883.1), a gene which strengthens and stabilizes the urothelial apical surface of the asymmetric unit membrane of mammalian bladder epithelium. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UPK1B.

[46309] The function of UPK1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Von hippel-lindau syndrome (VHL, Accession NP_000542.1) is another GAM3298 target gene, herein designated TARGET GENE. VHL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VHL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VHL BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46310] Another function of GAM3298 is therefore inhibition of

Von hippel-lindau syndrome (VHL, Accession NP_000542.1), a gene which may control rna stability through the selective degradation of rna- bound proteins. and therefore is associated with Von hippel- lindau disease. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of Von hippel- lindau disease, and of other diseases and clinical conditions associated with VHL.

[46311] The function of VHL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Vacuolar protein sorting 4b (yeast) (VPS4B, Accession NP_004860.2) is another GAM3298 target gene, herein designated TARGET GENE. VPS4B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VPS4B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VPS4B BINDING SITE, designated SEQ ID:19238, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46312] Another function of GAM3298 is therefore inhibition of

Vacuolar protein sorting 4b (yeast) (VPS4B, Accession NP_004860.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS4B.

[46313] Williams beuren syndrome chromosome region 21 (WBSCR21, Accession NP_683710.1) is another GAM3298 target gene, herein designated TARGET GENE. WBSCR21 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WBSCR21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR21 BINDING SITE, designated SEQ ID:6665, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46314] Another function of GAM3298 is therefore inhibition of Williams beuren syndrome chromosome region 21 (WBSCR21, Accession NP_683710.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR21.

[46315] Williams beuren syndrome chromosome region 21

(WBSCR21, Accession NP_683711.1) is another GAM3298 target gene, herein designated TARGET GENE. WBSCR21 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WBSCR21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR21 BINDING SITE, designated SEQ ID:6665, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46316] Another function of GAM3298 is therefore inhibition of Williams beuren syndrome chromosome region 21 (WBSCR21, Accession NP_683711.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR21.

[46317] Williams beuren syndrome chromosome region 21 (WBSCR21, Accession NP_112585.2) is another GAM3298 target gene, herein designated TARGET GENE. WBSCR21 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WBSCR21, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR21 BINDING SITE, designated SEQ ID:6665, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46318] Another function of GAM3298 is therefore inhibition of Williams beuren syndrome chromosome region 21 (WBSCR21, Accession NP_112585.2) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR21.

[46319] Williams beuren syndrome chromosome region 21 (WBSCR21, Accession NP_683713.1) is another GAM3298 target gene, herein designated TARGET GENE. WBSCR21 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WBSCR21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WBSCR21 BINDING SITE, designated SEQ ID:6665, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ

ID:259.

[46320] Another function of GAM3298 is therefore inhibition of Williams beuren syndrome chromosome region 21 (WBSCR21, Accession NP_683713.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WB-SCR21.

[46321] WDR23 (Accession NP_079506.3) is another GAM3298 target gene, herein designated TARGET GENE. WDR23 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WDR23, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WDR23 BINDING SITE, designated SEQ ID:1087, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46322] Another function of GAM3298 is therefore inhibition of WDR23 (Accession NP_079506.3) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDR23.

[46323] WDR23 (Accession NP_852002.1) is another GAM3298

target gene, herein designated TARGET GENE. WDR23 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WDR23, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WDR23 BINDING SITE, designated SEQ ID:1087, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46324] Another function of GAM3298 is therefore inhibition of WDR23 (Accession NP_852002.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDR23.

[46325] Wee1 homolog (s. pombe) (WEE1, Accession NP_003381.1) is another GAM3298 target gene, herein designated TARGET GENE. WEE1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WEE1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of WEE1 BINDING SITE, designated SEQ ID:5763, to the nucleotide sequence of GAM3298 RNA,

herein designated GAM RNA, also designated SEQ ID:259.

[46326] Another function of GAM3298 is therefore inhibition of Wee1 homolog (s. pombe) (WEE1, Accession NP_003381.1), a gene which negatively regulates entry into mitosis by catalyzing the inhibitory tyrosine phosphorylation of CDC2/cyclin. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WEE1.

[46327] The function of WEE1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM322.1.X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1) is another GAM3298 target gene, herein designated TARGET GENE. XRCC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by XRCC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of XRCC2 BINDING SITE, designated SEQ ID:2322, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46328] Another function of GAM3298 is therefore inhibition of X-ray repair complementing defective repair in chinese hamster cells 2 (XRCC2, Accession NP_005422.1), a gene which involves in the homologous recombination repair (hrr) pathway of double- stranded dna. Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XRCC2.

[46329] The function of XRCC2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.ZFP30 (Accession NP_055713.1) is another GAM3298 target gene, herein designated TARGET GENE. ZFP30 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZFP30, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP30 BINDING SITE, designated SEQ ID:1921, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46330] Another function of GAM3298 is therefore inhibition of ZFP30 (Accession NP_055713.1) . Accordingly, utilities of

GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP30.

[46331] Zinc finger protein 174 (ZNF174, Accession NP_003441.1) is another GAM3298 target gene, herein designated TARGET GENE. ZNF174 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZNF174, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF174 BINDING SITE, designated SEQ ID:7167, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46332] Another function of GAM3298 is therefore inhibition of Zinc finger protein 174 (ZNF174, Accession NP_003441.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF174.

[46333] Zinc finger protein 197 (ZNF197, Accession NP_008922.1) is another GAM3298 target gene, herein designated TARGET GENE. ZNF197 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF197, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF197 BINDING SITE, designated SEQ ID:12246, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46334] Another function of GAM3298 is therefore inhibition of Zinc finger protein 197 (ZNF197, Accession NP_008922.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF197.

[46335] Zinc finger protein 264 (ZNF264, Accession NP_003408.1) is another GAM3298 target gene, herein designated TARGET GENE. ZNF264 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF264, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF264 BINDING SITE, designated SEQ ID:8644, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46336] Another function of GAM3298 is therefore inhibition of

Zinc finger protein 264 (ZNF264, Accession NP_003408.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF264.

[46337] ZNF450 (Accession NP_055612.1) is another GAM3298 target gene, herein designated TARGET GENE. ZNF450 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF450, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF450 BINDING SITE, designated SEQ ID:3706, to the nucleotide sequence of GAM3298 RNA, herein designated GAM RNA, also designated SEQ ID:259.

[46338] Another function of GAM3298 is therefore inhibition of ZNF450 (Accession NP_055612.1) . Accordingly, utilities of GAM3298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF450.

[46339]

[46340] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 3418

(GAM3418), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[46341] GAM3418 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM3418 was detected is described hereinabove with reference to Figs. 8-15.

[46342] GAM3418 gene, herein designated GAM GENE, and GAM3418 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[46343] GAM3418 gene encodes a GAM3418 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM3418 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3418 precursor RNA is designated SEQ ID:147, and is provided hereinbelow with reference to the sequence listing part.

[46344] GAM3418 precursor RNA folds onto itself, forming GAM3418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA

genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[46345] GAM3418 precursor RNA folds onto itself, forming GAM3418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[46346] Nucleotide sequence of GAM3418 precursor RNA, designated SEQ-ID: 147, and a schematic representation of a predicted secondary folding of GAM3418 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[46347] An enzyme complex designated DICER COMPLEX, `dices` the GAM3418 folded precursor RNA into GAM3418 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM3418 RNA is designated SEQ ID:291, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[46348] GAM3418 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM3418 target RNA, herein designated GAM TARGET RNA. GAM3418 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[46349] GAM3418 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3418 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3418 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING

SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM3418 RNA may have a different number of target binding sites in untranslated regions of a GAM3418 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[46350] The complementary binding of GAM3418 RNA, herein designated GAM RNA, to target binding sites on GAM3418 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3418 target RNA into GAM3418 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[46351] It is appreciated that GAM3418 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM3418 target genes. The mRNA of each one of this plurality of GAM3418 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3418 RNA,

herein designated GAM RNA, and which when bound by GAM3418 RNA causes inhibition of translation of respective one or more GAM3418 target proteins.

[46352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM3418 gene, herein designated GAM GENE, on one or more GAM3418 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[46353] It is appreciated that specific functions and accordingly utilities of GAM3418 correlate with, and may be deduced from, the identity of the target genes which GAM3418 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[46354]

[46355]

[46356] A disintegrin and metalloproteinase domain 19 (meltrin beta) (ADAM19, Accession NP_150377.1) is a GAM3418 target gene, herein designated TARGET GENE. ADAM19 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ADAM19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAM19 BINDING SITE, designated SEQ ID:2787, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46357] A function of GAM3418 is therefore inhibition of A disintegrin and metalloproteinase domain 19 (meltrin beta) (ADAM19, Accession NP_150377.1), a gene which participates in the proteolytic processing of beta- type neuregulin isoforms . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM19.

[46358] The function of ADAM19 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM129.1.B1 (Accession NP_055266.1) is another GAM3418 target gene, herein designated TARGET GENE. B1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B1 BINDING SITE, designated SEQ ID:9166, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46359] Another function of GAM3418 is therefore inhibition of B1 (Accession NP_055266.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B1.

[46360] Cyclin-dependent kinase 4 (CDK4, Accession NP_000066.1) is another GAM3418 target gene, herein designated TARGET GENE. CDK4 BINDING SITE1 and CDK4 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CDK4, corresponding to target binding sites such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDK4 BINDING SITE1 and CDK4 BINDING SITE2, designated SEQ ID:5869 and SEQ ID:12296 respectively, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46361] Another function of GAM3418 is therefore inhibition of Cyclin-dependent kinase 4 (CDK4, Accession NP_000066.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDK4.

[46362] Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) is another GAM3418 target gene, herein designated TARGET GENE. CPSF2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CPSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPSF2 BINDING SITE, designated SEQ ID:20174, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46363] Another function of GAM3418 is therefore inhibition of Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPSF2.

[46364] Cylindromatosis (turban tumor syndrome) (CYLD, Accession NP_056062.1) is another GAM3418 target gene, herein designated TARGET GENE. CYLD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYLD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYLD BINDING SITE, designated SEQ ID:18734, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46365] Another function of GAM3418 is therefore inhibition of Cylindromatosis (turban tumor syndrome) (CYLD, Accession NP_056062.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYLD.

[46366] DKFZp547G0215 (Accession NP_775914.1) is another GAM3418 target gene, herein designated TARGET GENE.

DKFZp547G0215 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547G0215, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547G0215 BINDING SITE, designated SEQ ID:3848, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46367] Another function of GAM3418 is therefore inhibition of DKFZp547G0215 (Accession NP_775914.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547G0215.

[46368] Ells1 (Accession NP_690006.1) is another GAM3418 target gene, herein designated TARGET GENE. Ells1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Ells1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Ells1 BINDING SITE, designated SEQ ID:11977, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA,

also designated SEQ ID:291.

[46369] Another function of GAM3418 is therefore inhibition of Ells1 (Accession NP_690006.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Ells1.

[46370] Estrogen-related receptor gamma (ESRRG, Accession NP_001429.1) is another GAM3418 target gene, herein designated TARGET GENE. ESRRG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ESRRG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ESRRG BINDING SITE, designated SEQ ID:19845, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46371] Another function of GAM3418 is therefore inhibition of Estrogen-related receptor gamma (ESRRG, Accession NP_001429.1), a gene which Estrogen- related receptor gamma. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESRRG.

[46372] The function of ESRRG and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM200.1.FLJ11175 (Accession NP_060819.1) is another GAM3418 target gene, herein designated TARGET GENE. FLJ11175 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11175, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11175 BINDING SITE, designated SEQ ID:12392, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46373] Another function of GAM3418 is therefore inhibition of FLJ11175 (Accession NP_060819.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11175.

[46374] FLJ12660 (Accession NP_079428.1) is another GAM3418 target gene, herein designated TARGET GENE. FLJ12660 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12660, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12660 BINDING SITE, designated SEQ ID:9523, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46375] Another function of GAM3418 is therefore inhibition of FLJ12660 (Accession NP_079428.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12660.

[46376] FLJ13149 (Accession NP_068598.1) is another GAM3418 target gene, herein designated TARGET GENE. FLJ13149 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13149 BINDING SITE, designated SEQ ID:3760, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46377] Another function of GAM3418 is therefore inhibition of FLJ13149 (Accession NP_068598.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13149.

[46378] FLJ13912 (Accession NP_073607.2) is another GAM3418 target gene, herein designated TARGET GENE. FLJ13912 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13912, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13912 BINDING SITE, designated SEQ ID:16332, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46379] Another function of GAM3418 is therefore inhibition of FLJ13912 (Accession NP_073607.2) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13912.

[46380] FLJ14103 (Accession NP_078965.1) is another GAM3418 target gene, herein designated TARGET GENE. FLJ14103 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14103, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ14103 BINDING SITE, designated SEQ ID:15222, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46381] Another function of GAM3418 is therefore inhibition of FLJ14103 (Accession NP_078965.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14103.

[46382] FLJ31033 (Accession XP_037817.5) is another GAM3418 target gene, herein designated TARGET GENE. FLJ31033 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31033, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31033 BINDING SITE, designated SEQ ID:10323, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46383] Another function of GAM3418 is therefore inhibition of FLJ31033 (Accession XP_037817.5) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ31033.

[46384] GRIPE (Accession XP_170749.4) is another GAM3418 target gene, herein designated TARGET GENE. GRIPE BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GRIPE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRIPE BINDING SITE, designated SEQ ID:1088, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46385] Another function of GAM3418 is therefore inhibition of GRIPE (Accession XP_170749.4) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIPE.

[46386] General transcription factor iie, polypeptide 2, beta 34kda (GTF2E2, Accession NP_002086.1) is another GAM3418 target gene, herein designated TARGET GENE. GTF2E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GTF2E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

GTF2E2 BINDING SITE, designated SEQ ID:19529, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46387] Another function of GAM3418 is therefore inhibition of General transcription factor iie, polypeptide 2, beta 34kda (GTF2E2, Accession NP_002086.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2E2.

[46388] HH114 (Accession NP_115888.1) is another GAM3418 target gene, herein designated TARGET GENE. HH114 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HH114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HH114 BINDING SITE, designated SEQ ID:11665, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46389] Another function of GAM3418 is therefore inhibition of HH114 (Accession NP_115888.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HH114.

[46390] 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7, Accession NP_062874.1) is another GAM3418 target gene, herein designated TARGET GENE. HTR7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by HTR7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR7 BINDING SITE, designated SEQ ID:751, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46391] Another function of GAM3418 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7, Accession NP_062874.1), a gene which stimulates adenylate cyclase. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR7.

[46392] The function of HTR7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM492.2.5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7, Accession NP_000863.1) is another GAM3418 target gene, herein

designated TARGET GENE. HTR7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by HTR7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR7 BINDING SITE, designated SEQ ID:751, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46393] Another function of GAM3418 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7, Accession NP_000863.1), a gene which stimulates adenylate cyclase. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR7.

[46394] The function of HTR7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM492.2.5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7, Accession NP_062873.1) is another GAM3418 target gene, herein designated TARGET GENE. HTR7 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by HTR7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR7 BINDING SITE, designated SEQ ID:751, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46395] Another function of GAM3418 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7, Accession NP_062873.1), a gene which stimulates adenylate cyclase. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR7.

[46396] The function of HTR7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM492.2.KIAA1196 (Accession XP_028968.3) is another GAM3418 target gene, herein designated TARGET GENE. KIAA1196 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1196, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of KIAA1196 BINDING SITE, designated SEQ ID:3870, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46397] Another function of GAM3418 is therefore inhibition of KIAA1196 (Accession XP_028968.3) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1196.

[46398] KIAA1203 (Accession XP_049683.4) is another GAM3418 target gene, herein designated TARGET GENE. KIAA1203 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1203, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1203 BINDING SITE, designated SEQ ID:16550, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46399] Another function of GAM3418 is therefore inhibition of KIAA1203 (Accession XP_049683.4) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1203.

[46400] Lim domain kinase 2 (LIMK2, Accession NP_005560.1) is another GAM3418 target gene, herein designated TARGET GENE. LIMK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LIMK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LIMK2 BINDING SITE, designated SEQ ID:7977, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46401] Another function of GAM3418 is therefore inhibition of Lim domain kinase 2 (LIMK2, Accession NP_005560.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIMK2.

[46402] Lim domain kinase 2 (LIMK2, Accession NP_057952.1) is another GAM3418 target gene, herein designated TARGET GENE. LIMK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LIMK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LIMK2 BINDING SITE, designated SEQ ID:7977, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46403] Another function of GAM3418 is therefore inhibition of Lim domain kinase 2 (LIMK2, Accession NP_057952.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIMK2.

[46404] LOC126755 (Accession XP_059074.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC126755 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC126755, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126755 BINDING SITE, designated SEQ ID:16572, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46405] Another function of GAM3418 is therefore inhibition of LOC126755 (Accession XP_059074.1) . Accordingly, utili-

ties of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126755.

[46406] LOC129607 (Accession XP_059368.4) is another GAM3418 target gene, herein designated TARGET GENE. LOC129607 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC129607, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC129607 BINDING SITE, designated SEQ ID:3587, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46407] Another function of GAM3418 is therefore inhibition of LOC129607 (Accession XP_059368.4) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129607.

[46408] LOC145652 (Accession XP_096827.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC145652 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC145652, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145652 BINDING SITE, designated SEQ ID:8999, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46409] Another function of GAM3418 is therefore inhibition of LOC145652 (Accession XP_096827.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145652.

[46410] LOC145783 (Accession XP_085231.2) is another GAM3418 target gene, herein designated TARGET GENE. LOC145783 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145783, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145783 BINDING SITE, designated SEQ ID:8080, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46411] Another function of GAM3418 is therefore inhibition of LOC145783 (Accession XP_085231.2) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145783.

[46412] LOC152519 (Accession XP_087483.3) is another GAM3418 target gene, herein designated TARGET GENE. LOC152519 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152519, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152519 BINDING SITE, designated SEQ ID:10441, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46413] Another function of GAM3418 is therefore inhibition of LOC152519 (Accession XP_087483.3) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152519.

[46414] LOC283295 (Accession XP_210964.1) is another GAM3418 target gene, herein designated TARGET GENE.

LOC283295 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283295, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283295 BINDING SITE, designated SEQ ID:13815, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46415] Another function of GAM3418 is therefore inhibition of LOC283295 (Accession XP_210964.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283295.

[46416] LOC283505 (Accession XP_208702.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC283505 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283505, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283505 BINDING SITE, designated SEQ ID:9453, to the nucleotide sequence of

GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46417] Another function of GAM3418 is therefore inhibition of LOC283505 (Accession XP_208702.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283505.

[46418] LOC283596 (Accession XP_294746.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC283596 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283596, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283596 BINDING SITE, designated SEQ ID:604, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46419] Another function of GAM3418 is therefore inhibition of LOC283596 (Accession XP_294746.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283596.

[46420] LOC283817 (Accession XP_211215.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC283817 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283817 BINDING SITE, designated SEQ ID:12884, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46421] Another function of GAM3418 is therefore inhibition of LOC283817 (Accession XP_211215.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283817.

[46422] LOC283940 (Accession XP_208917.3) is another GAM3418 target gene, herein designated TARGET GENE. LOC283940 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283940, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC283940 BINDING SITE, designated SEQ ID:2801, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46423] Another function of GAM3418 is therefore inhibition of LOC283940 (Accession XP_208917.3) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283940.

[46424] LOC283980 (Accession XP_208940.2) is another GAM3418 target gene, herein designated TARGET GENE. LOC283980 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283980, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283980 BINDING SITE, designated SEQ ID:2801, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46425] Another function of GAM3418 is therefore inhibition of LOC283980 (Accession XP_208940.2) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283980.

[46426] LOC284542 (Accession XP_209254.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC284542 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284542, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284542 BINDING SITE, designated SEQ ID:11511, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46427] Another function of GAM3418 is therefore inhibition of LOC284542 (Accession XP_209254.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284542.

[46428] LOC284647 (Accession XP_211569.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC284647 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284647, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284647 BINDING SITE, designated SEQ ID:8747, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46429] Another function of GAM3418 is therefore inhibition of LOC284647 (Accession XP_211569.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284647.

[46430] LOC284719 (Accession XP_211601.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC284719 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284719 BINDING SITE, designated SEQ ID:13651, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46431] Another function of GAM3418 is therefore inhibition of

LOC284719 (Accession XP_211601.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284719.

[46432] LOC284950 (Accession XP_211703.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC284950 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284950, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284950 BINDING SITE, designated SEQ ID:6222, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46433] Another function of GAM3418 is therefore inhibition of LOC284950 (Accession XP_211703.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284950.

[46434] LOC285786 (Accession XP_208349.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC285786 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC285786, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285786 BINDING SITE, designated SEQ ID:8604, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46435] Another function of GAM3418 is therefore inhibition of LOC285786 (Accession XP_208349.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285786.

[46436] LOC347775 (Accession XP_302601.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC347775 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347775, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347775 BINDING SITE, designated SEQ ID:1860, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:291.

[46437] Another function of GAM3418 is therefore inhibition of LOC347775 (Accession XP_302601.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347775.

[46438] LOC348731 (Accession XP_300399.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC348731 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348731, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348731 BINDING SITE, designated SEQ ID:13922, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46439] Another function of GAM3418 is therefore inhibition of LOC348731 (Accession XP_300399.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348731.

[46440] LOC349257 (Accession XP_300996.1) is another

GAM3418 target gene, herein designated TARGET GENE. LOC349257 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349257, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349257 BINDING SITE, designated SEQ ID:17812, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46441] Another function of GAM3418 is therefore inhibition of LOC349257 (Accession XP_300996.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349257.

[46442] LOC349265 (Accession XP_301000.1) is another GAM3418 target gene, herein designated TARGET GENE. LOC349265 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349265, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349265 BINDING SITE, desig-

nated SEQ ID:17812, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46443] Another function of GAM3418 is therefore inhibition of LOC349265 (Accession XP_301000.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349265.

[46444] Mitogen-activated protein kinase 14 (MAPK14, Accession NP_001306.1) is another GAM3418 target gene, herein designated TARGET GENE. MAPK14 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPK14 BINDING SITE, designated SEQ ID:5165, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46445] Another function of GAM3418 is therefore inhibition of Mitogen-activated protein kinase 14 (MAPK14, Accession NP_001306.1), a gene which is important for cytokine production; responds to changes in extracellular osmolar-

ity. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK14.

[46446] The function of MAPK14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM473.1.Mitogen-activated protein kinase 14 (MAPK14, Accession NP_620581.1) is another GAM3418 target gene, herein designated TARGET GENE. MAPK14 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPK14 BINDING SITE, designated SEQ ID:5165, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46447] Another function of GAM3418 is therefore inhibition of Mitogen-activated protein kinase 14 (MAPK14, Accession NP_620581.1), a gene which is important for cytokine production; responds to changes in extracellular osmolarity. Accordingly, utilities of GAM3418 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with MAPK14.

[46448] The function of MAPK14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM473.1.Mitogen-activated protein kinase 14 (MAPK14, Accession NP_620583.1) is another GAM3418 target gene, herein designated TARGET GENE. MAPK14 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPK14 BINDING SITE, designated SEQ ID:5165, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46449] Another function of GAM3418 is therefore inhibition of Mitogen-activated protein kinase 14 (MAPK14, Accession NP_620583.1), a gene which is important for cytokine production; responds to changes in extracellular osmolarity. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with MAPK14.

[46450] The function of MAPK14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM473.1.MGC45866 (Accession NP_689472.2) is another GAM3418 target gene, herein designated TARGET GENE. MGC45866 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC45866, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC45866 BINDING SITE, designated SEQ ID:5930, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46451] Another function of GAM3418 is therefore inhibition of MGC45866 (Accession NP_689472.2) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC45866.

[46452] Nebulin (NEB, Accession NP_004534.1) is another GAM3418 target gene, herein designated TARGET GENE. NEB BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by NEB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NEB BINDING SITE, designated SEQ ID:14890, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46453] Another function of GAM3418 is therefore inhibition of Nebulin (NEB, Accession NP_004534.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEB.

[46454] NET-2 (Accession NP_036470.1) is another GAM3418 target gene, herein designated TARGET GENE. NET-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NET-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NET-2 BINDING SITE, designated SEQ ID:10940, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46455] Another function of GAM3418 is therefore inhibition of

NET-2 (Accession NP_036470.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NET-2.

[46456] 8-oxoguanine dna glycosylase (OGG1, Accession NP_058438.1) is another GAM3418 target gene, herein designated TARGET GENE. OGG1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OGG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OGG1 BINDING SITE, designated SEQ ID:20054, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46457] Another function of GAM3418 is therefore inhibition of 8-oxoguanine dna glycosylase (OGG1, Accession NP_058438.1), a gene which is involved in base excision DNA repair and removal of 8- oxyguanine and therefore may be associated with Tumorigenesis. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of Tumorigenesis, and of other diseases and clinical conditions associated with OGG1.

[46458] The function of OGG1 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Protocadherin 12 (PCDH12, Accession NP_057664.1) is another GAM3418 target gene, herein designated TARGET GENE. PCDH12 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PCDH12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDH12 BINDING SITE, designated SEQ ID:1606, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46459] Another function of GAM3418 is therefore inhibition of Protocadherin 12 (PCDH12, Accession NP_057664.1), a gene which is a member of a family of nonclassical cadherins. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH12.

[46460] The function of PCDH12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Polymerase (dna directed) sigma (POLS, Ac-

cession NP_008930.1) is another GAM3418 target gene, herein designated TARGET GENE. POLS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POLS BINDING SITE, designated SEQ ID:19359, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46461] Another function of GAM3418 is therefore inhibition of Polymerase (dna directed) sigma (POLS, Accession NP_008930.1), a gene which is necessary for chromosome segregation. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLS.

[46462] The function of POLS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.PP1665 (Accession NP_110419.3) is another GAM3418 target gene, herein designated TARGET GENE. PP1665 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PP1665, cor-

responding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PP1665 BINDING SITE, designated SEQ ID:1909, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46463] Another function of GAM3418 is therefore inhibition of PP1665 (Accession NP_110419.3) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1665.

[46464] Protein tyrosine phosphatase, non-receptor type 11 (noonan syndrome 1) (PTPN11, Accession NP_002825.2) is another GAM3418 target gene, herein designated TARGET GENE. PTPN11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTPN11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPN11 BINDING SITE, designated SEQ ID:13861, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46465] Another function of GAM3418 is therefore inhibition of

Protein tyrosine phosphatase, non-receptor type 11 (noonan syndrome 1) (PTPN11, Accession NP_002825.2) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN11.

[46466] Rab17, member ras oncogene family (RAB17, Accession NP_071894.1) is another GAM3418 target gene, herein designated TARGET GENE. RAB17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB17 BINDING SITE, designated SEQ ID:16304, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46467] Another function of GAM3418 is therefore inhibition of Rab17, member ras oncogene family (RAB17, Accession NP_071894.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB17.

[46468] SWAP70 (Accession XP_049197.2) is another GAM3418 target gene, herein designated TARGET GENE. SWAP70

BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SWAP70, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SWAP70 BINDING SITE, designated SEQ ID:18354, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46469] Another function of GAM3418 is therefore inhibition of SWAP70 (Accession XP_049197.2), a gene which is involved not only in nuclear events but also in signaling in B- cell activation. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SWAP70.

[46470] The function of SWAP70 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM257.1.SWAP70 (Accession NP_055870.1) is another GAM3418 target gene, herein designated TARGET GENE. SWAP70 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SWAP70, corresponding to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SWAP70 BINDING SITE, designated SEQ ID:18354, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46471] Another function of GAM3418 is therefore inhibition of SWAP70 (Accession NP_055870.1), a gene which is involved not only in nuclear events but also in signaling in B- cell activation. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SWAP70.

[46472] The function of SWAP70 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM257.1.Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_055734.1) is another GAM3418 target gene, herein designated TARGET GENE. WHSC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by WHSC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of WHSC1 BINDING SITE, designated SEQ ID:13876, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46473] Another function of GAM3418 is therefore inhibition of Wolf-hirschhorn syndrome candidate 1 (WHSC1, Accession NP_055734.1), a gene which binds covalently to and repairs g/t mismatches. and therefore may be associated with Wolf- hirschhorn syndrome. Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of Wolf- hirschhorn syndrome, and of other diseases and clinical conditions associated with WHSC1.

[46474] The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Zinc finger protein 323 (ZNF323, Accession NP_112161.2) is another GAM3418 target gene, herein designated TARGET GENE. ZNF323 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF323 BINDING

SITE, designated SEQ ID:11866, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46475] Another function of GAM3418 is therefore inhibition of Zinc finger protein 323 (ZNF323, Accession NP_112161.2) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF323.

[46476] Zinc finger protein 336 (ZNF336, Accession NP_071927.1) is another GAM3418 target gene, herein designated TARGET GENE. ZNF336 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF336 BINDING SITE, designated SEQ ID:11914, to the nucleotide sequence of GAM3418 RNA, herein designated GAM RNA, also designated SEQ ID:291.

[46477] Another function of GAM3418 is therefore inhibition of Zinc finger protein 336 (ZNF336, Accession NP_071927.1) . Accordingly, utilities of GAM3418 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with ZNF336.

[46478]

[46479] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 3431 (GAM3431), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[46480] GAM3431 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM3431 was detected is described hereinabove with reference to Figs. 8-15.

[46481] GAM3431 gene, herein designated GAM GENE, and GAM3431 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[46482] GAM3431 gene encodes a GAM3431 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM3431 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3431 precursor RNA is designated SEQ ID:105, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:105 is

located at position 6952115 relative to chromosome 12.

[46483] GAM3431 precursor RNA folds onto itself, forming GAM3431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[46484] GAM3431 precursor RNA folds onto itself, forming GAM3431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[46485] Nucleotide sequence of GAM3431 precursor RNA, designated SEQ-ID: 105, and a schematic representation of a predicted secondary folding of GAM3431 folded precursor RNA are further described with reference to Table 2,

hereby incorporated by reference.

[46486] An enzyme complex designated DICER COMPLEX, `dices` the GAM3431 folded precursor RNA into GAM3431 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM3431 RNA is designated SEQ ID:356, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[46487] GAM3431 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM3431 target RNA, herein designated GAM TARGET RNA. GAM3431 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[46488] GAM3431 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3431 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3431 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM3431 RNA may have a different number of target binding sites in untranslated regions of a GAM3431 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[46489] The complementary binding of GAM3431 RNA, herein designated GAM RNA, to target binding sites on GAM3431 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3431 target RNA into GAM3431 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[46490] It is appreciated that GAM3431 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM3431 target genes. The mRNA of each one of this plurality of GAM3431 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3431 RNA, herein designated GAM RNA, and which when bound by GAM3431 RNA causes inhibition of translation of respective one or more GAM3431 target proteins.

[46491] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM3431 gene, herein designated GAM GENE, on one or more GAM3431 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[46492] It is appreciated that specific functions and accordingly utilities of GAM3431 correlate with, and may be deduced from, the identity of the target genes which GAM3431 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[46493]

[46494]

[46495] A2BP1 (Accession NP_665900.1) is a GAM3431 target gene, herein designated TARGET GENE. A2BP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by A2BP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A2BP1 BINDING SITE, designated SEQ ID:7176, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46496] A function of GAM3431 is therefore inhibition of A2BP1 (Accession NP_665900.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with A2BP1.

[46497] A2BP1 (Accession NP_665898.1) is another GAM3431 target gene, herein designated TARGET GENE. A2BP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by A2BP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A2BP1 BINDING SITE, designated SEQ ID:7176, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46498] Another function of GAM3431 is therefore inhibition of A2BP1 (Accession NP_665898.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A2BP1.

[46499] A2BP1 (Accession NP_665899.1) is another GAM3431 target gene, herein designated TARGET GENE. A2BP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by A2BP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of A2BP1 BINDING SITE, designated SEQ ID:7176, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46500] Another function of GAM3431 is therefore inhibition of A2BP1 (Accession NP_665899.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A2BP1.

[46501] Atp-binding cassette, sub-family c (cftr/mrp), member 13 (ABCC13, Accession NP_620054.1) is another GAM3431 target gene, herein designated TARGET GENE. ABCC13 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABCC13, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCC13 BINDING SITE, designated SEQ ID:13374, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46502] Another function of GAM3431 is therefore inhibition of Atp-binding cassette, sub-family c (cftr/mrp), member 13 (ABCC13, Accession NP_620054.1) . Accordingly, utilities

of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC13.

[46503] Ras homolog gene family, member e (ARHE, Accession NP_005159.1) is another GAM3431 target gene, herein designated TARGET GENE. ARHE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHE BINDING SITE, designated SEQ ID:4853, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46504] Another function of GAM3431 is therefore inhibition of Ras homolog gene family, member e (ARHE, Accession NP_005159.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHE.

[46505] Chromosome 3 open reading frame 4 (C3orf4, Accession NP_063948.1) is another GAM3431 target gene, herein designated TARGET GENE. C3orf4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by C3orf4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C3orf4 BINDING SITE, designated SEQ ID:12739, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46506] Another function of GAM3431 is therefore inhibition of Chromosome 3 open reading frame 4 (C3orf4, Accession NP_063948.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C3orf4.

[46507] Cd59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3a5, ej16, ej30, el32 and g344) (CD59, Accession NP_000602.1) is another GAM3431 target gene, herein designated TARGET GENE. CD59 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD59, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD59 BINDING SITE, designated SEQ ID:18546, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:356.

[46508] Another function of GAM3431 is therefore inhibition of Cd59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3a5, ej16, ej30, el32 and g344) (CD59, Accession NP_000602.1), a gene which restricts lysis of human erythrocytes and leukocytes by homologous complement. and therefore may be associated with Cd59 deficiency (hemolytic anemia and thrombosis). Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of Cd59 deficiency (hemolytic anemia and thrombosis), and of other diseases and clinical conditions associated with CD59.

[46509] The function of CD59 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM401.1.DKFZP434G1411 (Accession XP_166383.1) is another GAM3431 target gene, herein designated TARGET GENE. DKFZP434G1411 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434G1411, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434G1411

BINDING SITE, designated SEQ ID:13982, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46510] Another function of GAM3431 is therefore inhibition of DKFZP434G1411 (Accession XP_166383.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434G1411.

[46511] DKFZP564I0422 (Accession NP_113623.1) is another GAM3431 target gene, herein designated TARGET GENE. DKFZP564I0422 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564I0422, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564I0422 BINDING SITE, designated SEQ ID:3040, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46512] Another function of GAM3431 is therefore inhibition of DKFZP564I0422 (Accession NP_113623.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZP564I0422.

[46513] FAT3 (Accession XP_061871.5) is another GAM3431 target gene, herein designated TARGET GENE. FAT3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FAT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FAT3 BINDING SITE, designated SEQ ID:3238, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46514] Another function of GAM3431 is therefore inhibition of FAT3 (Accession XP_061871.5) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAT3.

[46515] FLJ13197 (Accession NP_078890.1) is another GAM3431 target gene, herein designated TARGET GENE. FLJ13197 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13197, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13197 BINDING SITE, designated SEQ ID:14915, to the

nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46516] Another function of GAM3431 is therefore inhibition of FLJ13197 (Accession NP_078890.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13197.

[46517] FLJ32191 (Accession NP_653290.2) is another GAM3431 target gene, herein designated TARGET GENE. FLJ32191 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32191, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32191 BINDING SITE, designated SEQ ID:4685, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46518] Another function of GAM3431 is therefore inhibition of FLJ32191 (Accession NP_653290.2) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32191.

[46519] FLJ33918 (Accession NP_689620.1) is another GAM3431

target gene, herein designated TARGET GENE. FLJ33918 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33918, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33918 BINDING SITE, designated SEQ ID:9000, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46520] Another function of GAM3431 is therefore inhibition of FLJ33918 (Accession NP_689620.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33918.

[46521] FLJ40298 (Accession XP_059377.5) is another GAM3431 target gene, herein designated TARGET GENE. FLJ40298 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ40298, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ40298 BINDING SITE, designated SEQ ID:6666, to the nucleotide sequence of GAM3431 RNA, herein designated

GAM RNA, also designated SEQ ID:356.

[46522] Another function of GAM3431 is therefore inhibition of FLJ40298 (Accession XP_059377.5) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ40298.

[46523] Forkhead box p1 (FOXP1, Accession NP_116071.2) is another GAM3431 target gene, herein designated TARGET GENE. FOXP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FOXP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FOXP1 BINDING SITE, designated SEQ ID:7666, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46524] Another function of GAM3431 is therefore inhibition of Forkhead box p1 (FOXP1, Accession NP_116071.2) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXP1.

[46525] HSPC177 (Accession NP_057494.2) is another GAM3431 target gene, herein designated TARGET GENE. HSPC177

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSPC177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPC177 BINDING SITE, designated SEQ ID:19777, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46526] Another function of GAM3431 is therefore inhibition of HSPC177 (Accession NP_057494.2) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC177.

[46527] KIAA1155 (Accession XP_030864.2) is another GAM3431 target gene, herein designated TARGET GENE. KIAA1155 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1155, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1155 BINDING SITE, designated SEQ ID:2654, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46528] Another function of GAM3431 is therefore inhibition of KIAA1155 (Accession XP_030864.2) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1155.

[46529] KIAA1432 (Accession XP_039698.3) is another GAM3431 target gene, herein designated TARGET GENE. KIAA1432 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1432, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1432 BINDING SITE, designated SEQ ID:18507, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46530] Another function of GAM3431 is therefore inhibition of KIAA1432 (Accession XP_039698.3) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1432.

[46531] KIAA1576 (Accession NP_065978.1) is another GAM3431 target gene, herein designated TARGET GENE. KIAA1576 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1576, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1576 BINDING SITE, designated SEQ ID:4405, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46532] Another function of GAM3431 is therefore inhibition of KIAA1576 (Accession NP_065978.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1576.

[46533] KIAA1587 (Accession NP_065983.1) is another GAM3431 target gene, herein designated TARGET GENE. KIAA1587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1587 BINDING SITE, designated SEQ ID:10648, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46534] Another function of GAM3431 is therefore inhibition of

KIAA1587 (Accession NP_065983.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1587.

[46535] KIAA1673 (Accession XP_047672.4) is another GAM3431 target gene, herein designated TARGET GENE. KIAA1673 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1673, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1673 BINDING SITE, designated SEQ ID:17033, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46536] Another function of GAM3431 is therefore inhibition of KIAA1673 (Accession XP_047672.4) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1673.

[46537] Kelch-like 3 (drosophila) (KLHL3, Accession NP_059111.1) is another GAM3431 target gene, herein designated TARGET GENE. KLHL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

KLHL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLHL3 BINDING SITE, designated SEQ ID:2902, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46538] Another function of GAM3431 is therefore inhibition of Kelch-like 3 (drosophila) (KLHL3, Accession NP_059111.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLHL3.

[46539] LOC126669 (Accession XP_060121.4) is another GAM3431 target gene, herein designated TARGET GENE. LOC126669 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC126669, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126669 BINDING SITE, designated SEQ ID:8765, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46540] Another function of GAM3431 is therefore inhibition of LOC126669 (Accession XP_060121.4) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126669.

[46541] LOC144874 (Accession XP_096696.1) is another GAM3431 target gene, herein designated TARGET GENE. LOC144874 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144874, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144874 BINDING SITE, designated SEQ ID:552, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46542] Another function of GAM3431 is therefore inhibition of LOC144874 (Accession XP_096696.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144874.

[46543] LOC150587 (Accession XP_097917.1) is another GAM3431 target gene, herein designated TARGET GENE.

LOC150587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150587 BINDING SITE, designated SEQ ID:6328, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46544] Another function of GAM3431 is therefore inhibition of LOC150587 (Accession XP_097917.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150587.

[46545] LOC254532 (Accession XP_172961.1) is another GAM3431 target gene, herein designated TARGET GENE. LOC254532 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC254532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254532 BINDING SITE, designated SEQ ID:18418, to the nucleotide sequence of

GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46546] Another function of GAM3431 is therefore inhibition of LOC254532 (Accession XP_172961.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254532.

[46547] LOC283053 (Accession XP_210869.1) is another GAM3431 target gene, herein designated TARGET GENE. LOC283053 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283053, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283053 BINDING SITE, designated SEQ ID:6480, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46548] Another function of GAM3431 is therefore inhibition of LOC283053 (Accession XP_210869.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283053.

[46549] LOC284317 (Accession XP_209162.1) is another GAM3431 target gene, herein designated TARGET GENE. LOC284317 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284317, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284317 BINDING SITE, designated SEQ ID:4230, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46550] Another function of GAM3431 is therefore inhibition of LOC284317 (Accession XP_209162.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284317.

[46551] LOC284325 (Accession XP_209143.1) is another GAM3431 target gene, herein designated TARGET GENE. LOC284325 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284325, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284325 BINDING SITE, designated SEQ ID:10520, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46552] Another function of GAM3431 is therefore inhibition of LOC284325 (Accession XP_209143.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284325.

[46553] LOC285082 (Accession XP_211759.1) is another GAM3431 target gene, herein designated TARGET GENE. LOC285082 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285082, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285082 BINDING SITE, designated SEQ ID:19819, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46554] Another function of GAM3431 is therefore inhibition of LOC285082 (Accession XP_211759.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC285082.

[46555] LOC285147 (Accession XP_211784.1) is another GAM3431 target gene, herein designated TARGET GENE. LOC285147 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285147, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285147 BINDING SITE, designated SEQ ID:6394, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46556] Another function of GAM3431 is therefore inhibition of LOC285147 (Accession XP_211784.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285147.

[46557] LOC286416 (Accession XP_210041.1) is another GAM3431 target gene, herein designated TARGET GENE. LOC286416 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286416, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286416 BINDING SITE, designated SEQ ID:494, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46558] Another function of GAM3431 is therefore inhibition of LOC286416 (Accession XP_210041.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286416.

[46559] LOC339987 (Accession XP_295123.1) is another GAM3431 target gene, herein designated TARGET GENE. LOC339987 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339987, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339987 BINDING SITE, designated SEQ ID:6821, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46560] Another function of GAM3431 is therefore inhibition of

LOC339987 (Accession XP_295123.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339987.

[46561] MGC24180 (Accession NP_689565.1) is another GAM3431 target gene, herein designated TARGET GENE. MGC24180 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC24180, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC24180 BINDING SITE, designated SEQ ID:15915, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46562] Another function of GAM3431 is therefore inhibition of MGC24180 (Accession NP_689565.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC24180.

[46563] MGC50559 (Accession NP_776163.1) is another GAM3431 target gene, herein designated TARGET GENE. MGC50559 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC50559, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC50559 BINDING SITE, designated SEQ ID:4039, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46564] Another function of GAM3431 is therefore inhibition of MGC50559 (Accession NP_776163.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC50559.

[46565] Pim-2 oncogene (PIM2, Accession NP_006866.1) is another GAM3431 target gene, herein designated TARGET GENE. PIM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PIM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PIM2 BINDING SITE, designated SEQ ID:2828, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46566] Another function of GAM3431 is therefore inhibition of Pim-2 oncogene (PIM2, Accession NP_006866.1) . Accord-

ingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIM2.

[46567] Peroxisome proliferative activated receptor, delta (PPARD, Accession NP_006229.1) is another GAM3431 target gene, herein designated TARGET GENE. PPARD BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPARD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPARD BINDING SITE, designated SEQ ID:10291, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46568] Another function of GAM3431 is therefore inhibition of Peroxisome proliferative activated receptor, delta (PPARD, Accession NP_006229.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPARD.

[46569] Pleckstrin homology, sec7 and coiled/coil domains 3 (PSCD3, Accession NP_004218.1) is another GAM3431 target gene, herein designated TARGET GENE. PSCD3 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by PSCD3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSCD3 BINDING SITE, designated SEQ ID:6586, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46570] Another function of GAM3431 is therefore inhibition of Pleckstrin homology, sec7 and coiled/coil domains 3 (PSCD3, Accession NP_004218.1), a gene which regulates vesicle trafficking in eukaryotic cells. Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSCD3.

[46571] The function of PSCD3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM650.2.Reelin (RELN, Accession NP_774959.1) is another GAM3431 target gene, herein designated TARGET GENE. RELN BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RELN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of RELN BINDING SITE, designated SEQ ID:615, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46572] Another function of GAM3431 is therefore inhibition of Reelin (RELN, Accession NP_774959.1), a gene which regulates microtubule function in neurons and neuronal migration. and therefore is associated with Norman- roberts syndrome. Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of Norman- roberts syndrome, and of other diseases and clinical conditions associated with RELN.

[46573] The function of RELN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM700.2.Reelin (RELN, Accession NP_005036.2) is another GAM3431 target gene, herein designated TARGET GENE. RELN BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RELN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RELN BINDING SITE,

designated SEQ ID:615, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46574] Another function of GAM3431 is therefore inhibition of Reelin (RELN, Accession NP_005036.2), a gene which regulates microtubule function in neurons and neuronal migration. and therefore is associated with Norman- roberts syndrome. Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of Norman- roberts syndrome, and of other diseases and clinical conditions associated with RELN.

[46575] The function of RELN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM700.2.Rna guanylyltransferase and 5'-phosphatase (RNGTT, Accession NP_003791.1) is another GAM3431 target gene, herein designated TARGET GENE. RNGTT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNGTT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNGTT BINDING SITE, designated SEQ ID:19971, to the

nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46576] Another function of GAM3431 is therefore inhibition of Rna guanylyltransferase and 5'-phosphatase (RNGTT, Accession NP_003791.1), a gene which is an MRNA capping enzyme; bifunctional enzyme containing both 5'- triphosphatase and mRNA guanylyltransferase activity. Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNGTT.

[46577] The function of RNGTT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM475.2.RTKN2 (Accession NP_660350.2) is another GAM3431 target gene, herein designated TARGET GENE. RTKN2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RTKN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RTKN2 BINDING SITE, designated SEQ ID:8705, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46578] Another function of GAM3431 is therefore inhibition of RTKN2 (Accession NP_660350.2) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RTKN2.

[46579] Solute carrier family 25 (mitochondrial carrier, aralar), member 12 (SLC25A12, Accession NP_003696.2) is another GAM3431 target gene, herein designated TARGET GENE. SLC25A12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC25A12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC25A12 BINDING SITE, designated SEQ ID:801, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46580] Another function of GAM3431 is therefore inhibition of Solute carrier family 25 (mitochondrial carrier, aralar), member 12 (SLC25A12, Accession NP_003696.2), a gene which is a calcium - dependent mitochondrial solute carrier.may have a function in the urea cycle (by similarity). Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC25A12.

[46581] The function of SLC25A12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM522.2.SNX16 (Accession NP_071416.2) is another GAM3431 target gene, herein designated TARGET GENE. SNX16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX16 BINDING SITE, designated SEQ ID:9454, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46582] Another function of GAM3431 is therefore inhibition of SNX16 (Accession NP_071416.2) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX16.

[46583] SNX16 (Accession NP_690049.1) is another GAM3431 target gene, herein designated TARGET GENE. SNX16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX16, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX16 BINDING SITE, designated SEQ ID:9454, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46584] Another function of GAM3431 is therefore inhibition of SNX16 (Accession NP_690049.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX16.

[46585] SNX16 (Accession NP_690050.1) is another GAM3431 target gene, herein designated TARGET GENE. SNX16 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SNX16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX16 BINDING SITE, designated SEQ ID:9454, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46586] Another function of GAM3431 is therefore inhibition of SNX16 (Accession NP_690050.1) . Accordingly, utilities of

GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX16.

[46587] SRGAP2 (Accession NP_055665.1) is another GAM3431 target gene, herein designated TARGET GENE. SRGAP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SRGAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRGAP2 BINDING SITE, designated SEQ ID:5806, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46588] Another function of GAM3431 is therefore inhibition of SRGAP2 (Accession NP_055665.1) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRGAP2.

[46589] T-box 4 (TBX4, Accession NP_060958.2) is another GAM3431 target gene, herein designated TARGET GENE. TBX4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TBX4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of TBX4 BINDING SITE, designated SEQ ID:19579, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46590] Another function of GAM3431 is therefore inhibition of T-box 4 (TBX4, Accession NP_060958.2) . Accordingly, utilities of GAM3431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBX4.

[46591] Zinc finger protein 183-like 1 (ZNF183L1, Accession NP_849192.1) is another GAM3431 target gene, herein designated TARGET GENE. ZNF183L1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF183L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF183L1 BINDING SITE, designated SEQ ID:13659, to the nucleotide sequence of GAM3431 RNA, herein designated GAM RNA, also designated SEQ ID:356.

[46592] Another function of GAM3431 is therefore inhibition of Zinc finger protein 183-like 1 (ZNF183L1, Accession NP_849192.1) . Accordingly, utilities of GAM3431 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF183L1.

[46593]

[46594] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 3499 (GAM3499), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[46595] GAM3499 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM3499 was detected is described hereinabove with reference to Figs. 8-15.

[46596] GAM3499 gene, herein designated GAM GENE, and GAM3499 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[46597] GAM3499 gene encodes a GAM3499 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM3499 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3499 precursor RNA is designated SEQ ID:38, and is provided hereinbelow with reference to the

sequence listing part.

[46598] GAM3499 precursor RNA folds onto itself, forming GAM3499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[46599] GAM3499 precursor RNA folds onto itself, forming GAM3499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[46600] Nucleotide sequence of GAM3499 precursor RNA, designated SEQ-ID: 38, and a schematic representation of a predicted secondary folding of GAM3499 folded precursor RNA are further described with reference to Table 2,

hereby incorporated by reference.

[46601] An enzyme complex designated DICER COMPLEX, `dices` the GAM3499 folded precursor RNA into GAM3499 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM3499 RNA is designated SEQ ID:226, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[46602] GAM3499 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM3499 target RNA, herein designated GAM TARGET RNA. GAM3499 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[46603] GAM3499 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3499 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3499 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM3499 RNA may have a different number of target binding sites in untranslated regions of a GAM3499 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[46604] The complementary binding of GAM3499 RNA, herein designated GAM RNA, to target binding sites on GAM3499 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3499 target RNA into GAM3499 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[46605] It is appreciated that GAM3499 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM3499 target genes. The mRNA of each one of this plurality of GAM3499 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3499 RNA, herein designated GAM RNA, and which when bound by GAM3499 RNA causes inhibition of translation of respective one or more GAM3499 target proteins.

[46606] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM3499 gene, herein designated GAM GENE, on one or more GAM3499 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[46607] It is appreciated that specific functions and accordingly utilities of GAM3499 correlate with, and may be deduced from, the identity of the target genes which GAM3499 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[46608]

[46609]

[46610] Agmatine ureohydrolase (agmatinase) (AGMAT, Accession NP_079034.2) is a GAM3499 target gene, herein designated TARGET GENE. AGMAT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AGMAT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGMAT BINDING SITE, designated SEQ ID:17623, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46611] A function of GAM3499 is therefore inhibition of Agmatine ureohydrolase (agmatinase) (AGMAT, Accession

NP_079034.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGMAT.

[46612] BTBD9 (Accession NP_689946.1) is another GAM3499 target gene, herein designated TARGET GENE. BTBD9 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BTBD9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTBD9 BINDING SITE, designated SEQ ID:1931, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46613] Another function of GAM3499 is therefore inhibition of BTBD9 (Accession NP_689946.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTBD9.

[46614] C14orf117 (Accession NP_061148.1) is another GAM3499 target gene, herein designated TARGET GENE. C14orf117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C14orf117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of C14orf117 BINDING SITE, designated SEQ ID:9472, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46615] Another function of GAM3499 is therefore inhibition of C14orf117 (Accession NP_061148.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf117.

[46616] Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) is another GAM3499 target gene, herein designated TARGET GENE. C1orf24 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C1orf24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:18867, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46617] Another function of GAM3499 is therefore inhibition of Chromosome 1 open reading frame 24 (C1orf24, Accession NP_443198.1) . Accordingly, utilities of GAM3499 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24.

[46618] Cyclin d2 (CCND2, Accession NP_001750.1) is another GAM3499 target gene, herein designated TARGET GENE. CCND2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCND2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCND2 BINDING SITE, designated SEQ ID:10931, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46619] Another function of GAM3499 is therefore inhibition of Cyclin d2 (CCND2, Accession NP_001750.1), a gene which is essential for the control of the cell cycle at the g1/s (start) transition. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCND2.

[46620] The function of CCND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Cyclin-dependent kinase inhibitor 2b (p15, inhibits cdk4) (CDKN2B, Accession NP_511042.1) is an-

other GAM3499 target gene, herein designated TARGET GENE. CDKN2B BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CDKN2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDKN2B BINDING SITE, designated SEQ ID:7140, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46621] Another function of GAM3499 is therefore inhibition of Cyclin-dependent kinase inhibitor 2b (p15, inhibits cdk4) (CDKN2B, Accession NP_511042.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKN2B.

[46622] Cyclin-dependent kinase inhibitor 2b (p15, inhibits cdk4) (CDKN2B, Accession NP_004927.2) is another GAM3499 target gene, herein designated TARGET GENE. CDKN2B BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CDKN2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDKN2B BINDING SITE, designated SEQ ID:7140, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46623] Another function of GAM3499 is therefore inhibition of Cyclin-dependent kinase inhibitor 2b (p15, inhibits cdk4) (CDKN2B, Accession NP_004927.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKN2B.

[46624] CGI-31 (Accession NP_057043.1) is another GAM3499 target gene, herein designated TARGET GENE. CGI-31 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CGI-31, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-31 BINDING SITE, designated SEQ ID:16300, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46625] Another function of GAM3499 is therefore inhibition of CGI-31 (Accession NP_057043.1) . Accordingly, utilities of

GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-31.

[46626] CHD6 (Accession NP_115597.3) is another GAM3499 target gene, herein designated TARGET GENE. CHD6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHD6 BINDING SITE, designated SEQ ID:11177, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46627] Another function of GAM3499 is therefore inhibition of CHD6 (Accession NP_115597.3) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHD6.

[46628] Chloride channel 6 (CLCN6, Accession NP_068504.1) is another GAM3499 target gene, herein designated TARGET GENE. CLCN6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLCN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of CLCN6 BINDING SITE, designated SEQ ID:10812, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46629] Another function of GAM3499 is therefore inhibition of Chloride channel 6 (CLCN6, Accession NP_068504.1), a gene which is a voltage- gated chloride channel. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN6.

[46630] The function of CLCN6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Chloride channel 6 (CLCN6, Accession NP_001277.1) is another GAM3499 target gene, herein designated TARGET GENE. CLCN6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLCN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLCN6 BINDING SITE, designated SEQ ID:10812, to the nucleotide sequence of GAM3499 RNA, herein designated

GAM RNA, also designated SEQ ID:226.

[46631] Another function of GAM3499 is therefore inhibition of Chloride channel 6 (CLCN6, Accession NP_001277.1), a gene which is a voltage- gated chloride channel. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN6.

[46632] The function of CLCN6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Chloride channel 6 (CLCN6, Accession NP_068505.1) is another GAM3499 target gene, herein designated TARGET GENE. CLCN6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLCN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLCN6 BINDING SITE, designated SEQ ID:10812, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46633] Another function of GAM3499 is therefore inhibition of Chloride channel 6 (CLCN6, Accession NP_068505.1), a

gene which is a voltage- gated chloride channel. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN6.

[46634] The function of CLCN6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Chloride channel 6 (CLCN6, Accession NP_068503.1) is another GAM3499 target gene, herein designated TARGET GENE. CLCN6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CLCN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLCN6 BINDING SITE, designated SEQ ID:10812, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46635] Another function of GAM3499 is therefore inhibition of Chloride channel 6 (CLCN6, Accession NP_068503.1), a gene which is a voltage- gated chloride channel. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with CLCN6.

[46636] The function of CLCN6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Claudin 1 (CLDN1, Accession NP_066924.1) is another GAM3499 target gene, herein designated TARGET GENE. CLDN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLDN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLDN1 BINDING SITE, designated SEQ ID:19530, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46637] Another function of GAM3499 is therefore inhibition of Claudin 1 (CLDN1, Accession NP_066924.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLDN1.

[46638] CYP19A1 (Accession NP_112503.1) is another GAM3499 target gene, herein designated TARGET GENE. CYP19A1 BINDING SITE is a target binding site found in the 3` un-

translated region of multiple transcripts of mRNA encoded by CYP19A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP19A1 BINDING SITE, designated SEQ ID:13808, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46639] Another function of GAM3499 is therefore inhibition of CYP19A1 (Accession NP_112503.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP19A1.

[46640] CYP19A1 (Accession NP_000094.2) is another GAM3499 target gene, herein designated TARGET GENE. CYP19A1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CYP19A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP19A1 BINDING SITE, designated SEQ ID:13808, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ

ID:226.

[46641] Another function of GAM3499 is therefore inhibition of CYP19A1 (Accession NP_000094.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP19A1.

[46642] Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1) is another GAM3499 target gene, herein designated TARGET GENE. DIAPH2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DIAPH2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DIAPH2 BINDING SITE, designated SEQ ID:9117, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46643] Another function of GAM3499 is therefore inhibition of Diaphanous homolog 2 (drosophila) (DIAPH2, Accession NP_006720.1), a gene which may affect in oogenesis and therefore may be associated with Premature ovarian failure . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of Premature ovarian failure .,

and of other diseases and clinical conditions associated with DIAPH2.

[46644] The function of DIAPH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.DKFZp434E0519 (Accession NP_115623.1) is another GAM3499 target gene, herein designated TARGET GENE. DKFZp434E0519 BINDING SITE1 and DKFZp434E0519 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DKFZp434E0519, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434E0519 BINDING SITE1 and DKFZp434E0519 BINDING SITE2, designated SEQ ID:2462 and SEQ ID:3588 respectively, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46645] Another function of GAM3499 is therefore inhibition of DKFZp434E0519 (Accession NP_115623.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E0519.

[46646] DKFZP434G072 (Accession NP_115525.1) is another GAM3499 target gene, herein designated TARGET GENE. DKFZP434G072 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434G072, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434G072 BINDING SITE, designated SEQ ID:14688, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46647] Another function of GAM3499 is therefore inhibition of DKFZP434G072 (Accession NP_115525.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434G072.

[46648] DKFZP434I092 (Accession NP_056483.1) is another GAM3499 target gene, herein designated TARGET GENE. DKFZP434I092 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434I092, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of DKFZP434I092 BINDING SITE, designated SEQ ID:4289, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46649] Another function of GAM3499 is therefore inhibition of DKFZP434I092 (Accession NP_056483.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434I092.

[46650] DKFZP564M182 (Accession XP_085525.3) is another GAM3499 target gene, herein designated TARGET GENE. DKFZP564M182 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564M182, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564M182 BINDING SITE, designated SEQ ID:4069, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46651] Another function of GAM3499 is therefore inhibition of DKFZP564M182 (Accession XP_085525.3) . Accordingly, utilities of GAM3499 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZP564M182.

[46652] DKFZp762C1112 (Accession XP_095568.5) is another GAM3499 target gene, herein designated TARGET GENE. DKFZp762C1112 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp762C1112, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762C1112 BINDING SITE, designated SEQ ID:964, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46653] Another function of GAM3499 is therefore inhibition of DKFZp762C1112 (Accession XP_095568.5) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762C1112.

[46654] DKFZP762N2316 (Accession XP_040560.4) is another GAM3499 target gene, herein designated TARGET GENE. DKFZP762N2316 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DKFZP762N2316, corresponding to

a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP762N2316 BINDING SITE, designated SEQ ID:10932, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46655] Another function of GAM3499 is therefore inhibition of DKFZP762N2316 (Accession XP_040560.4) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP762N2316.

[46656] FLJ12892 (Accession NP_073594.2) is another GAM3499 target gene, herein designated TARGET GENE. FLJ12892 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ12892, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12892 BINDING SITE, designated SEQ ID:18919, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46657] Another function of GAM3499 is therefore inhibition of FLJ12892 (Accession NP_073594.2) . Accordingly, utilities

of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12892.

[46658] FLJ13456 (Accession XP_038291.5) is another GAM3499 target gene, herein designated TARGET GENE. FLJ13456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13456 BINDING SITE, designated SEQ ID:12797, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46659] Another function of GAM3499 is therefore inhibition of FLJ13456 (Accession XP_038291.5) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13456.

[46660] FLJ20582 (Accession XP_090970.4) is another GAM3499 target gene, herein designated TARGET GENE. FLJ20582 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20582, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20582 BINDING SITE, designated SEQ ID:12014, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46661] Another function of GAM3499 is therefore inhibition of FLJ20582 (Accession XP_090970.4) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20582.

[46662] FLJ23447 (Accession NP_079101.1) is another GAM3499 target gene, herein designated TARGET GENE. FLJ23447 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23447, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23447 BINDING SITE, designated SEQ ID:18407, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46663] Another function of GAM3499 is therefore inhibition of FLJ23447 (Accession NP_079101.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ23447.

[46664] FLJ23537 (Accession NP_079165.1) is another GAM3499 target gene, herein designated TARGET GENE. FLJ23537 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23537, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23537 BINDING SITE, designated SEQ ID:18841, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46665] Another function of GAM3499 is therefore inhibition of FLJ23537 (Accession NP_079165.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23537.

[46666] FLJ30681 (Accession XP_166291.1) is another GAM3499 target gene, herein designated TARGET GENE. FLJ30681 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30681, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ30681 BINDING SITE, designated SEQ ID:16626, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46667] Another function of GAM3499 is therefore inhibition of FLJ30681 (Accession XP_166291.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30681.

[46668] FLJ31208 (Accession NP_694568.1) is another GAM3499 target gene, herein designated TARGET GENE. FLJ31208 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31208, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31208 BINDING SITE, designated SEQ ID:5760, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46669] Another function of GAM3499 is therefore inhibition of FLJ31208 (Accession NP_694568.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ31208.

[46670] FLJ35693 (Accession NP_694972.2) is another GAM3499 target gene, herein designated TARGET GENE. FLJ35693 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ35693, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35693 BINDING SITE, designated SEQ ID:7369, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46671] Another function of GAM3499 is therefore inhibition of FLJ35693 (Accession NP_694972.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35693.

[46672] FLJ36754 (Accession NP_776190.1) is another GAM3499 target gene, herein designated TARGET GENE. FLJ36754 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36754, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ36754 BINDING SITE, designated SEQ ID:7444, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46673] Another function of GAM3499 is therefore inhibition of FLJ36754 (Accession NP_776190.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36754.

[46674] FLJ37131 (Accession NP_775958.1) is another GAM3499 target gene, herein designated TARGET GENE. FLJ37131 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37131, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37131 BINDING SITE, designated SEQ ID:16721, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46675] Another function of GAM3499 is therefore inhibition of FLJ37131 (Accession NP_775958.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37131.

[46676] Glycoprotein 2 (zymogen granule membrane) (GP2, Accession NP_001493.1) is another GAM3499 target gene, herein designated TARGET GENE. GP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GP2 BINDING SITE, designated SEQ ID:3890, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46677] Another function of GAM3499 is therefore inhibition of Glycoprotein 2 (zymogen granule membrane) (GP2, Accession NP_001493.1), a gene which expresses in the secretory granule of the exocrine pancreas. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GP2.

[46678] The function of GP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.1.G protein-coupled receptor 105 (GPR105, Accession NP_055694.1) is another GAM3499 target gene,

herein designated TARGET GENE. GPR105 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR105, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR105 BINDING SITE, designated SEQ ID:7994, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46679] Another function of GAM3499 is therefore inhibition of G protein-coupled receptor 105 (GPR105, Accession NP_055694.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR105.

[46680] Glutamate receptor, ionotropic, n-methyl-d-aspartate 3a (GRIN3A, Accession NP_597702.1) is another GAM3499 target gene, herein designated TARGET GENE. GRIN3A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRIN3A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRIN3A BINDING SITE, designated SEQ ID:19610, to the

nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46681] Another function of GAM3499 is therefore inhibition of Glutamate receptor, ionotropic, n-methyl-d-aspartate 3a (GRIN3A, Accession NP_597702.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIN3A.

[46682] High-mobility group 20a (HMG20A, Accession NP_060670.1) is another GAM3499 target gene, herein designated TARGET GENE. HMG20A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HMG20A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HMG20A BINDING SITE, designated SEQ ID:17461, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46683] Another function of GAM3499 is therefore inhibition of High-mobility group 20a (HMG20A, Accession NP_060670.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with HMG20A.

[46684] Heterogeneous nuclear ribonucleoprotein a0 (HNRPA0, Accession NP_006796.1) is another GAM3499 target gene, herein designated TARGET GENE. HNRPA0 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HNRPA0, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HNRPA0 BINDING SITE, designated SEQ ID:10813, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46685] Another function of GAM3499 is therefore inhibition of Heterogeneous nuclear ribonucleoprotein a0 (HNRPA0, Accession NP_006796.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNRPA0.

[46686] KIAA0514 (Accession NP_055511.1) is another GAM3499 target gene, herein designated TARGET GENE. KIAA0514 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0514, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA0514 BINDING SITE, designated SEQ ID:18061, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46687] Another function of GAM3499 is therefore inhibition of KIAA0514 (Accession NP_055511.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0514.

[46688] KIAA1735 (Accession XP_290496.1) is another GAM3499 target gene, herein designated TARGET GENE. KIAA1735 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1735 BINDING SITE, designated SEQ ID:12467, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46689] Another function of GAM3499 is therefore inhibition of KIAA1735 (Accession XP_290496.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1735.

[46690] KIAA1985 (Accession NP_078853.1) is another GAM3499 target gene, herein designated TARGET GENE. KIAA1985 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1985, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1985 BINDING SITE, designated SEQ ID:6965, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46691] Another function of GAM3499 is therefore inhibition of KIAA1985 (Accession NP_078853.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1985.

[46692] KIAA2024 (Accession NP_742067.1) is another GAM3499 target gene, herein designated TARGET GENE. KIAA2024 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA2024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA2024 BINDING SITE, designated SEQ ID:18702, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46693] Another function of GAM3499 is therefore inhibition of KIAA2024 (Accession NP_742067.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2024.

[46694] Legumain (LGMN, Accession NP_005597.2) is another GAM3499 target gene, herein designated TARGET GENE. LGMN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LGMN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LGMN BINDING SITE, designated SEQ ID:10662, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46695] Another function of GAM3499 is therefore inhibition of Legumain (LGMN, Accession NP_005597.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGMN.

[46696] LOC115219 (Accession XP_055499.2) is another GAM3499 target gene, herein designated TARGET GENE. LOC115219 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC115219, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115219 BINDING SITE, designated SEQ ID:2334, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46697] Another function of GAM3499 is therefore inhibition of LOC115219 (Accession XP_055499.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115219.

[46698] LOC137485 (Accession XP_059909.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC137485 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC137485, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC137485 BINDING SITE, designated SEQ ID:8695, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46699] Another function of GAM3499 is therefore inhibition of LOC137485 (Accession XP_059909.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137485.

[46700] LOC143381 (Accession XP_084501.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC143381 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC143381, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143381 BINDING SITE, designated SEQ ID:14117, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46701] Another function of GAM3499 is therefore inhibition of LOC143381 (Accession XP_084501.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC143381.

[46702] LOC145844 (Accession XP_085255.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC145844 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145844, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145844 BINDING SITE, designated SEQ ID:4635, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46703] Another function of GAM3499 is therefore inhibition of LOC145844 (Accession XP_085255.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145844.

[46704] LOC147727 (Accession XP_085862.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC147727 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147727, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147727 BINDING SITE, designated SEQ ID:5469, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46705] Another function of GAM3499 is therefore inhibition of LOC147727 (Accession XP_085862.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147727.

[46706] LOC149371 (Accession NP_787072.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC149371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149371 BINDING SITE, designated SEQ ID:7415, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46707] Another function of GAM3499 is therefore inhibition of

LOC149371 (Accession NP_787072.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149371.

[46708] LOC149420 (Accession NP_690048.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC149420 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149420, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149420 BINDING SITE, designated SEQ ID:2383, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46709] Another function of GAM3499 is therefore inhibition of LOC149420 (Accession NP_690048.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149420.

[46710] LOC149619 (Accession XP_097690.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC149619 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC149619, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149619 BINDING SITE, designated SEQ ID:5200, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46711] Another function of GAM3499 is therefore inhibition of LOC149619 (Accession XP_097690.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149619.

[46712] LOC150174 (Accession XP_086802.2) is another GAM3499 target gene, herein designated TARGET GENE. LOC150174 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150174, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150174 BINDING SITE, designated SEQ ID:1768, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:226.

[46713] Another function of GAM3499 is therefore inhibition of LOC150174 (Accession XP_086802.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150174.

[46714] LOC150212 (Accession XP_086827.2) is another GAM3499 target gene, herein designated TARGET GENE. LOC150212 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150212, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150212 BINDING SITE, designated SEQ ID:11780, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46715] Another function of GAM3499 is therefore inhibition of LOC150212 (Accession XP_086827.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150212.

[46716] LOC150213 (Accession XP_059324.1) is another

GAM3499 target gene, herein designated TARGET GENE. LOC150213 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150213, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150213 BINDING SITE, designated SEQ ID:1768, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46717] Another function of GAM3499 is therefore inhibition of LOC150213 (Accession XP_059324.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150213.

[46718] LOC155081 (Accession XP_088145.2) is another GAM3499 target gene, herein designated TARGET GENE. LOC155081 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC155081, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC155081 BINDING SITE, desig-

nated SEQ ID:3019, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46719] Another function of GAM3499 is therefore inhibition of LOC155081 (Accession XP_088145.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155081.

[46720] LOC157556 (Accession XP_098783.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC157556 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC157556, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157556 BINDING SITE, designated SEQ ID:4290, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46721] Another function of GAM3499 is therefore inhibition of LOC157556 (Accession XP_098783.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC157556.

[46722] LOC197201 (Accession XP_113839.2) is another GAM3499 target gene, herein designated TARGET GENE. LOC197201 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC197201, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC197201 BINDING SITE, designated SEQ ID:19865, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46723] Another function of GAM3499 is therefore inhibition of LOC197201 (Accession XP_113839.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197201.

[46724] LOC200339 (Accession XP_117226.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC200339 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200339, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200339 BINDING SITE, designated SEQ ID:2412, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46725] Another function of GAM3499 is therefore inhibition of LOC200339 (Accession XP_117226.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200339.

[46726] LOC201510 (Accession XP_113972.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC201510 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201510, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201510 BINDING SITE, designated SEQ ID:8805, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46727] Another function of GAM3499 is therefore inhibition of LOC201510 (Accession XP_113972.1) . Accordingly, utili-

ties of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201510.

[46728] LOC202802 (Accession XP_114560.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC202802 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC202802, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202802 BINDING SITE, designated SEQ ID:3019, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46729] Another function of GAM3499 is therefore inhibition of LOC202802 (Accession XP_114560.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202802.

[46730] LOC256895 (Accession XP_173029.2) is another GAM3499 target gene, herein designated TARGET GENE. LOC256895 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC256895, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC256895 BINDING SITE, designated SEQ ID:18534, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46731] Another function of GAM3499 is therefore inhibition of LOC256895 (Accession XP_173029.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256895.

[46732] LOC283038 (Accession XP_302599.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC283038 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283038, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283038 BINDING SITE, designated SEQ ID:10213, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46733] Another function of GAM3499 is therefore inhibition of LOC283038 (Accession XP_302599.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283038.

[46734] LOC283070 (Accession XP_210878.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC283070 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283070, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283070 BINDING SITE, designated SEQ ID:16956, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46735] Another function of GAM3499 is therefore inhibition of LOC283070 (Accession XP_210878.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283070.

[46736] LOC283655 (Accession XP_211144.1) is another GAM3499 target gene, herein designated TARGET GENE.

LOC283655 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283655, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283655 BINDING SITE, designated SEQ ID:3498, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46737] Another function of GAM3499 is therefore inhibition of LOC283655 (Accession XP_211144.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283655.

[46738] LOC283682 (Accession XP_211161.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC283682 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283682, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283682 BINDING SITE, designated SEQ ID:11367, to the nucleotide sequence of

GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46739] Another function of GAM3499 is therefore inhibition of LOC283682 (Accession XP_211161.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283682.

[46740] LOC284360 (Accession XP_211433.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC284360 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284360, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284360 BINDING SITE, designated SEQ ID:14189, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46741] Another function of GAM3499 is therefore inhibition of LOC284360 (Accession XP_211433.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284360.

[46742] LOC284650 (Accession XP_211571.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC284650 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284650, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284650 BINDING SITE, designated SEQ ID:10960, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46743] Another function of GAM3499 is therefore inhibition of LOC284650 (Accession XP_211571.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284650.

[46744] LOC284899 (Accession XP_211680.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC284899 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284899 BINDING SITE, designated SEQ ID:2091, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46745] Another function of GAM3499 is therefore inhibition of LOC284899 (Accession XP_211680.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284899.

[46746] LOC284999 (Accession XP_211728.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC284999 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284999, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284999 BINDING SITE, designated SEQ ID:15988, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46747] Another function of GAM3499 is therefore inhibition of LOC284999 (Accession XP_211728.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284999.

[46748] LOC338564 (Accession XP_290466.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC338564 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338564, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338564 BINDING SITE, designated SEQ ID:18841, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46749] Another function of GAM3499 is therefore inhibition of LOC338564 (Accession XP_290466.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338564.

[46750] LOC339083 (Accession XP_290697.2) is another GAM3499 target gene, herein designated TARGET GENE. LOC339083 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339083, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339083 BINDING SITE, designated SEQ ID:4465, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46751] Another function of GAM3499 is therefore inhibition of LOC339083 (Accession XP_290697.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339083.

[46752] LOC347042 (Accession XP_299969.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC347042 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC347042, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC347042 BINDING SITE, designated SEQ ID:15492, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46753] Another function of GAM3499 is therefore inhibition of

LOC347042 (Accession XP_299969.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347042.

[46754] LOC348171 (Accession XP_302672.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC348171 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348171, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348171 BINDING SITE, designated SEQ ID:11763, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46755] Another function of GAM3499 is therefore inhibition of LOC348171 (Accession XP_302672.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348171.

[46756] LOC349081 (Accession XP_300935.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC349081 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC349081, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349081 BINDING SITE, designated SEQ ID:8658, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46757] Another function of GAM3499 is therefore inhibition of LOC349081 (Accession XP_300935.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349081.

[46758] LOC349094 (Accession XP_300945.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC349094 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349094, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349094 BINDING SITE, designated SEQ ID:3536, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:226.

[46759] Another function of GAM3499 is therefore inhibition of LOC349094 (Accession XP_300945.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349094.

[46760] LOC349097 (Accession XP_300940.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC349097 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349097, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349097 BINDING SITE, designated SEQ ID:3536, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46761] Another function of GAM3499 is therefore inhibition of LOC349097 (Accession XP_300940.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349097.

[46762] LOC349138 (Accession XP_300960.1) is another

GAM3499 target gene, herein designated TARGET GENE. LOC349138 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349138, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349138 BINDING SITE, designated SEQ ID:3536, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46763] Another function of GAM3499 is therefore inhibition of LOC349138 (Accession XP_300960.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349138.

[46764] LOC90826 (Accession NP_612373.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC90826 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC90826, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90826 BINDING SITE, designated SEQ ID:8249, to the

nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46765] Another function of GAM3499 is therefore inhibition of LOC90826 (Accession NP_612373.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90826.

[46766] LOC92912 (Accession NP_775740.1) is another GAM3499 target gene, herein designated TARGET GENE. LOC92912 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC92912, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC92912 BINDING SITE, designated SEQ ID:16021, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46767] Another function of GAM3499 is therefore inhibition of LOC92912 (Accession NP_775740.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92912.

[46768] Leucine-rich repeat protein, neuronal 1 (LRRN1, Accession

NP_065924.1) is another GAM3499 target gene, herein designated TARGET GENE. LRRN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LRRN1 BINDING SITE, designated SEQ ID:7636, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46769] Another function of GAM3499 is therefore inhibition of Leucine-rich repeat protein, neuronal 1 (LRRN1, Accession NP_065924.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRRN1.

[46770] Leucine zipper transcription factor-like 1 (LZTFL1, Accession NP_065080.1) is another GAM3499 target gene, herein designated TARGET GENE. LZTFL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LZTFL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LZTFL1 BINDING

SITE, designated SEQ ID:4713, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46771] Another function of GAM3499 is therefore inhibition of Leucine zipper transcription factor-like 1 (LZTFL1, Accession NP_065080.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTFL1.

[46772] Mcf.2 cell line derived transforming sequence (MCF2, Accession NP_005360.2) is another GAM3499 target gene, herein designated TARGET GENE. MCF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MCF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCF2 BINDING SITE, designated SEQ ID:17926, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46773] Another function of GAM3499 is therefore inhibition of Mcf.2 cell line derived transforming sequence (MCF2, Accession NP_005360.2), a gene which Cytoplasmic oncoprotein similar to vimentin and therefore may be associ-

ated with B- cell lymphoma (dbl) oncogene. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of B- cell lymphoma (dbl) oncogene., and of other diseases and clinical conditions associated with MCF2.

[46774] The function of MCF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM619.1.MGC14836 (Accession NP_219480.1) is another GAM3499 target gene, herein designated TARGET GENE. MGC14836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC14836, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14836 BINDING SITE, designated SEQ ID:6981, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46775] Another function of GAM3499 is therefore inhibition of MGC14836 (Accession NP_219480.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC14836.

[46776] Membrane protein, palmitoylated 3 (maguk p55 subfamily member 3) (MPP3, Accession NP_001923.2) is another GAM3499 target gene, herein designated TARGET GENE. MPP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPP3 BINDING SITE, designated SEQ ID:6425, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46777] Another function of GAM3499 is therefore inhibition of Membrane protein, palmitoylated 3 (maguk p55 subfamily member 3) (MPP3, Accession NP_001923.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPP3.

[46778] MPPE1 (Accession NP_075563.2) is another GAM3499 target gene, herein designated TARGET GENE. MPPE1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPPE1, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPPE1 BINDING SITE, designated SEQ ID:13939, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46779] Another function of GAM3499 is therefore inhibition of MPPE1 (Accession NP_075563.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPPE1.

[46780] Myosin, heavy polypeptide 11, smooth muscle (MYH11, Accession NP_002465.1) is another GAM3499 target gene, herein designated TARGET GENE. MYH11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MYH11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYH11 BINDING SITE, designated SEQ ID:6924, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46781] Another function of GAM3499 is therefore inhibition of Myosin, heavy polypeptide 11, smooth muscle (MYH11, Accession NP_002465.1), a gene which is involved in

muscle contraction. and therefore may be associated with Acute myeloid leukemia. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of Acute myeloid leukemia., and of other diseases and clinical conditions associated with MYH11.

[46782] The function of MYH11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM291.1.Myosin, heavy polypeptide 11, smooth muscle (MYH11, Accession NP_074035.1) is another GAM3499 target gene, herein designated TARGET GENE. MYH11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MYH11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYH11 BINDING SITE, designated SEQ ID:6924, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46783] Another function of GAM3499 is therefore inhibition of Myosin, heavy polypeptide 11, smooth muscle (MYH11, Accession NP_074035.1), a gene which is involved in

muscle contraction. and therefore may be associated with Acute myeloid leukemia. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of Acute myeloid leukemia., and of other diseases and clinical conditions associated with MYH11.

[46784] The function of MYH11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM291.1.Nuclear receptor interacting protein 1 (NRIP1, Accession NP_003480.1) is another GAM3499 target gene, herein designated TARGET GENE. NRIP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NRIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRIP1 BINDING SITE, designated SEQ ID:11880, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46785] Another function of GAM3499 is therefore inhibition of Nuclear receptor interacting protein 1 (NRIP1, Accession NP_003480.1), a gene which modulates transcriptional activation by the estrogen receptor. Accordingly, utilities

of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRIP1.

[46786] The function of NRIP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Nuclear receptor interacting protein 1 (NRIP1, Accession XP_009699.1) is another GAM3499 target gene, herein designated TARGET GENE. NRIP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NRIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NRIP1 BINDING SITE, designated SEQ ID:11880, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46787] Another function of GAM3499 is therefore inhibition of Nuclear receptor interacting protein 1 (NRIP1, Accession XP_009699.1), a gene which modulates transcriptional activation by the estrogen receptor. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRIP1.

[46788] The function of NRIP1 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Origin recognition complex, subunit 4-like (yeast) (ORC4L, Accession NP_002543.1) is another GAM3499 target gene, herein designated TARGET GENE. ORC4L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ORC4L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ORC4L BINDING SITE, designated SEQ ID:5097, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46789] Another function of GAM3499 is therefore inhibition of Origin recognition complex, subunit 4-like (yeast) (ORC4L, Accession NP_002543.1), a gene which may be required for initiation of DNA replication and has a putative nucleotide triphosphate binding motif. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ORC4L.

[46790] The function of ORC4L and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM203.2.Protocadherin beta 7 (PCDHB7, Accession NP_061763.1) is another GAM3499 target gene, herein designated TARGET GENE. PCDHB7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB7 BINDING SITE, designated SEQ ID:9936, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46791] Another function of GAM3499 is therefore inhibition of Protocadherin beta 7 (PCDHB7, Accession NP_061763.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB7.

[46792] PRO0478 (Accession NP_054848.1) is another GAM3499 target gene, herein designated TARGET GENE. PRO0478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRO0478, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of PRO0478 BINDING SITE, designated SEQ ID:2029, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46793] Another function of GAM3499 is therefore inhibition of PRO0478 (Accession NP_054848.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0478.

[46794] Ptk2 protein tyrosine kinase 2 (PTK2, Accession NP_005598.3) is another GAM3499 target gene, herein designated TARGET GENE. PTK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTK2 BINDING SITE, designated SEQ ID:9167, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46795] Another function of GAM3499 is therefore inhibition of Ptk2 protein tyrosine kinase 2 (PTK2, Accession NP_005598.3), a gene which involves in intracellular sig-

nal transduction pathway and is a putative homolog of chicken focal adhesion associated kinase. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTK2.

[46796] The function of PTK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.2.Ptk2 protein tyrosine kinase 2 (PTK2, Accession NP_722560.1) is another GAM3499 target gene, herein designated TARGET GENE. PTK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTK2 BINDING SITE, designated SEQ ID:9167, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46797] Another function of GAM3499 is therefore inhibition of Ptk2 protein tyrosine kinase 2 (PTK2, Accession NP_722560.1), a gene which involves in intracellular signal transduction pathway and is a putative homolog of

chicken focal adhesion associated kinase. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTK2.

[46798] The function of PTK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.2.Protein tyrosine phosphatase, receptor type, c (PTPRC, Accession NP_002829.2) is another GAM3499 target gene, herein designated TARGET GENE. PTPRC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTPRC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPRC BINDING SITE, designated SEQ ID:18645, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46799] Another function of GAM3499 is therefore inhibition of Protein tyrosine phosphatase, receptor type, c (PTPRC, Accession NP_002829.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with PTPRC.

[46800] Protein tyrosine phosphatase, receptor type, c (PTPRC, Accession NP_563579.1) is another GAM3499 target gene, herein designated TARGET GENE. PTPRC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTPRC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPRC BINDING SITE, designated SEQ ID:18645, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46801] Another function of GAM3499 is therefore inhibition of Protein tyrosine phosphatase, receptor type, c (PTPRC, Accession NP_563579.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRC.

[46802] Protein tyrosine phosphatase, receptor type, c (PTPRC, Accession NP_563578.1) is another GAM3499 target gene, herein designated TARGET GENE. PTPRC BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTPRC, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPRC BINDING SITE, designated SEQ ID:18645, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46803] Another function of GAM3499 is therefore inhibition of Protein tyrosine phosphatase, receptor type, c (PTPRC, Accession NP_563578.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRC.

[46804] RAD18 (Accession NP_064550.2) is another GAM3499 target gene, herein designated TARGET GENE. RAD18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAD18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD18 BINDING SITE, designated SEQ ID:3162, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46805] Another function of GAM3499 is therefore inhibition of RAD18 (Accession NP_064550.2), a gene which functions with dna repair protein rad5 in error- free postreplication

dna repair and therefore may be associated with Cancer. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of Cancer, and of other diseases and clinical conditions associated with RAD18.

[46806] The function of RAD18 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.2.SB52 (Accession NP_612208.1) is another GAM3499 target gene, herein designated TARGET GENE. SB52 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SB52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SB52 BINDING SITE, designated SEQ ID:6196, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46807] Another function of GAM3499 is therefore inhibition of SB52 (Accession NP_612208.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SB52.

[46808] SEC15B (Accession XP_039570.3) is another GAM3499 target gene, herein designated TARGET GENE. SEC15B

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEC15B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEC15B BINDING SITE, designated SEQ ID:4566, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46809] Another function of GAM3499 is therefore inhibition of SEC15B (Accession XP_039570.3) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC15B.

[46810] SLC35E2 (Accession XP_049733.6) is another GAM3499 target gene, herein designated TARGET GENE. SLC35E2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC35E2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC35E2 BINDING SITE, designated SEQ ID:8532, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46811] Another function of GAM3499 is therefore inhibition of

SLC35E2 (Accession XP_049733.6) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35E2.

[46812] SNX22 (Accession NP_079074.1) is another GAM3499 target gene, herein designated TARGET GENE. SNX22 BINDING SITE1 and SNX22 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by SNX22, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SNX22 BINDING SITE1 and SNX22 BINDING SITE2, designated SEQ ID:7099 and SEQ ID:11732 respectively, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46813] Another function of GAM3499 is therefore inhibition of SNX22 (Accession NP_079074.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX22.

[46814] Sprouty homolog 3 (drosophila) (SPRY3, Accession NP_005831.1) is another GAM3499 target gene, herein designated TARGET GENE. SPRY3 BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by SPRY3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPRY3 BINDING SITE, designated SEQ ID:428, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46815] Another function of GAM3499 is therefore inhibition of Sprouty homolog 3 (drosophila) (SPRY3, Accession NP_005831.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPRY3.

[46816] Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) is another GAM3499 target gene, herein designated TARGET GENE. TGIF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TGIF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TGIF2 BINDING SITE, designated SEQ ID:7688, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46817] Another function of GAM3499 is therefore inhibition of Tgfb-induced factor 2 (tale family homeobox) (TGIF2, Accession NP_068581.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGIF2.

[46818] Triple homeobox 1 (TIX1, Accession NP_055850.1) is another GAM3499 target gene, herein designated TARGET GENE. TIX1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TIX1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TIX1 BINDING SITE, designated SEQ ID:17199, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46819] Another function of GAM3499 is therefore inhibition of Triple homeobox 1 (TIX1, Accession NP_055850.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIX1.

[46820] Toll-like receptor 3 (TLR3, Accession NP_003256.1) is another GAM3499 target gene, herein designated TARGET GENE. TLR3 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by TLR3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLR3 BINDING SITE, designated SEQ ID:13708, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46821] Another function of GAM3499 is therefore inhibition of Toll-like receptor 3 (TLR3, Accession NP_003256.1), a gene which involves in host defense against viruses. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLR3.

[46822] The function of TLR3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1490.1.Topoisomerase (dna) ii alpha 170kda (TOP2A, Accession NP_001058.2) is another GAM3499 target gene, herein designated TARGET GENE. TOP2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TOP2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of TOP2A BINDING SITE, designated SEQ ID:14864, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46823] Another function of GAM3499 is therefore inhibition of Topoisomerase (dna) ii alpha 170kda (TOP2A, Accession NP_001058.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOP2A.

[46824] TP53BPL (Accession NP_005793.1) is another GAM3499 target gene, herein designated TARGET GENE. TP53BPL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TP53BPL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TP53BPL BINDING SITE, designated SEQ ID:1710, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46825] Another function of GAM3499 is therefore inhibition of TP53BPL (Accession NP_005793.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

TP53BPL.

[46826] VN1R1 (Accession NP_065684.1) is another GAM3499 target gene, herein designated TARGET GENE. VN1R1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VN1R1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VN1R1 BINDING SITE, designated SEQ ID:14407, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46827] Another function of GAM3499 is therefore inhibition of VN1R1 (Accession NP_065684.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VN1R1.

[46828] Williams beuren syndrome chromosome region 19 (WBSCR19, Accession NP_778234.2) is another GAM3499 target gene, herein designated TARGET GENE. WBSCR19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by WBSCR19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

WBSCR19 BINDING SITE, designated SEQ ID:3019, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46829] Another function of GAM3499 is therefore inhibition of Williams beuren syndrome chromosome region 19 (WBSCR19, Accession NP_778234.2) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WB-SCR19.

[46830] Zinc finger protein 214 (ZNF214, Accession NP_037381.1) is another GAM3499 target gene, herein designated TAR-GET GENE. ZNF214 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF214, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-cleotide sequences of ZNF214 BINDING SITE, designated SEQ ID:6248, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46831] Another function of GAM3499 is therefore inhibition of Zinc finger protein 214 (ZNF214, Accession NP_037381.1) . Accordingly, utilities of GAM3499 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with ZNF214.

[46832] ZNF333 (Accession NP_115809.1) is another GAM3499 target gene, herein designated TARGET GENE. ZNF333 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF333, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF333 BINDING SITE, designated SEQ ID:15527, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46833] Another function of GAM3499 is therefore inhibition of ZNF333 (Accession NP_115809.1) . Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF333.

[46834] Zinc finger protein 36 (kox 18) (ZNF36, Accession XP_168302.1) is another GAM3499 target gene, herein designated TARGET GENE. ZNF36 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF36, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF36 BINDING SITE, designated SEQ ID:10965, to the nucleotide sequence of GAM3499 RNA, herein designated GAM RNA, also designated SEQ ID:226.

[46835] Another function of GAM3499 is therefore inhibition of Zinc finger protein 36 (kox 18) (ZNF36, Accession XP_168302.1), a gene which may be involved in transcriptional regulation. Accordingly, utilities of GAM3499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF36.

[46836] The function of ZNF36 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM31.1.

[46837] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 3770 (GAM3770), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[46838] GAM3770 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM3770 was detected is described hereinabove with reference to Figs. 8-15.

[46839] GAM3770 gene, herein designated GAM GENE, and GAM3770 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[46840] GAM3770 gene encodes a GAM3770 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM3770 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM3770 precursor RNA is designated SEQ ID:29, and is provided hereinbelow with reference to the sequence listing part.

[46841] GAM3770 precursor RNA folds onto itself, forming GAM3770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[46842] GAM3770 precursor RNA folds onto itself, forming

GAM3770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[46843] Nucleotide sequence of GAM3770 precursor RNA, designated SEQ-ID: 29, and a schematic representation of a predicted secondary folding of GAM3770 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[46844] An enzyme complex designated DICER COMPLEX, `dices` the GAM3770 folded precursor RNA into GAM3770 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM3770 RNA is designated SEQ ID:281, and is provided hereinbelow with refer-

ences to the sequence listing part and Table 3, hereby incorporated by reference.

[46845] GAM3770 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM3770 target RNA, herein designated GAM TARGET RNA. GAM3770 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[46846] GAM3770 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM3770 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM3770 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM3770 RNA may have a different number of target binding sites in untranslated regions of a GAM3770 target

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[46847] The complementary binding of GAM3770 RNA, herein designated GAM RNA, to target binding sites on GAM3770 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM3770 target RNA into GAM3770 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[46848] It is appreciated that GAM3770 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM3770 target genes. The mRNA of each one of this plurality of GAM3770 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM3770 RNA, herein designated GAM RNA, and which when bound by GAM3770 RNA causes inhibition of translation of respective one or more GAM3770 target proteins.

[46849] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM3770 gene, herein designated GAM GENE, on one or more GAM3770 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[46850] It is appreciated that specific functions and accordingly utilities of GAM3770 correlate with, and may be deduced from, the identity of the target genes which GAM3770 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[46851]

[46852]

[46853] Atp-binding cassette, sub-family d (ald), member 2

(ABCD2, Accession NP_005155.1) is a GAM3770 target gene, herein designated TARGET GENE. ABCD2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ABCD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCD2 BINDING SITE, designated SEQ ID:19013, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46854] A function of GAM3770 is therefore inhibition of Atp-binding cassette, sub-family d (ald), member 2 (ABCD2, Accession NP_005155.1), a gene which probable transporter. and therefore may be associated with Adrenoleukodystrophy. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Adrenoleukodystrophy, and of other diseases and clinical conditions associated with ABCD2.

[46855] The function of ABCD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Atp-binding cassette, sub-family f (gcn20), member 2 (ABCF2, Accession NP_009120.1) is another

GAM3770 target gene, herein designated TARGET GENE. ABCF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABCF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCF2 BINDING SITE, designated SEQ ID:484, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46856] Another function of GAM3770 is therefore inhibition of Atp-binding cassette, sub-family f (gcn20), member 2 (ABCF2, Accession NP_009120.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCF2.

[46857] Arp1 actin-related protein 1 homolog a, centractin alpha (yeast) (ACTR1A, Accession NP_005727.1) is another GAM3770 target gene, herein designated TARGET GENE. ACTR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACTR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACTR1A BINDING SITE, designated SEQ

ID:6045, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46858] Another function of GAM3770 is therefore inhibition of Arp1 actin-related protein 1 homolog a, centractin alpha (yeast) (ACTR1A, Accession NP_005727.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACTR1A.

[46859] A kinase (prka) anchor protein 2 (AKAP2, Accession NP_009134.1) is another GAM3770 target gene, herein designated TARGET GENE. AKAP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AKAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKAP2 BINDING SITE, designated SEQ ID:7250, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46860] Another function of GAM3770 is therefore inhibition of A kinase (prka) anchor protein 2 (AKAP2, Accession NP_009134.1), a gene which binds to regulatory subunit (rii) of protein kinase a. Accordingly, utilities of GAM3770

include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP2.

[46861] The function of AKAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Aldehyde dehydrogenase 3 family, member a2 (ALDH3A2, Accession NP_000373.1) is another GAM3770 target gene, herein designated TARGET GENE. ALDH3A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALDH3A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALDH3A2 BINDING SITE, designated SEQ ID:15493, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46862] Another function of GAM3770 is therefore inhibition of Aldehyde dehydrogenase 3 family, member a2 (ALDH3A2, Accession NP_000373.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH3A2.

[46863] Aldehyde dehydrogenase 6 family, member a1 (ALDH6A1,

Accession NP_005580.1) is another GAM3770 target gene, herein designated TARGET GENE. ALDH6A1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ALDH6A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALDH6A1 BINDING SITE, designated SEQ ID:7652, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46864] Another function of GAM3770 is therefore inhibition of Aldehyde dehydrogenase 6 family, member a1 (ALDH6A1, Accession NP_005580.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH6A1.

[46865] Aldehyde dehydrogenase 9 family, member a1 (ALDH9A1, Accession NP_000687.2) is another GAM3770 target gene, herein designated TARGET GENE. ALDH9A1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ALDH9A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALDH9A1

BINDING SITE, designated SEQ ID:4064, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46866] Another function of GAM3770 is therefore inhibition of Aldehyde dehydrogenase 9 family, member a1 (ALDH9A1, Accession NP_000687.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH9A1.

[46867] Autocrine motility factor receptor (AMFR, Accession NP_620408.1) is another GAM3770 target gene, herein designated TARGET GENE. AMFR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AMFR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMFR BINDING SITE, designated SEQ ID:6822, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46868] Another function of GAM3770 is therefore inhibition of Autocrine motility factor receptor (AMFR, Accession NP_620408.1), a gene which acts to stimulate migration of fibrosarcoma cells and therefore may be associated

with Tumors. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Tumors, and of other diseases and clinical conditions associated with AMFR.

[46869] The function of AMFR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Autocrine motility factor receptor (AMFR, Accession NP_001135.3) is another GAM3770 target gene, herein designated TARGET GENE. AMFR BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AMFR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMFR BINDING SITE, designated SEQ ID:6822, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46870] Another function of GAM3770 is therefore inhibition of Autocrine motility factor receptor (AMFR, Accession NP_001135.3), a gene which acts to stimulate migration of fibrosarcoma cells and therefore may be associated with Tumors. Accordingly, utilities of GAM3770 include

diagnosis, prevention and treatment of Tumors, and of other diseases and clinical conditions associated with AMFR.

[46871] The function of AMFR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Adenosine monophosphate deaminase (isoform e) (AMPD3, Accession NP_000471.1) is another GAM3770 target gene, herein designated TARGET GENE. AMPD3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AMPD3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMPD3 BINDING SITE, designated SEQ ID:2981, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46872] Another function of GAM3770 is therefore inhibition of Adenosine monophosphate deaminase (isoform e) (AMPD3, Accession NP_000471.1), a gene which plays a critical role in energy metabolism. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMPD3.

[46873] The function of AMPD3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM584.1.Rac/cdc42 guanine nucleotide exchange factor (gef) 6 (ARHGEF6, Accession NP_004831.1) is another GAM3770 target gene, herein designated TARGET GENE. ARHGEF6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGEF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGEF6 BINDING SITE, designated SEQ ID:4040, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46874] Another function of GAM3770 is therefore inhibition of Rac/cdc42 guanine nucleotide exchange factor (gef) 6 (ARHGEF6, Accession NP_004831.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF6.

[46875] ARPP-21 (Accession NP_057384.1) is another GAM3770 target gene, herein designated TARGET GENE. ARPP-21

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ARPP-21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARPP-21 BINDING SITE, designated SEQ ID:4251, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46876] Another function of GAM3770 is therefore inhibition of ARPP-21 (Accession NP_057384.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARPP-21.

[46877] Arylsulfatase b (ARSB, Accession NP_000037.1) is another GAM3770 target gene, herein designated TARGET GENE. ARSB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARSB BINDING SITE, designated SEQ ID:11835, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46878] Another function of GAM3770 is therefore inhibition of Arylsulfatase b (ARSB, Accession NP_000037.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARSB.

[46879] Atpase, class i, type 8b, member 2 (ATP8B2, Accession XP_290875.1) is another GAM3770 target gene, herein designated TARGET GENE. ATP8B2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP8B2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP8B2 BINDING SITE, designated SEQ ID:17310, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46880] Another function of GAM3770 is therefore inhibition of Atpase, class i, type 8b, member 2 (ATP8B2, Accession XP_290875.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8B2.

[46881] Bai1-associated protein 2 (BAIAP2, Accession NP_059345.1) is another GAM3770 target gene, herein

designated TARGET GENE. BAIAP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAIAP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAIAP2 BINDING SITE, designated SEQ ID:6156, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46882] Another function of GAM3770 is therefore inhibition of Bai1-associated protein 2 (BAIAP2, Accession NP_059345.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAIAP2.

[46883] BCAP31 (Accession NP_005736.2) is another GAM3770 target gene, herein designated TARGET GENE. BCAP31 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCAP31, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCAP31 BINDING SITE, designated SEQ ID:13375, to the nucleotide sequence of GAM3770 RNA, herein designated

GAM RNA, also designated SEQ ID:281.

[46884] Another function of GAM3770 is therefore inhibition of BCAP31 (Accession NP_005736.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCAP31.

[46885] B-cell cll/lymphoma 7a (BCL7A, Accession NP_066273.1) is another GAM3770 target gene, herein designated TARGET GENE. BCL7A BINDING SITE1 and BCL7A BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by BCL7A, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCL7A BINDING SITE1 and BCL7A BINDING SITE2, designated SEQ ID:16792 and SEQ ID:8131 respectively, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46886] Another function of GAM3770 is therefore inhibition of B-cell cll/lymphoma 7a (BCL7A, Accession NP_066273.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL7A.

[46887] Baculoviral iap repeat-containing 8 (BIRC8, Accession NP_203127.2) is another GAM3770 target gene, herein designated TARGET GENE. BIRC8 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BIRC8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BIRC8 BINDING SITE, designated SEQ ID:2524, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46888] Another function of GAM3770 is therefore inhibition of Baculoviral iap repeat-containing 8 (BIRC8, Accession NP_203127.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIRC8.

[46889] BLAME (Accession NP_064510.1) is another GAM3770 target gene, herein designated TARGET GENE. BLAME BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BLAME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BLAME

BINDING SITE, designated SEQ ID:14865, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46890] Another function of GAM3770 is therefore inhibition of BLAME (Accession NP_064510.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BLAME.

[46891] Brf2, subunit of rna polymerase iii transcription initiation factor, brf1-like (BRF2, Accession NP_060780.2) is another GAM3770 target gene, herein designated TARGET GENE. BRF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BRF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BRF2 BINDING SITE, designated SEQ ID:4164, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46892] Another function of GAM3770 is therefore inhibition of Brf2, subunit of rna polymerase iii transcription initiation factor, brf1-like (BRF2, Accession NP_060780.2), a gene which is one of the multiple subunits of the RNA polymerase III transcription factor complex. Accordingly, utili-

ties of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRF2.

[46893] The function of BRF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1095.1.Bassoon (presynaptic cytomatrix protein) (BSN, Accession NP_003449.1) is another GAM3770 target gene, herein designated TARGET GENE. BSN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BSN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BSN BINDING SITE, designated SEQ ID:11733, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46894] Another function of GAM3770 is therefore inhibition of Bassoon (presynaptic cytomatrix protein) (BSN, Accession NP_003449.1), a gene which may be involved in cytomatrix organization at the site of neurotransmitter release and therefore may be associated with Multiple system atrophy (msa). Accordingly, utilities of GAM3770 include di-

agnosis, prevention and treatment of Multiple system atrophy (msa), and of other diseases and clinical conditions associated with BSN.

[46895] The function of BSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM146.1.Btb (poz) domain containing 6 (BTBD6, Accession NP_150374.1) is another GAM3770 target gene, herein designated TARGET GENE. BTBD6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTBD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTBD6 BINDING SITE, designated SEQ ID:14701, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46896] Another function of GAM3770 is therefore inhibition of Btb (poz) domain containing 6 (BTBD6, Accession NP_150374.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTBD6.

[46897] BZRAP1 (Accession NP_004749.1) is another GAM3770 target gene, herein designated TARGET GENE. BZRAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BZRAP1, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BZRAP1 BINDING SITE, designated SEQ ID:7707, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46898] Another function of GAM3770 is therefore inhibition of BZRAP1 (Accession NP_004749.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BZRAP1.

[46899] Chromosome 1 open reading frame 25 (C1orf25, Accession NP_112196.2) is another GAM3770 target gene, herein designated TARGET GENE. C1orf25 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1orf25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf25 BINDING SITE, designated SEQ ID:8737, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46900] Another function of GAM3770 is therefore inhibition of Chromosome 1 open reading frame 25 (C1orf25, Acces-

sion NP_112196.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf25.

[46901] Chromosome 20 open reading frame 103 (C20orf103, Accession NP_036393.1) is another GAM3770 target gene, herein designated TARGET GENE. C20orf103 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf103, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf103 BINDING SITE, designated SEQ ID:8221, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46902] Another function of GAM3770 is therefore inhibition of Chromosome 20 open reading frame 103 (C20orf103, Accession NP_036393.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf103.

[46903] Chromosome 20 open reading frame 152 (C20orf152, Accession NP_543024.1) is another GAM3770 target gene, herein designated TARGET GENE. C20orf152 BINDING SITE is a target binding site found in the 5` untranslated re-

gion of mRNA encoded by C20orf152, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf152 BINDING SITE, designated SEQ ID:9895, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46904] Another function of GAM3770 is therefore inhibition of Chromosome 20 open reading frame 152 (C20orf152, Accession NP_543024.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf152.

[46905] Chromosome 20 open reading frame 175 (C20orf175, Accession NP_543019.1) is another GAM3770 target gene, herein designated TARGET GENE. C20orf175 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C20orf175, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf175 BINDING SITE, designated SEQ ID:13674, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46906] Another function of GAM3770 is therefore inhibition of Chromosome 20 open reading frame 175 (C20orf175, Accession NP_543019.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf175.

[46907] C20orf194 (Accession XP_045421.1) is another GAM3770 target gene, herein designated TARGET GENE. C20orf194 BINDING SITE1 and C20orf194 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by C20orf194, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf194 BINDING SITE1 and C20orf194 BINDING SITE2, designated SEQ ID:20123 and SEQ ID:12486 respectively, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46908] Another function of GAM3770 is therefore inhibition of C20orf194 (Accession XP_045421.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf194.

[46909] Chromosome 5 open reading frame 4 (C5orf4, Accession

NP_057432.1) is another GAM3770 target gene, herein designated TARGET GENE. C5orf4 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by C5orf4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C5orf4 BINDING SITE, designated SEQ ID:7312, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46910] Another function of GAM3770 is therefore inhibition of Chromosome 5 open reading frame 4 (C5orf4, Accession NP_057432.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf4.

[46911] Chromosome 5 open reading frame 4 (C5orf4, Accession NP_115761.1) is another GAM3770 target gene, herein designated TARGET GENE. C5orf4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C5orf4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

C5orf4 BINDING SITE, designated SEQ ID:7312, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46912] Another function of GAM3770 is therefore inhibition of Chromosome 5 open reading frame 4 (C5orf4, Accession NP_115761.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf4.

[46913] Caspase recruitment domain family, member 9 (CARD9, Accession NP_071747.2) is another GAM3770 target gene, herein designated TARGET GENE. CARD9 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CARD9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CARD9 BINDING SITE, designated SEQ ID:9215, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46914] Another function of GAM3770 is therefore inhibition of Caspase recruitment domain family, member 9 (CARD9, Accession NP_071747.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with CARD9.

[46915] Chemokine (c-c motif) ligand 1 (CCL1, Accession NP_002972.1) is another GAM3770 target gene, herein designated TARGET GENE. CCL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CCL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL1 BINDING SITE, designated SEQ ID:11794, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46916] Another function of GAM3770 is therefore inhibition of Chemokine (c-c motif) ligand 1 (CCL1, Accession NP_002972.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL1.

[46917] Chemokine (c-c motif) receptor 1 (CCR1, Accession NP_001286.1) is another GAM3770 target gene, herein designated TARGET GENE. CCR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCR1 BINDING SITE, designated SEQ ID:17877, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46918] Another function of GAM3770 is therefore inhibition of Chemokine (c-c motif) receptor 1 (CCR1, Accession NP_001286.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCR1.

[46919] Cd1a antigen, a polypeptide (CD1A, Accession NP_001754.1) is another GAM3770 target gene, herein designated TARGET GENE. CD1A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CD1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD1A BINDING SITE, designated SEQ ID:6426, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46920] Another function of GAM3770 is therefore inhibition of Cd1a antigen, a polypeptide (CD1A, Accession

NP_001754.1), a gene which is involved in antigen presentation. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD1A.

[46921] The function of CD1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Cd1d antigen, d polypeptide (CD1D, Accession NP_001757.1) is another GAM3770 target gene, herein designated TARGET GENE. CD1D BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CD1D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD1D BINDING SITE, designated SEQ ID:3178, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46922] Another function of GAM3770 is therefore inhibition of Cd1d antigen, d polypeptide (CD1D, Accession NP_001757.1), a gene which is a member D of the CD1 family; involved in antigen presentation . Accordingly, utilities of GAM3770 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with CD1D.

[46923] The function of CD1D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM550.1.Congenital dyserythropoietic anemia, type i (CDAN1, Accession XP_085300.3) is another GAM3770 target gene, herein designated TARGET GENE. CDAN1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CDAN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDAN1 BINDING SITE, designated SEQ ID:6457, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46924] Another function of GAM3770 is therefore inhibition of Congenital dyserythropoietic anemia, type i (CDAN1, Accession XP_085300.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDAN1.

[46925] Cdc42 effector protein (rho gtpase binding) 3 (CDC42EP3, Accession NP_006440.2) is another GAM3770 target gene,

herein designated TARGET GENE. CDC42EP3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CDC42EP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC42EP3 BINDING SITE, designated SEQ ID:19072, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46926] Another function of GAM3770 is therefore inhibition of Cdc42 effector protein (rho gtpase binding) 3 (CDC42EP3, Accession NP_006440.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC42EP3.

[46927] Cdc91 cell division cycle 91-like 1 (s. cerevisiae) (CDC91L1, Accession NP_536724.1) is another GAM3770 target gene, herein designated TARGET GENE. CDC91L1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDC91L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

CDC91L1 BINDING SITE, designated SEQ ID:3448, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46928] Another function of GAM3770 is therefore inhibition of Cdc91 cell division cycle 91-like 1 (s. cerevisiae) (CDC91L1, Accession NP_536724.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC91L1.

[46929] Cadherin 5, type 2, ve-cadherin (vascular epithelium) (CDH5, Accession NP_001786.1) is another GAM3770 target gene, herein designated TARGET GENE. CDH5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDH5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH5 BINDING SITE, designated SEQ ID:10833, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46930] Another function of GAM3770 is therefore inhibition of Cadherin 5, type 2, ve-cadherin (vascular epithelium) (CDH5, Accession NP_001786.1), a gene which associates

with alpha- catenin forming a link to the cytoskeleton. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH5.

[46931] The function of CDH5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.Cysteine dioxygenase, type i (CDO1, Accession NP_001792.1) is another GAM3770 target gene, herein designated TARGET GENE. CDO1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CDO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDO1 BINDING SITE, designated SEQ ID:4009, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46932] Another function of GAM3770 is therefore inhibition of Cysteine dioxygenase, type i (CDO1, Accession NP_001792.1), a gene which is involved in degradation of cysteine to pyruvate. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with CDO1.

[46933] The function of CDO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM475.1.Claudin 1 (CLDN1, Accession NP_066924.1) is another GAM3770 target gene, herein designated TARGET GENE. CLDN1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CLDN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLDN1 BINDING SITE, designated SEQ ID:17449, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46934] Another function of GAM3770 is therefore inhibition of Claudin 1 (CLDN1, Accession NP_066924.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLDN1.

[46935] cPLA2delta (Accession NP_828848.1) is another GAM3770 target gene, herein designated TARGET GENE. cPLA2delta BINDING SITE is a target binding site found in the 3` un-

translated region of multiple transcripts of mRNA encoded by cPLA2delta, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of cPLA2delta BINDING SITE, designated SEQ ID:17982, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46936] Another function of GAM3770 is therefore inhibition of cPLA2delta (Accession NP_828848.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with cPLA2delta.

[46937] cPLA2delta (Accession XP_208820.2) is another GAM3770 target gene, herein designated TARGET GENE. cPLA2delta BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by cPLA2delta, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of cPLA2delta BINDING SITE, designated SEQ ID:17982, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:281.

[46938] Another function of GAM3770 is therefore inhibition of cPLA2delta (Accession XP_208820.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with cPLA2delta.

[46939] C-reactive protein, pentraxin-related (CRP, Accession NP_000558.1) is another GAM3770 target gene, herein designated TARGET GENE. CRP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRP BINDING SITE, designated SEQ ID:11630, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46940] Another function of GAM3770 is therefore inhibition of C-reactive protein, pentraxin-related (CRP, Accession NP_000558.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRP.

[46941] Cofactor required for sp1 transcriptional activation, sub-

unit 2, 150kda (CRSP2, Accession NP_004220.2) is another GAM3770 target gene, herein designated TARGET GENE. CRSP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRSP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRSP2 BINDING SITE, designated SEQ ID:10521, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46942] Another function of GAM3770 is therefore inhibition of Cofactor required for sp1 transcriptional activation, subunit 2, 150kda (CRSP2, Accession NP_004220.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRSP2.

[46943] Cullin 3 (CUL3, Accession NP_003581.1) is another GAM3770 target gene, herein designated TARGET GENE. CUL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CUL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

CUL3 BINDING SITE, designated SEQ ID:9467, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46944] Another function of GAM3770 is therefore inhibition of Cullin 3 (CUL3, Accession NP_003581.1), a gene which may target other proteins for ubiquitin- dependent proteolysis. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CUL3.

[46945] The function of CUL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM32.1.Cytoplasmic linker 2 (CYLN2, Accession NP_003379.2) is another GAM3770 target gene, herein designated TARGET GENE. CYLN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CYLN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYLN2 BINDING SITE, designated SEQ ID:9937, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46946] Another function of GAM3770 is therefore inhibition of Cytoplasmic linker 2 (CYLN2, Accession NP_003379.2), a gene which associates with microtubules and dendritic lamellar bodies. and therefore may be associated with Williams- beuren syndrome. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Williams- beuren syndrome, and of other diseases and clinical conditions associated with CYLN2.

[46947] The function of CYLN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM330.2.Cytoplasmic linker 2 (CYLN2, Accession NP_115797.1) is another GAM3770 target gene, herein designated TARGET GENE. CYLN2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CYLN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYLN2 BINDING SITE, designated SEQ ID:9937, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46948] Another function of GAM3770 is therefore inhibition of

Cytoplasmic linker 2 (CYLN2, Accession NP_115797.1), a gene which associates with microtubules and dendritic lamellar bodies. and therefore may be associated with Williams- beuren syndrome. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Williams- beuren syndrome, and of other diseases and clinical conditions associated with CYLN2.

[46949] The function of CYLN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM330.2.DBC-1 (Accession NP_066997.3) is another GAM3770 target gene, herein designated TARGET GENE. DBC-1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DBC-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DBC-1 BINDING SITE, designated SEQ ID:17305, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46950] Another function of GAM3770 is therefore inhibition of DBC-1 (Accession NP_066997.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with DBC-1.

[46951] Digeorge syndrome critical region gene 14 (DGCR14, Accession NP_073210.1) is another GAM3770 target gene, herein designated TARGET GENE. DGCR14 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DGCR14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DGCR14 BINDING SITE, designated SEQ ID:10110, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46952] Another function of GAM3770 is therefore inhibition of Digeorge syndrome critical region gene 14 (DGCR14, Accession NP_073210.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGCR14.

[46953] DKFZp434D177-like (Accession XP_209288.2) is another GAM3770 target gene, herein designated TARGET GENE. DKFZp434D177-like BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434D177-like, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434D177-like BINDING SITE, designated SEQ ID:8952, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46954] Another function of GAM3770 is therefore inhibition of DKFZp434D177-like (Accession XP_209288.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434D177-like.

[46955] DKFZp434E2321 (Accession XP_038298.1) is another GAM3770 target gene, herein designated TARGET GENE. DKFZp434E2321 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434E2321, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434E2321 BINDING SITE, designated SEQ ID:4827, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46956] Another function of GAM3770 is therefore inhibition of DKFZp434E2321 (Accession XP_038298.1) . Accordingly,

utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E2321.

[46957] DKFZP434H132 (Accession NP_056307.1) is another GAM3770 target gene, herein designated TARGET GENE. DKFZP434H132 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP434H132, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434H132 BINDING SITE, designated SEQ ID:9323, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46958] Another function of GAM3770 is therefore inhibition of DKFZP434H132 (Accession NP_056307.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434H132.

[46959] DKFZP761D0211 (Accession NP_114428.1) is another GAM3770 target gene, herein designated TARGET GENE. DKFZP761D0211 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

DKFZP761D0211, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP761D0211 BINDING SITE, designated SEQ ID:14838, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46960] Another function of GAM3770 is therefore inhibition of DKFZP761D0211 (Accession NP_114428.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761D0211.

[46961] DKFZp761L1518 (Accession XP_294685.2) is another GAM3770 target gene, herein designated TARGET GENE. DKFZp761L1518 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761L1518, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761L1518 BINDING SITE, designated SEQ ID:10498, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46962] Another function of GAM3770 is therefore inhibition of DKFZp761L1518 (Accession XP_294685.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761L1518.

[46963] EDEM (Accession NP_055489.1) is another GAM3770 target gene, herein designated TARGET GENE. EDEM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EDEM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDEM BINDING SITE, designated SEQ ID:4285, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46964] Another function of GAM3770 is therefore inhibition of EDEM (Accession NP_055489.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDEM.

[46965] Endothelin 3 (EDN3, Accession NP_000105.1) is another GAM3770 target gene, herein designated TARGET GENE. EDN3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by EDN3, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDN3 BINDING SITE, designated SEQ ID:6587, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46966] Another function of GAM3770 is therefore inhibition of Endothelin 3 (EDN3, Accession NP_000105.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDN3.

[46967] Ells1 (Accession NP_690006.1) is another GAM3770 target gene, herein designated TARGET GENE. Ells1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by Ells1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of Ells1 BINDING SITE, designated SEQ ID:12892, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46968] Another function of GAM3770 is therefore inhibition of Ells1 (Accession NP_690006.1) . Accordingly, utilities of

GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Ells1.

[46969] Engulfment and cell motility 1 (ced-12 homolog, c. elegans) (ELMO1, Accession NP_055615.8) is another GAM3770 target gene, herein designated TARGET GENE. ELMO1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ELMO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ELMO1 BINDING SITE, designated SEQ ID:16847, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46970] Another function of GAM3770 is therefore inhibition of Engulfment and cell motility 1 (ced-12 homolog, c. elegans) (ELMO1, Accession NP_055615.8) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELMO1.

[46971] ERdj5 (Accession NP_061854.1) is another GAM3770 target gene, herein designated TARGET GENE. ERdj5 BINDING SITE is a target binding site found in the 3` untranslated

region of mRNA encoded by ERdj5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ERdj5 BINDING SITE, designated SEQ ID:5195, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46972] Another function of GAM3770 is therefore inhibition of ERdj5 (Accession NP_061854.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERdj5.

[46973] Ets variant gene 4 (e1a enhancer binding protein, e1af) (ETV4, Accession NP_001977.1) is another GAM3770 target gene, herein designated TARGET GENE. ETV4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ETV4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ETV4 BINDING SITE, designated SEQ ID:12526, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46974] Another function of GAM3770 is therefore inhibition of Ets

variant gene 4 (e1a enhancer binding protein, e1af) (ETV4, Accession NP_001977.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ETV4.

[46975] F-box only protein 2 (FBXO2, Accession NP_036300.2) is another GAM3770 target gene, herein designated TARGET GENE. FBXO2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FBXO2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXO2 BINDING SITE, designated SEQ ID:4915, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46976] Another function of GAM3770 is therefore inhibition of F-box only protein 2 (FBXO2, Accession NP_036300.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO2.

[46977] FLJ10751 (Accession NP_060709.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ10751 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded

by FLJ10751, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10751 BINDING SITE, designated SEQ ID:764, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46978] Another function of GAM3770 is therefore inhibition of FLJ10751 (Accession NP_060709.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10751.

[46979] FLJ10751 (Accession NP_060675.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ10751 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ10751, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10751 BINDING SITE, designated SEQ ID:764, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46980] Another function of GAM3770 is therefore inhibition of FLJ10751 (Accession NP_060675.1) . Accordingly, utilities

of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10751.

[46981] FLJ10901 (Accession NP_060735.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ10901 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10901, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10901 BINDING SITE, designated SEQ ID:18342, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46982] Another function of GAM3770 is therefore inhibition of FLJ10901 (Accession NP_060735.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10901.

[46983] FLJ10945 (Accession NP_060750.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ10945 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10945, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10945 BINDING SITE, designated SEQ ID:17908, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46984] Another function of GAM3770 is therefore inhibition of FLJ10945 (Accession NP_060750.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10945.

[46985] FLJ12121 (Accession NP_079254.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ12121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12121 BINDING SITE, designated SEQ ID:6795, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46986] Another function of GAM3770 is therefore inhibition of FLJ12121 (Accession NP_079254.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12121.

[46987] FLJ12788 (Accession NP_071937.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ12788 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12788, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12788 BINDING SITE, designated SEQ ID:18045, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46988] Another function of GAM3770 is therefore inhibition of FLJ12788 (Accession NP_071937.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12788.

[46989] FLJ13114 (Accession NP_078817.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ13114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ13114 BINDING SITE, designated SEQ ID:14164, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46990] Another function of GAM3770 is therefore inhibition of FLJ13114 (Accession NP_078817.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13114.

[46991] FLJ13224 (Accession NP_079075.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ13224 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13224, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13224 BINDING SITE, designated SEQ ID:2074, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46992] Another function of GAM3770 is therefore inhibition of FLJ13224 (Accession NP_079075.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ13224.

[46993] FLJ13646 (Accession NP_078860.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ13646 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13646, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13646 BINDING SITE, designated SEQ ID:19731, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46994] Another function of GAM3770 is therefore inhibition of FLJ13646 (Accession NP_078860.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13646.

[46995] FLJ20320 (Accession NP_060235.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ20320 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ20320, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ20320 BINDING SITE, designated SEQ ID:14004, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[46996] Another function of GAM3770 is therefore inhibition of FLJ20320 (Accession NP_060235.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20320.

[46997] FLJ20445 (Accession NP_060294.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ20445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20445 BINDING SITE, designated SEQ ID:3014, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[46998] Another function of GAM3770 is therefore inhibition of FLJ20445 (Accession NP_060294.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20445.

[46999] FLJ22222 (Accession NP_078924.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ22222 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ22222, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22222 BINDING SITE, designated SEQ ID:8328, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47000] Another function of GAM3770 is therefore inhibition of FLJ22222 (Accession NP_078924.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22222.

[47001] FLJ22222 (Accession NP_787098.2) is another GAM3770 target gene, herein designated TARGET GENE. FLJ22222 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ22222, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of FLJ22222 BINDING SITE, designated SEQ ID:8328, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47002] Another function of GAM3770 is therefore inhibition of FLJ22222 (Accession NP_787098.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22222.

[47003] FLJ23186 (Accession NP_078892.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ23186 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23186 BINDING SITE, designated SEQ ID:3020, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47004] Another function of GAM3770 is therefore inhibition of FLJ23186 (Accession NP_078892.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ23186.

[47005] FLJ23323 (Accession NP_078930.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ23323 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23323, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23323 BINDING SITE, designated SEQ ID:12687, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47006] Another function of GAM3770 is therefore inhibition of FLJ23323 (Accession NP_078930.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23323.

[47007] FLJ23867 (Accession NP_689875.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ23867 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23867, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ23867 BINDING SITE, designated SEQ ID:1191, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47008] Another function of GAM3770 is therefore inhibition of FLJ23867 (Accession NP_689875.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23867.

[47009] FLJ32096 (Accession NP_776156.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ32096 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32096, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32096 BINDING SITE, designated SEQ ID:12027, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47010] Another function of GAM3770 is therefore inhibition of FLJ32096 (Accession NP_776156.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32096.

[47011] FLJ32334 (Accession NP_653166.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ32334 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32334, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32334 BINDING SITE, designated SEQ ID:14094, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47012] Another function of GAM3770 is therefore inhibition of FLJ32334 (Accession NP_653166.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32334.

[47013] FLJ32389 (Accession NP_653218.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ32389 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32389, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32389 BINDING SITE, designated SEQ ID:18343, to the

nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47014] Another function of GAM3770 is therefore inhibition of FLJ32389 (Accession NP_653218.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32389.

[47015] FLJ32833 (Accession NP_689701.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ32833 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32833, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32833 BINDING SITE, designated SEQ ID:8952, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47016] Another function of GAM3770 is therefore inhibition of FLJ32833 (Accession NP_689701.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32833.

[47017] FLJ37078 (Accession NP_694588.1) is another GAM3770

target gene, herein designated TARGET GENE. FLJ37078 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ37078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37078 BINDING SITE, designated SEQ ID:924, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47018] Another function of GAM3770 is therefore inhibition of FLJ37078 (Accession NP_694588.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37078.

[47019] FLJ38607 (Accession NP_689867.1) is another GAM3770 target gene, herein designated TARGET GENE. FLJ38607 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38607, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38607 BINDING SITE, designated SEQ ID:1795, to the nucleotide sequence of GAM3770 RNA, herein designated

GAM RNA, also designated SEQ ID:241.

[47020] Another function of GAM3770 is therefore inhibition of FLJ38607 (Accession NP_689867.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38607.

[47021] FRCP2 (Accession NP_715637.1) is another GAM3770 target gene, herein designated TARGET GENE. FRCP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FRCP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FRCP2 BINDING SITE, designated SEQ ID:8098, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47022] Another function of GAM3770 is therefore inhibition of FRCP2 (Accession NP_715637.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FRCP2.

[47023] Frequenin homolog (drosophila) (FREQ, Accession NP_055101.2) is another GAM3770 target gene, herein designated TARGET GENE. FREQ BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by FREQ, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FREQ BINDING SITE, designated SEQ ID:12562, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47024] Another function of GAM3770 is therefore inhibition of Frequenin homolog (drosophila) (FREQ, Accession NP_055101.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FREQ.

[47025] Gamma-aminobutyric acid (gaba) a receptor, epsilon (GABRE, Accession NP_068822.1) is another GAM3770 target gene, herein designated TARGET GENE. GABRE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GABRE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GABRE BINDING SITE, designated SEQ ID:10097, to the nucleotide sequence of GAM3770

RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47026] Another function of GAM3770 is therefore inhibition of Gamma-aminobutyric acid (gaba) a receptor, epsilon (GABRE, Accession NP_068822.1), a gene which mediates neuronal inhibition by binding to the gaba/ benzodiazepine receptor and opening an integral chloride channel. and therefore may be associated with Early- onset parkinsonism (or waisman syndrome), mrx3 (a form of x- linked mental retardation). Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Early- onset parkinsonism (or waisman syndrome), mrx3 (a form of x- linked mental retardation), and of other diseases and clinical conditions associated with GABRE.

[47027] The function of GABRE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.Gamma-aminobutyric acid (gaba) a receptor, epsilon (GABRE, Accession NP_068830.1) is another GAM3770 target gene, herein designated TARGET GENE. GABRE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GABRE, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GABRE BINDING SITE, designated SEQ ID:10097, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47028] Another function of GAM3770 is therefore inhibition of Gamma-aminobutyric acid (gaba) a receptor, epsilon (GABRE, Accession NP_068830.1), a gene which mediates neuronal inhibition by binding to the gaba/ benzodiazepine receptor and opening an integral chloride channel. and therefore may be associated with Early- onset parkinsonism (or waisman syndrome), mrx3 (a form of x- linked mental retardation). Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Early- onset parkinsonism (or waisman syndrome), mrx3 (a form of x- linked mental retardation), and of other diseases and clinical conditions associated with GABRE.

[47029] The function of GABRE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.Gamma-aminobutyric acid (gaba) a receptor, epsilon (GABRE, Accession NP_068819.1) is another

GAM3770 target gene, herein designated TARGET GENE. GABRE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GABRE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GABRE BINDING SITE, designated SEQ ID:10097, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47030] Another function of GAM3770 is therefore inhibition of Gamma-aminobutyric acid (gaba) a receptor, epsilon (GABRE, Accession NP_068819.1), a gene which mediates neuronal inhibition by binding to the gaba/ benzodiazepine receptor and opening an integral chloride channel. and therefore may be associated with Early- onset parkinsonism (or waisman syndrome), mrx3 (a form of x- linked mental retardation). Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Early- onset parkinsonism (or waisman syndrome), mrx3 (a form of x- linked mental retardation), and of other diseases and clinical conditions associated with GABRE.

[47031] The function of GABRE and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.Gamma-aminobutyric acid (gaba) a receptor, epsilon (GABRE, Accession NP_004952.1) is another GAM3770 target gene, herein designated TARGET GENE. GABRE BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GABRE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GABRE BINDING SITE, designated SEQ ID:10097, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47032] Another function of GAM3770 is therefore inhibition of Gamma-aminobutyric acid (gaba) a receptor, epsilon (GABRE, Accession NP_004952.1), a gene which mediates neuronal inhibition by binding to the gaba/ benzodiazepine receptor and opening an integral chloride channel. and therefore may be associated with Early- on-set parkinsonism (or waisman syndrome), mrx3 (a form of x- linked mental retardation). Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of

Early- onset parkinsonism (or waisman syndrome), mrx3 (a form of x- linked mental retardation), and of other diseases and clinical conditions associated with GABRE.

[47033] The function of GABRE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.Udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 2 (galnac-t2) (GALNT2, Accession NP_004472.1) is another GAM3770 target gene, herein designated TARGET GENE. GALNT2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GALNT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GALNT2 BINDING SITE, designated SEQ ID:6744, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47034] Another function of GAM3770 is therefore inhibition of Udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 2 (galnac-t2) (GALNT2, Accession NP_004472.1), a gene which catalyzes the ini-

tial reaction in o- linked oligosaccharide biosynthesis. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNT2.

[47035] The function of GALNT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Glycine amidinotransferase (l-arginine:glycine amidinotransferase) (GATM, Accession NP_001473.1) is another GAM3770 target gene, herein designated TARGET GENE. GATM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GATM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GATM BINDING SITE, designated SEQ ID:19758, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47036] Another function of GAM3770 is therefore inhibition of Glycine amidinotransferase (l-arginine:glycine amidinotransferase) (GATM, Accession NP_001473.1), a gene which glycine amidinotransferase; component of the creatine biosynthetic pathway and therefore may be associ-

ated with Agat deficiency. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Agat deficiency., and of other diseases and clinical conditions associated with GATM.

[47037] The function of GATM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM367.1.Ganglioside-induced differentiation-associated protein 1-like 1 (GDAP1L1, Accession NP_076939.3) is another GAM3770 target gene, herein designated TARGET GENE. GDAP1L1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GDAP1L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GDAP1L1 BINDING SITE, designated SEQ ID:1628, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47038] Another function of GAM3770 is therefore inhibition of Ganglioside-induced differentiation-associated protein 1-like 1 (GDAP1L1, Accession NP_076939.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with GDAP1L1.

[47039] Growth differentiation factor 10 (GDF10, Accession NP_004953.1) is another GAM3770 target gene, herein designated TARGET GENE. GDF10 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GDF10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GDF10 BINDING SITE, designated SEQ ID:15145, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47040] Another function of GAM3770 is therefore inhibition of Growth differentiation factor 10 (GDF10, Accession NP_004953.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GDF10.

[47041] Glycine receptor, alpha 3 (GLRA3, Accession NP_006520.1) is another GAM3770 target gene, herein designated TARGET GENE. GLRA3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GLRA3, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GLRA3 BINDING SITE, designated SEQ ID:12548, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47042] Another function of GAM3770 is therefore inhibition of Glycine receptor, alpha 3 (GLRA3, Accession NP_006520.1), a gene which increases the chloride conductance and thus produces hyperpolarization (inhibition of neuronal firing). Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLRA3.

[47043] The function of GLRA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM785.1.GNB4 (Accession NP_067642.1) is another GAM3770 target gene, herein designated TARGET GENE. GNB4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GNB4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

GNB4 BINDING SITE, designated SEQ ID:19919, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47044] Another function of GAM3770 is therefore inhibition of GNB4 (Accession NP_067642.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNB4.

[47045] GNPNAT1 (Accession XP_085119.1) is another GAM3770 target gene, herein designated TARGET GENE. GNPNAT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNPNAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNPNAT1 BINDING SITE, designated SEQ ID:12686, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47046] Another function of GAM3770 is therefore inhibition of GNPNAT1 (Accession XP_085119.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNPNAT1.

[47047] Glycoprotein a33 (transmembrane) (GPA33, Accession

NP_005805.1) is another GAM3770 target gene, herein designated TARGET GENE. GPA33 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPA33, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPA33 BINDING SITE, designated SEQ ID:11566, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47048] Another function of GAM3770 is therefore inhibition of Glycoprotein a33 (transmembrane) (GPA33, Accession NP_005805.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPA33.

[47049] GTR2 (Accession NP_071440.1) is another GAM3770 target gene, herein designated TARGET GENE. GTR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GTR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTR2 BINDING SITE, designated SEQ ID:18842, to the nucleotide se-

quence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47050] Another function of GAM3770 is therefore inhibition of GTR2 (Accession NP_071440.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTR2.

[47051] Huntingtin (huntington disease) (HD, Accession NP_002102.2) is another GAM3770 target gene, herein designated TARGET GENE. HD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HD BINDING SITE, designated SEQ ID:17396, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47052] Another function of GAM3770 is therefore inhibition of Huntingtin (huntington disease) (HD, Accession NP_002102.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HD.

[47053] HEMK (Accession NP_057257.1) is another GAM3770 target gene, herein designated TARGET GENE. HEMK BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HEMK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HEMK BINDING SITE, designated SEQ ID:18413, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47054] Another function of GAM3770 is therefore inhibition of HEMK (Accession NP_057257.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEMK.

[47055] Hect domain and rld 3 (HERC3, Accession NP_055421.1) is another GAM3770 target gene, herein designated TARGET GENE. HERC3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HERC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HERC3 BINDING SITE, designated SEQ ID:13951, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47056] Another function of GAM3770 is therefore inhibition of Hect domain and rld 3 (HERC3, Accession NP_055421.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HERC3.

[47057] HFL-EDDG1 (Accession NP_006544.1) is another GAM3770 target gene, herein designated TARGET GENE. HFL-EDDG1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HFL-EDDG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HFL-EDDG1 BINDING SITE, designated SEQ ID:13232, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47058] Another function of GAM3770 is therefore inhibition of HFL-EDDG1 (Accession NP_006544.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HFL-EDDG1.

[47059] hIAN2 (Accession NP_078987.2) is another GAM3770 target gene, herein designated TARGET GENE. hIAN2 BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by hIAN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of hIAN2 BINDING SITE, designated SEQ ID:19907, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47060] Another function of GAM3770 is therefore inhibition of hIAN2 (Accession NP_078987.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with hIAN2.

[47061] Hypermethylated in cancer 2 (HIC2, Accession NP_055909.1) is another GAM3770 target gene, herein designated TARGET GENE. HIC2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by HIC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIC2 BINDING SITE, designated SEQ ID:3402, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47062] Another function of GAM3770 is therefore inhibition of Hypermethylated in cancer 2 (HIC2, Accession NP_055909.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIC2.

[47063] Hypermethylated in cancer 2 (HIC2, Accession XP_036937.2) is another GAM3770 target gene, herein designated TARGET GENE. HIC2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by HIC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIC2 BINDING SITE, designated SEQ ID:3402, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47064] Another function of GAM3770 is therefore inhibition of Hypermethylated in cancer 2 (HIC2, Accession XP_036937.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIC2.

[47065] HIP1R (Accession XP_290592.1) is another GAM3770 target gene, herein designated TARGET GENE. HIP1R BINDING

SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HIP1R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIP1R BINDING SITE, designated SEQ ID:16778, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47066] Another function of GAM3770 is therefore inhibition of HIP1R (Accession XP_290592.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIP1R.

[47067] High-mobility group box 3 (HMGB3, Accession NP_005333.1) is another GAM3770 target gene, herein designated TARGET GENE. HMGB3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HMGB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HMGB3 BINDING SITE, designated SEQ ID:4089, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47068] Another function of GAM3770 is therefore inhibition of High-mobility group box 3 (HMGB3, Accession NP_005333.1), a gene which plays a fundamental role in DNA replication, nucleosome assembly, and transcription. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMGB3.

[47069] The function of HMGB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM409.1.Heparan sulfate (glucosamine) 3-o-sulfotransferase 4 (HS3ST4, Accession XP_056254.4) is another GAM3770 target gene, herein designated TARGET GENE. HS3ST4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HS3ST4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HS3ST4 BINDING SITE, designated SEQ ID:1736, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47070] Another function of GAM3770 is therefore inhibition of

Heparan sulfate (glucosamine) 3-o-sulfotransferase 4 (HS3ST4, Accession XP_056254.4) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HS3ST4.

[47071] Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 (HSD3B2, Accession NP_000189.1) is another GAM3770 target gene, herein designated TARGET GENE. HSD3B2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSD3B2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSD3B2 BINDING SITE, designated SEQ ID:10226, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47072] Another function of GAM3770 is therefore inhibition of Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 (HSD3B2, Accession NP_000189.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSD3B2.

[47073] HUMPPA (Accession XP_290730.2) is another GAM3770 target gene, herein designated TARGET GENE. HUMPPA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HUMPPA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUMPPA BINDING SITE, designated SEQ ID:1054, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47074] Another function of GAM3770 is therefore inhibition of HUMPPA (Accession XP_290730.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUMPPA.

[47075] Inhibitor of dna binding 4, dominant negative helix-loop-helix protein (ID4, Accession NP_001537.1) is another GAM3770 target gene, herein designated TARGET GENE. ID4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ID4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of ID4 BINDING SITE, designated SEQ ID:2437, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47076] Another function of GAM3770 is therefore inhibition of Inhibitor of dna binding 4, dominant negative helix-loop-helix protein (ID4, Accession NP_001537.1), a gene which negatively regulates cell differentiation. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ID4.

[47077] The function of ID4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM71.1.Interferon induced transmembrane protein 2 (1-8d) (IFITM2, Accession NP_006426.1) is another GAM3770 target gene, herein designated TARGET GENE. IFITM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IFITM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IFITM2 BINDING SITE, designated SEQ ID:3118, to the nucleotide sequence of GAM3770 RNA, herein designated

GAM RNA, also designated SEQ ID:281.

[47078] Another function of GAM3770 is therefore inhibition of Interferon induced transmembrane protein 2 (1-8d) (IFITM2, Accession NP_006426.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IFITM2.

[47079] Interleukin 6 receptor (IL6R, Accession NP_000556.1) is another GAM3770 target gene, herein designated TARGET GENE. IL6R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL6R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL6R BINDING SITE, designated SEQ ID:10573, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47080] Another function of GAM3770 is therefore inhibition of Interleukin 6 receptor (IL6R, Accession NP_000556.1), a gene which is essential to the regulation of the immune response, hematopoiesis, and acute- phase reactions. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with IL6R.

[47081] The function of IL6R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Interleukin 6 receptor (IL6R, Accession NP_852004.1) is another GAM3770 target gene, herein designated TARGET GENE. IL6R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL6R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL6R BINDING SITE, designated SEQ ID:10573, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47082] Another function of GAM3770 is therefore inhibition of Interleukin 6 receptor (IL6R, Accession NP_852004.1), a gene which is essential to the regulation of the immune response, hematopoiesis, and acute- phase reactions. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL6R.

[47083] The function of IL6R and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Inhibin, beta b (activin ab beta polypeptide) (INHBB, Accession NP_002184.1) is another GAM3770 target gene, herein designated TARGET GENE. INHBB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INHBB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of INHBB BINDING SITE, designated SEQ ID:14744, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47084] Another function of GAM3770 is therefore inhibition of Inhibin, beta b (activin ab beta polypeptide) (INHBB, Accession NP_002184.1), a gene which inhibins inhibit the secretion of follitropin by the pituitary gland. and therefore may be associated with Tumors. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Tumors, and of other diseases and clinical conditions associated with INHBB.

[47085] The function of INHBB and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM174.1.Potassium voltage-gated channel, shab-related subfamily, member 2 (KCNB2, Accession NP_004761.2) is another GAM3770 target gene, herein designated TARGET GENE. KCNB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KCNB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNB2 BINDING SITE, designated SEQ ID:6452, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47086] Another function of GAM3770 is therefore inhibition of Potassium voltage-gated channel, shab-related subfamily, member 2 (KCNB2, Accession NP_004761.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNB2.

[47087] Potassium voltage-gated channel, shal-related subfamily, member 1 (KCND1, Accession NP_004970.3) is another GAM3770 target gene, herein designated TARGET GENE. KCND1 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by KCND1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCND1 BINDING SITE, designated SEQ ID:12525, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47088] Another function of GAM3770 is therefore inhibition of Potassium voltage-gated channel, shal-related subfamily, member 1 (KCND1, Accession NP_004970.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCND1.

[47089] Kdel (lys-asp-glu-leu) endoplasmic reticulum protein retention receptor 1 (KDELR1, Accession NP_006792.1) is another GAM3770 target gene, herein designated TARGET GENE. KDELR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KDELR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KDELR1 BINDING SITE, designated SEQ ID:1055, to the nucleotide sequence of GAM3770

RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47090] Another function of GAM3770 is therefore inhibition of Kdel (lys-asp-glu-leu) endoplasmic reticulum protein retention receptor 1 (KDELR1, Accession NP_006792.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KDELR1.

[47091] KIAA0194 (Accession XP_038362.3) is another GAM3770 target gene, herein designated TARGET GENE. KIAA0194 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0194 BINDING SITE, designated SEQ ID:19314, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47092] Another function of GAM3770 is therefore inhibition of KIAA0194 (Accession XP_038362.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0194.

[47093] KIAA0252 (Accession NP_055953.1) is another GAM3770 target gene, herein designated TARGET GENE. KIAA0252 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0252, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0252 BINDING SITE, designated SEQ ID:19417, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47094] Another function of GAM3770 is therefore inhibition of KIAA0252 (Accession NP_055953.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0252.

[47095] KIAA0570 (Accession XP_291018.1) is another GAM3770 target gene, herein designated TARGET GENE. KIAA0570 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0570, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0570 BINDING SITE, designated SEQ ID:3719, to the

nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47096] Another function of GAM3770 is therefore inhibition of KIAA0570 (Accession XP_291018.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0570.

[47097] KIAA0657 (Accession XP_051017.2) is another GAM3770 target gene, herein designated TARGET GENE. KIAA0657 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0657, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0657 BINDING SITE, designated SEQ ID:10072, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47098] Another function of GAM3770 is therefore inhibition of KIAA0657 (Accession XP_051017.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0657.

[47099] KIAA1032 (Accession XP_038604.4) is another GAM3770

target gene, herein designated TARGET GENE. KIAA1032 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1032, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1032 BINDING SITE, designated SEQ ID:12901, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47100] Another function of GAM3770 is therefore inhibition of KIAA1032 (Accession XP_038604.4) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1032.

[47101] KIAA1209 (Accession XP_027307.2) is another GAM3770 target gene, herein designated TARGET GENE. KIAA1209 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1209, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1209 BINDING SITE, designated SEQ ID:11915, to the nucleotide sequence of GAM3770 RNA, herein designated

GAM RNA, also designated SEQ ID:281.

[47102] Another function of GAM3770 is therefore inhibition of KIAA1209 (Accession XP_027307.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1209.

[47103] KIAA1522 (Accession XP_036299.6) is another GAM3770 target gene, herein designated TARGET GENE. KIAA1522 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1522, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1522 BINDING SITE, designated SEQ ID:17568, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47104] Another function of GAM3770 is therefore inhibition of KIAA1522 (Accession XP_036299.6) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1522.

[47105] KIAA1813 (Accession XP_046743.2) is another GAM3770 target gene, herein designated TARGET GENE. KIAA1813

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1813 BINDING SITE, designated SEQ ID:6050, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47106] Another function of GAM3770 is therefore inhibition of KIAA1813 (Accession XP_046743.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1813.

[47107] KIAA1939 (Accession NP_079113.1) is another GAM3770 target gene, herein designated TARGET GENE. KIAA1939 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1939, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1939 BINDING SITE, designated SEQ ID:4111, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47108] Another function of GAM3770 is therefore inhibition of KIAA1939 (Accession NP_079113.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1939.

[47109] Kinesin family member 5a (KIF5A, Accession NP_004975.1) is another GAM3770 target gene, herein designated TARGET GENE. KIF5A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIF5A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIF5A BINDING SITE, designated SEQ ID:14793, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47110] Another function of GAM3770 is therefore inhibition of Kinesin family member 5a (KIF5A, Accession NP_004975.1), a gene which is a microtubule- associated force- producing protein that may play a role in organelle transport. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF5A.

[47111] The function of KIF5A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Kallikrein 12 (KLK12, Accession NP_665901.1) is another GAM3770 target gene, herein designated TARGET GENE. KLK12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLK12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLK12 BINDING SITE, designated SEQ ID:12199, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47112] Another function of GAM3770 is therefore inhibition of Kallikrein 12 (KLK12, Accession NP_665901.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLK12.

[47113] Kallikrein 12 (KLK12, Accession NP_665902.1) is another GAM3770 target gene, herein designated TARGET GENE. KLK12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA

encoded by KLK12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLK12 BINDING SITE, designated SEQ ID:12199, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47114] Another function of GAM3770 is therefore inhibition of Kallikrein 12 (KLK12, Accession NP_665902.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLK12.

[47115] KRTHBP2 (Accession XP_303553.1) is another GAM3770 target gene, herein designated TARGET GENE. KRTHBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KRTHBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KRTHBP2 BINDING SITE, designated SEQ ID:12132, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47116] Another function of GAM3770 is therefore inhibition of

KRTHBP2 (Accession XP_303553.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KRTHBP2.

[47117] LCHN (Accession XP_098615.2) is another GAM3770 target gene, herein designated TARGET GENE. LCHN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LCHN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LCHN BINDING SITE, designated SEQ ID:19437, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47118] Another function of GAM3770 is therefore inhibition of LCHN (Accession XP_098615.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCHN.

[47119] LOC115219 (Accession XP_055499.2) is another GAM3770 target gene, herein designated TARGET GENE. LOC115219 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC115219, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115219 BINDING SITE, designated SEQ ID:13877, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47120] Another function of GAM3770 is therefore inhibition of LOC115219 (Accession XP_055499.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115219.

[47121] LOC122704 (Accession XP_058647.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC122704 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC122704, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC122704 BINDING SITE, designated SEQ ID:12936, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47122] Another function of GAM3770 is therefore inhibition of

LOC122704 (Accession XP_058647.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122704.

[47123] LOC124842 (Accession XP_064333.3) is another GAM3770 target gene, herein designated TARGET GENE. LOC124842 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC124842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC124842 BINDING SITE, designated SEQ ID:15407, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47124] Another function of GAM3770 is therefore inhibition of LOC124842 (Accession XP_064333.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124842.

[47125] LOC137886 (Accession XP_059929.3) is another GAM3770 target gene, herein designated TARGET GENE. LOC137886 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC137886, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC137886 BINDING SITE, designated SEQ ID:4502, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47126] Another function of GAM3770 is therefore inhibition of LOC137886 (Accession XP_059929.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137886.

[47127] LOC143310 (Accession XP_084485.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC143310 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC143310, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143310 BINDING SITE, designated SEQ ID:17009, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:281.

[47128] Another function of GAM3770 is therefore inhibition of LOC143310 (Accession XP_084485.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143310.

[47129] LOC143680 (Accession XP_096474.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC143680 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC143680, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143680 BINDING SITE, designated SEQ ID:11678, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47130] Another function of GAM3770 is therefore inhibition of LOC143680 (Accession XP_096474.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143680.

[47131] LOC144248 (Accession XP_084786.1) is another

GAM3770 target gene, herein designated TARGET GENE. LOC144248 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144248 BINDING SITE, designated SEQ ID:16663, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47132] Another function of GAM3770 is therefore inhibition of LOC144248 (Accession XP_084786.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144248.

[47133] LOC144438 (Accession XP_084860.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC144438 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144438, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144438 BINDING SITE, desig-

nated SEQ ID:6020, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47134] Another function of GAM3770 is therefore inhibition of LOC144438 (Accession XP_084860.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144438.

[47135] LOC146229 (Accession XP_085387.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC146229 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146229, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146229 BINDING SITE, designated SEQ ID:5022, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47136] Another function of GAM3770 is therefore inhibition of LOC146229 (Accession XP_085387.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC146229.

[47137] LOC146325 (Accession NP_660313.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC146325 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146325, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146325 BINDING SITE, designated SEQ ID:16441, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47138] Another function of GAM3770 is therefore inhibition of LOC146325 (Accession NP_660313.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146325.

[47139] LOC146350 (Accession XP_096985.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC146350 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146350, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146350 BINDING SITE, designated SEQ ID:17607, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47140] Another function of GAM3770 is therefore inhibition of LOC146350 (Accession XP_096985.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146350.

[47141] LOC148918 (Accession XP_086361.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC148918 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC148918, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148918 BINDING SITE, designated SEQ ID:17967, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47142] Another function of GAM3770 is therefore inhibition of LOC148918 (Accession XP_086361.1) . Accordingly, utili-

ties of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148918.

[47143] LOC150157 (Accession XP_097823.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC150157 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150157, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150157 BINDING SITE, designated SEQ ID:6127, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47144] Another function of GAM3770 is therefore inhibition of LOC150157 (Accession XP_097823.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150157.

[47145] LOC150935 (Accession XP_087049.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC150935 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC150935, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150935 BINDING SITE, designated SEQ ID:9952, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47146] Another function of GAM3770 is therefore inhibition of LOC150935 (Accession XP_087049.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150935.

[47147] LOC151154 (Accession XP_098008.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC151154 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151154, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151154 BINDING SITE, designated SEQ ID:14042, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47148] Another function of GAM3770 is therefore inhibition of LOC151154 (Accession XP_098008.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151154.

[47149] LOC151647 (Accession XP_087261.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC151647 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151647, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151647 BINDING SITE, designated SEQ ID:13550, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47150] Another function of GAM3770 is therefore inhibition of LOC151647 (Accession XP_087261.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151647.

[47151] LOC152719 (Accession XP_098257.1) is another GAM3770 target gene, herein designated TARGET GENE.

LOC152719 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152719 BINDING SITE, designated SEQ ID:6325, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47152] Another function of GAM3770 is therefore inhibition of LOC152719 (Accession XP_098257.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152719.

[47153] LOC152790 (Accession XP_098264.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC152790 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152790, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152790 BINDING SITE, designated SEQ ID:9283, to the nucleotide sequence of

GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47154] Another function of GAM3770 is therefore inhibition of LOC152790 (Accession XP_098264.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152790.

[47155] LOC154822 (Accession XP_098618.3) is another GAM3770 target gene, herein designated TARGET GENE. LOC154822 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154822 BINDING SITE, designated SEQ ID:5835, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47156] Another function of GAM3770 is therefore inhibition of LOC154822 (Accession XP_098618.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154822.

[47157] LOC154860 (Accession XP_098623.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC154860 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154860, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154860 BINDING SITE, designated SEQ ID:13099, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47158] Another function of GAM3770 is therefore inhibition of LOC154860 (Accession XP_098623.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154860.

[47159] LOC155036 (Accession XP_098651.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC155036 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC155036, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC155036 BINDING SITE, designated SEQ ID:2202, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47160] Another function of GAM3770 is therefore inhibition of LOC155036 (Accession XP_098651.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155036.

[47161] LOC158062 (Accession XP_098861.2) is another GAM3770 target gene, herein designated TARGET GENE. LOC158062 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158062, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158062 BINDING SITE, designated SEQ ID:19866, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47162] Another function of GAM3770 is therefore inhibition of LOC158062 (Accession XP_098861.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC158062.

[47163] LOC170371 (Accession XP_096316.5) is another GAM3770 target gene, herein designated TARGET GENE. LOC170371 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC170371, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC170371 BINDING SITE, designated SEQ ID:17257, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47164] Another function of GAM3770 is therefore inhibition of LOC170371 (Accession XP_096316.5) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170371.

[47165] LOC196484 (Accession XP_031807.3) is another GAM3770 target gene, herein designated TARGET GENE. LOC196484 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196484, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196484 BINDING SITE, designated SEQ ID:19892, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47166] Another function of GAM3770 is therefore inhibition of LOC196484 (Accession XP_031807.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196484.

[47167] LOC197322 (Accession NP_777577.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC197322 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC197322, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC197322 BINDING SITE, designated SEQ ID:1678, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47168] Another function of GAM3770 is therefore inhibition of

LOC197322 (Accession NP_777577.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197322.

[47169] LOC202404 (Accession XP_114481.4) is another GAM3770 target gene, herein designated TARGET GENE. LOC202404 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC202404, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202404 BINDING SITE, designated SEQ ID:3891, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47170] Another function of GAM3770 is therefore inhibition of LOC202404 (Accession XP_114481.4) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202404.

[47171] LOC221218 (Accession XP_166281.3) is another GAM3770 target gene, herein designated TARGET GENE. LOC221218 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC221218, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221218 BINDING SITE, designated SEQ ID:18010, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47172] Another function of GAM3770 is therefore inhibition of LOC221218 (Accession XP_166281.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221218.

[47173] LOC221442 (Accession XP_166432.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC221442 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221442 BINDING SITE, designated SEQ ID:11963, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:241.

[47174] Another function of GAM3770 is therefore inhibition of LOC221442 (Accession XP_166432.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221442.

[47175] LOC253559 (Accession NP_694854.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC253559 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253559, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253559 BINDING SITE, designated SEQ ID:6427, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47176] Another function of GAM3770 is therefore inhibition of LOC253559 (Accession NP_694854.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253559.

[47177] LOC254099 (Accession XP_173023.1) is another

GAM3770 target gene, herein designated TARGET GENE. LOC254099 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC254099, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254099 BINDING SITE, designated SEQ ID:3792, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47178] Another function of GAM3770 is therefore inhibition of LOC254099 (Accession XP_173023.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254099.

[47179] LOC255783 (Accession XP_170871.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC255783 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC255783, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255783

BINDING SITE, designated SEQ ID:746, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47180] Another function of GAM3770 is therefore inhibition of LOC255783 (Accession XP_170871.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255783.

[47181] LOC255783 (Accession NP_848606.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC255783 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC255783, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255783 BINDING SITE, designated SEQ ID:746, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47182] Another function of GAM3770 is therefore inhibition of LOC255783 (Accession NP_848606.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC255783.

[47183] LOC282965 (Accession XP_210833.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC282965 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282965, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282965 BINDING SITE, designated SEQ ID:20085, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47184] Another function of GAM3770 is therefore inhibition of LOC282965 (Accession XP_210833.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282965.

[47185] LOC283005 (Accession XP_208481.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC283005 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283005, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283005 BINDING SITE, designated SEQ ID:14676, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47186] Another function of GAM3770 is therefore inhibition of LOC283005 (Accession XP_208481.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283005.

[47187] LOC283045 (Accession XP_210866.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC283045 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283045 BINDING SITE, designated SEQ ID:19707, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47188] Another function of GAM3770 is therefore inhibition of LOC283045 (Accession XP_210866.1) . Accordingly, utili-

ties of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283045.

[47189] LOC283048 (Accession XP_210867.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC283048 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283048, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283048 BINDING SITE, designated SEQ ID:12366, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47190] Another function of GAM3770 is therefore inhibition of LOC283048 (Accession XP_210867.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283048.

[47191] LOC283454 (Accession XP_211049.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC283454 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC283454, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283454 BINDING SITE, designated SEQ ID:15833, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47192] Another function of GAM3770 is therefore inhibition of LOC283454 (Accession XP_211049.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283454.

[47193] LOC283491 (Accession XP_208695.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC283491 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283491, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283491 BINDING SITE, designated SEQ ID:14118, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47194] Another function of GAM3770 is therefore inhibition of LOC283491 (Accession XP_208695.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283491.

[47195] LOC283526 (Accession XP_211081.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC283526 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283526, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283526 BINDING SITE, designated SEQ ID:4485, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47196] Another function of GAM3770 is therefore inhibition of LOC283526 (Accession XP_211081.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283526.

[47197] LOC283851 (Accession XP_211229.1) is another GAM3770 target gene, herein designated TARGET GENE.

LOC283851 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283851, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283851 BINDING SITE, designated SEQ ID:9696, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47198] Another function of GAM3770 is therefore inhibition of LOC283851 (Accession XP_211229.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283851.

[47199] LOC283875 (Accession XP_211241.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC283875 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283875, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283875 BINDING SITE, designated SEQ ID:12309, to the nucleotide sequence of

GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47200] Another function of GAM3770 is therefore inhibition of LOC283875 (Accession XP_211241.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283875.

[47201] LOC283921 (Accession XP_211263.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC283921 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283921, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283921 BINDING SITE, designated SEQ ID:13328, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47202] Another function of GAM3770 is therefore inhibition of LOC283921 (Accession XP_211263.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283921.

[47203] LOC284084 (Accession XP_211325.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC284084 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284084, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284084 BINDING SITE, designated SEQ ID:14562, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47204] Another function of GAM3770 is therefore inhibition of LOC284084 (Accession XP_211325.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284084.

[47205] LOC284118 (Accession XP_211336.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC284118 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284118, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284118 BINDING SITE, designated SEQ ID:15952, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47206] Another function of GAM3770 is therefore inhibition of LOC284118 (Accession XP_211336.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284118.

[47207] LOC284130 (Accession XP_209031.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC284130 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284130, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284130 BINDING SITE, designated SEQ ID:18185, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47208] Another function of GAM3770 is therefore inhibition of LOC284130 (Accession XP_209031.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284130.

[47209] LOC284336 (Accession XP_211438.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC284336 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284336, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284336 BINDING SITE, designated SEQ ID:13309, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47210] Another function of GAM3770 is therefore inhibition of LOC284336 (Accession XP_211438.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284336.

[47211] LOC284570 (Accession XP_211521.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC284570 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284570, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284570 BINDING SITE, designated SEQ ID:4065, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47212] Another function of GAM3770 is therefore inhibition of LOC284570 (Accession XP_211521.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284570.

[47213] LOC284708 (Accession XP_209332.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC284708 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284708 BINDING SITE, designated SEQ ID:9883, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47214] Another function of GAM3770 is therefore inhibition of

LOC284708 (Accession XP_209332.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284708.

[47215] LOC284736 (Accession XP_209343.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC284736 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284736, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284736 BINDING SITE, designated SEQ ID:1836, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47216] Another function of GAM3770 is therefore inhibition of LOC284736 (Accession XP_209343.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284736.

[47217] LOC284751 (Accession XP_211622.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC284751 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC284751, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284751 BINDING SITE, designated SEQ ID:7838, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47218] Another function of GAM3770 is therefore inhibition of LOC284751 (Accession XP_211622.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284751.

[47219] LOC284997 (Accession XP_211723.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC284997 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284997, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284997 BINDING SITE, designated SEQ ID:19759, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:281.

[47220] Another function of GAM3770 is therefore inhibition of LOC284997 (Accession XP_211723.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284997.

[47221] LOC285085 (Accession XP_209463.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC285085 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285085, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285085 BINDING SITE, designated SEQ ID:9957, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47222] Another function of GAM3770 is therefore inhibition of LOC285085 (Accession XP_209463.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285085.

[47223] LOC285582 (Accession XP_211943.1) is another

GAM3770 target gene, herein designated TARGET GENE. LOC285582 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285582, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285582 BINDING SITE, designated SEQ ID:12902, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47224] Another function of GAM3770 is therefore inhibition of LOC285582 (Accession XP_211943.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285582.

[47225] LOC285589 (Accession XP_209671.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC285589 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285589, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285589 BINDING SITE, desig-

nated SEQ ID:10045, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47226] Another function of GAM3770 is therefore inhibition of LOC285589 (Accession XP_209671.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285589.

[47227] LOC285622 (Accession XP_208333.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC285622 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285622, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285622 BINDING SITE, designated SEQ ID:8952, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47228] Another function of GAM3770 is therefore inhibition of LOC285622 (Accession XP_208333.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285622.

[47229] LOC285727 (Accession XP_212000.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC285727 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285727, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285727 BINDING SITE, designated SEQ ID:2857, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47230] Another function of GAM3770 is therefore inhibition of LOC285727 (Accession XP_212000.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285727.

[47231] LOC285772 (Accession XP_212014.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC285772 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285772, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285772 BINDING SITE, designated SEQ ID:2909, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47232] Another function of GAM3770 is therefore inhibition of LOC285772 (Accession XP_212014.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285772.

[47233] LOC285951 (Accession XP_212090.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC285951 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285951, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285951 BINDING SITE, designated SEQ ID:3942, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47234] Another function of GAM3770 is therefore inhibition of LOC285951 (Accession XP_212090.1) . Accordingly, utili-

ties of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285951.

[47235] LOC286058 (Accession XP_212158.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC286058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286058 BINDING SITE, designated SEQ ID:1673, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47236] Another function of GAM3770 is therefore inhibition of LOC286058 (Accession XP_212158.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286058.

[47237] LOC286078 (Accession XP_212163.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC286078 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC286078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286078 BINDING SITE, designated SEQ ID:11859, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47238] Another function of GAM3770 is therefore inhibition of LOC286078 (Accession XP_212163.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286078.

[47239] LOC286206 (Accession XP_209953.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC286206 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286206, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286206 BINDING SITE, designated SEQ ID:5166, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47240] Another function of GAM3770 is therefore inhibition of LOC286206 (Accession XP_209953.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286206.

[47241] LOC286214 (Accession XP_212231.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC286214 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286214, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286214 BINDING SITE, designated SEQ ID:19388, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47242] Another function of GAM3770 is therefore inhibition of LOC286214 (Accession XP_212231.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286214.

[47243] LOC286381 (Accession XP_212298.1) is another GAM3770 target gene, herein designated TARGET GENE.

LOC286381 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286381, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286381 BINDING SITE, designated SEQ ID:13537, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47244] Another function of GAM3770 is therefore inhibition of LOC286381 (Accession XP_212298.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286381.

[47245] LOC286493 (Accession XP_208437.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC286493 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286493 BINDING SITE, designated SEQ ID:18478, to the nucleotide sequence of

GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47246] Another function of GAM3770 is therefore inhibition of LOC286493 (Accession XP_208437.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286493.

[47247] LOC338769 (Accession XP_294696.2) is another GAM3770 target gene, herein designated TARGET GENE. LOC338769 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC338769, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338769 BINDING SITE, designated SEQ ID:2578, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47248] Another function of GAM3770 is therefore inhibition of LOC338769 (Accession XP_294696.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338769.

[47249] LOC339149 (Accession XP_294830.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC339149 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339149, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339149 BINDING SITE, designated SEQ ID:19949, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47250] Another function of GAM3770 is therefore inhibition of LOC339149 (Accession XP_294830.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339149.

[47251] LOC339392 (Accession XP_294925.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC339392 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339392, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC339392 BINDING SITE, designated SEQ ID:4480, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47252] Another function of GAM3770 is therefore inhibition of LOC339392 (Accession XP_294925.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339392.

[47253] LOC339442 (Accession XP_294957.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC339442 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339442 BINDING SITE, designated SEQ ID:995, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47254] Another function of GAM3770 is therefore inhibition of LOC339442 (Accession XP_294957.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC339442.

[47255] LOC339492 (Accession XP_290919.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC339492 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339492, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339492 BINDING SITE, designated SEQ ID:17748, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47256] Another function of GAM3770 is therefore inhibition of LOC339492 (Accession XP_290919.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339492.

[47257] LOC339502 (Accession XP_294983.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC339502 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339502, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339502 BINDING SITE, designated SEQ ID:18035, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47258] Another function of GAM3770 is therefore inhibition of LOC339502 (Accession XP_294983.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339502.

[47259] LOC339975 (Accession XP_295115.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC339975 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339975, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339975 BINDING SITE, designated SEQ ID:5687, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47260] Another function of GAM3770 is therefore inhibition of

LOC339975 (Accession XP_295115.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339975.

[47261] LOC340319 (Accession XP_295216.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC340319 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340319, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340319 BINDING SITE, designated SEQ ID:3583, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47262] Another function of GAM3770 is therefore inhibition of LOC340319 (Accession XP_295216.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340319.

[47263] LOC348549 (Accession XP_211637.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC348549 BINDING SITE1 and LOC348549 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC348549, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348549 BINDING SITE1 and LOC348549 BINDING SITE2, designated SEQ ID:12486 and SEQ ID:20123 respectively, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47264] Another function of GAM3770 is therefore inhibition of LOC348549 (Accession XP_211637.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348549.

[47265] LOC348897 (Accession XP_300874.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC348897 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348897, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348897 BINDING SITE, designated SEQ ID:14363, to the nucleotide sequence of

GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47266] Another function of GAM3770 is therefore inhibition of LOC348897 (Accession XP_300874.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348897.

[47267] LOC349312 (Accession XP_303025.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC349312 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349312, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349312 BINDING SITE, designated SEQ ID:13537, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47268] Another function of GAM3770 is therefore inhibition of LOC349312 (Accession XP_303025.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349312.

[47269] LOC349364 (Accession XP_303037.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC349364 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349364, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349364 BINDING SITE, designated SEQ ID:12158, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47270] Another function of GAM3770 is therefore inhibition of LOC349364 (Accession XP_303037.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349364.

[47271] LOC349613 (Accession XP_303409.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC349613 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349613, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC349613 BINDING SITE, designated SEQ ID:19525, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47272] Another function of GAM3770 is therefore inhibition of LOC349613 (Accession XP_303409.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349613.

[47273] LOC350154 (Accession XP_301527.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC350154 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC350154, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC350154 BINDING SITE, designated SEQ ID:13364, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47274] Another function of GAM3770 is therefore inhibition of LOC350154 (Accession XP_301527.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC350154.

[47275] LOC352856 (Accession XP_304742.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC352856 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC352856, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC352856 BINDING SITE, designated SEQ ID:8614, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47276] Another function of GAM3770 is therefore inhibition of LOC352856 (Accession XP_304742.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC352856.

[47277] LOC63928 (Accession NP_071380.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC63928 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC63928, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC63928 BINDING SITE, designated SEQ ID:6921, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47278] Another function of GAM3770 is therefore inhibition of LOC63928 (Accession NP_071380.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC63928.

[47279] LOC90110 (Accession XP_029046.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC90110 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC90110, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90110 BINDING SITE, designated SEQ ID:3656, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47280] Another function of GAM3770 is therefore inhibition of LOC90110 (Accession XP_029046.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC90110.

[47281] LOC90170 (Accession XP_029589.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC90170 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90170, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90170 BINDING SITE, designated SEQ ID:8664, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47282] Another function of GAM3770 is therefore inhibition of LOC90170 (Accession XP_029589.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90170.

[47283] LOC90668 (Accession XP_090790.7) is another GAM3770 target gene, herein designated TARGET GENE. LOC90668 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90668, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of LOC90668 BINDING SITE, designated SEQ ID:9653, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47284] Another function of GAM3770 is therefore inhibition of LOC90668 (Accession XP_090790.7) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90668.

[47285] LOC91661 (Accession NP_612381.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC91661 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC91661, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91661 BINDING SITE, designated SEQ ID:2238, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47286] Another function of GAM3770 is therefore inhibition of LOC91661 (Accession NP_612381.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC91661.

[47287] LOC96597 (Accession XP_039922.1) is another GAM3770 target gene, herein designated TARGET GENE. LOC96597 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC96597, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC96597 BINDING SITE, designated SEQ ID:9043, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47288] Another function of GAM3770 is therefore inhibition of LOC96597 (Accession XP_039922.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC96597.

[47289] LRRC8 (Accession XP_026998.2) is another GAM3770 target gene, herein designated TARGET GENE. LRRC8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LRRC8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LRRC8

BINDING SITE, designated SEQ ID:11922, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47290] Another function of GAM3770 is therefore inhibition of LRRC8 (Accession XP_026998.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRRC8.

[47291] Mitogen-activated protein kinase 8 interacting protein 3 (MAPK8IP3, Accession NP_203750.1) is another GAM3770 target gene, herein designated TARGET GENE. MAPK8IP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAPK8IP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAPK8IP3 BINDING SITE, designated SEQ ID:11255, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47292] Another function of GAM3770 is therefore inhibition of Mitogen-activated protein kinase 8 interacting protein 3 (MAPK8IP3, Accession NP_203750.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MAPK8IP3.

[47293] MDS018 (Accession NP_068595.2) is another GAM3770 target gene, herein designated TARGET GENE. MDS018 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MDS018, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDS018 BINDING SITE, designated SEQ ID:7934, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47294] Another function of GAM3770 is therefore inhibition of MDS018 (Accession NP_068595.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDS018.

[47295] Antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 (MFI2, Accession NP_201573.1) is another GAM3770 target gene, herein designated TARGET GENE. MFI2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MFI2, corresponding

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MFI2 BINDING SITE, designated SEQ ID:10773, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47296] Another function of GAM3770 is therefore inhibition of Antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 (MFI2, Accession NP_201573.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MFI2.

[47297] MFN1 (Accession NP_060397.1) is another GAM3770 target gene, herein designated TARGET GENE. MFN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MFN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MFN1 BINDING SITE, designated SEQ ID:8117, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47298] Another function of GAM3770 is therefore inhibition of

MFN1 (Accession NP_060397.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MFN1.

[47299] MFN1 (Accession NP_284941.1) is another GAM3770 target gene, herein designated TARGET GENE. MFN1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MFN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MFN1 BINDING SITE, designated SEQ ID:8117, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47300] Another function of GAM3770 is therefore inhibition of MFN1 (Accession NP_284941.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MFN1.

[47301] MGC11134 (Accession NP_113660.1) is another GAM3770 target gene, herein designated TARGET GENE. MGC11134 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC11134, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC11134 BINDING SITE, designated SEQ ID:7280, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47302] Another function of GAM3770 is therefore inhibition of MGC11134 (Accession NP_113660.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11134.

[47303] MGC21688 (Accession NP_653236.1) is another GAM3770 target gene, herein designated TARGET GENE. MGC21688 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC21688, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC21688 BINDING SITE, designated SEQ ID:10713, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47304] Another function of GAM3770 is therefore inhibition of MGC21688 (Accession NP_653236.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC21688.

[47305] MGC2734 (Accession NP_149108.1) is another GAM3770 target gene, herein designated TARGET GENE. MGC2734 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC2734, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC2734 BINDING SITE, designated SEQ ID:1723, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47306] Another function of GAM3770 is therefore inhibition of MGC2734 (Accession NP_149108.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2734.

[47307] MGC2793 (Accession NP_659501.1) is another GAM3770 target gene, herein designated TARGET GENE. MGC2793 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC2793, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC2793 BINDING SITE, designated SEQ ID:13614, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47308] Another function of GAM3770 is therefore inhibition of MGC2793 (Accession NP_659501.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2793.

[47309] MGC29649 (Accession NP_776171.1) is another GAM3770 target gene, herein designated TARGET GENE. MGC29649 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC29649, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC29649 BINDING SITE, designated SEQ ID:9449, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47310] Another function of GAM3770 is therefore inhibition of MGC29649 (Accession NP_776171.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29649.

[47311] MGC4238 (Accession NP_115708.1) is another GAM3770 target gene, herein designated TARGET GENE. MGC4238 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC4238, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC4238 BINDING SITE, designated SEQ ID:7861, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47312] Another function of GAM3770 is therefore inhibition of MGC4238 (Accession NP_115708.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4238.

[47313] MGC46719 (Accession NP_714924.1) is another GAM3770 target gene, herein designated TARGET GENE. MGC46719 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC46719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC46719 BINDING SITE, designated SEQ ID:9825, to the

nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47314] Another function of GAM3770 is therefore inhibition of MGC46719 (Accession NP_714924.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC46719.

[47315] MGC5576 (Accession NP_076961.1) is another GAM3770 target gene, herein designated TARGET GENE. MGC5576 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC5576, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC5576 BINDING SITE, designated SEQ ID:11789, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47316] Another function of GAM3770 is therefore inhibition of MGC5576 (Accession NP_076961.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5576.

[47317] Midline 1 (opitz/bbb syndrome) (MID1, Accession

NP_150632.1) is another GAM3770 target gene, herein designated TARGET GENE. MID1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by MID1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MID1 BINDING SITE, designated SEQ ID:2966, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47318] Another function of GAM3770 is therefore inhibition of Midline 1 (opitz/bbb syndrome) (MID1, Accession NP_150632.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MID1.

[47319] MONDOA (Accession NP_055753.1) is another GAM3770 target gene, herein designated TARGET GENE. MONDOA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MONDOA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MONDOA BINDING SITE, designated SEQ ID:17392, to the

nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47320] Another function of GAM3770 is therefore inhibition of MONDOA (Accession NP_055753.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MONDOA.

[47321] Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_848026.1) is another GAM3770 target gene, herein designated TARGET GENE. MRPL52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL52 BINDING SITE, designated SEQ ID:12936, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47322] Another function of GAM3770 is therefore inhibition of Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_848026.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL52.

[47323] Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851313.1) is another GAM3770 target gene, herein designated TARGET GENE. MRPL52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL52 BINDING SITE, designated SEQ ID:12936, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47324] Another function of GAM3770 is therefore inhibition of Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851313.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL52.

[47325] Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851822.1) is another GAM3770 target gene, herein designated TARGET GENE. MRPL52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MRPL52 BINDING SITE, designated SEQ ID:12936, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47326] Another function of GAM3770 is therefore inhibition of Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851822.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL52.

[47327] Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851823.1) is another GAM3770 target gene, herein designated TARGET GENE. MRPL52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL52 BINDING SITE, designated SEQ ID:12936, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47328] Another function of GAM3770 is therefore inhibition of Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851823.1) . Accordingly, utilities of GAM3770 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL52.

[47329] Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851821.1) is another GAM3770 target gene, herein designated TARGET GENE. MRPL52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL52 BINDING SITE, designated SEQ ID:12936, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47330] Another function of GAM3770 is therefore inhibition of Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851821.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL52.

[47331] Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851312.1) is another GAM3770 target gene, herein designated TARGET GENE. MRPL52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL52, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL52 BINDING SITE, designated SEQ ID:12936, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47332] Another function of GAM3770 is therefore inhibition of Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851312.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL52.

[47333] Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851824.1) is another GAM3770 target gene, herein designated TARGET GENE. MRPL52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MRPL52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRPL52 BINDING SITE, designated SEQ ID:12936, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47334] Another function of GAM3770 is therefore inhibition of

Mitochondrial ribosomal protein l52 (MRPL52, Accession NP_851824.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL52.

[47335] MRS3/4 (Accession NP_112489.2) is another GAM3770 target gene, herein designated TARGET GENE. MRS3/4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MRS3/4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MRS3/4 BINDING SITE, designated SEQ ID:4406, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47336] Another function of GAM3770 is therefore inhibition of MRS3/4 (Accession NP_112489.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRS3/4.

[47337] Musculin (activated b-cell factor-1) (MSC, Accession NP_005089.1) is another GAM3770 target gene, herein designated TARGET GENE. MSC BINDING SITE is a target binding site found in the 5` untranslated region of mRNA

encoded by MSC, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MSC BINDING SITE, designated SEQ ID:10452, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47338] Another function of GAM3770 is therefore inhibition of Musculin (activated b-cell factor-1) (MSC, Accession NP_005089.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSC.

[47339] Neutrophil cytosolic factor 4, 40kda (NCF4, Accession NP_000622.1) is another GAM3770 target gene, herein designated TARGET GENE. NCF4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NCF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NCF4 BINDING SITE, designated SEQ ID:11268, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47340] Another function of GAM3770 is therefore inhibition of Neutrophil cytosolic factor 4, 40kda (NCF4, Accession NP_000622.1), a gene which may be important for the assembly and/or activation of the nadph- oxidase complex. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCF4.

[47341] The function of NCF4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM967.1.NID67 (Accession NP_116565.1) is another GAM3770 target gene, herein designated TARGET GENE. NID67 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NID67, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NID67 BINDING SITE, designated SEQ ID:1378, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47342] Another function of GAM3770 is therefore inhibition of NID67 (Accession NP_116565.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with NID67.

[47343] Nk3 transcription factor related, locus 1 (drosophila) (NKX3-1, Accession NP_006158.2) is another GAM3770 target gene, herein designated TARGET GENE. NKX3-1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NKX3-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NKX3-1 BINDING SITE, designated SEQ ID:5499, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47344] Another function of GAM3770 is therefore inhibition of Nk3 transcription factor related, locus 1 (drosophila) (NKX3-1, Accession NP_006158.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NKX3-1.

[47345] NMNAT2 (Accession NP_055854.1) is another GAM3770 target gene, herein designated TARGET GENE. NMNAT2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NMNAT2, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NMNAT2 BINDING SITE, designated SEQ ID:1983, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47346] Another function of GAM3770 is therefore inhibition of NMNAT2 (Accession NP_055854.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NMNAT2.

[47347] Npc1 (niemann-pick disease, type c1, gene)-like 1 (NPC1L1, Accession NP_037521.1) is another GAM3770 target gene, herein designated TARGET GENE. NPC1L1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NPC1L1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NPC1L1 BINDING SITE, designated SEQ ID:17761, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47348] Another function of GAM3770 is therefore inhibition of

Npc1 (niemann-pick disease, type c1, gene)-like 1 (NPC1L1, Accession NP_037521.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPC1L1.

[47349] Oxidative-stress responsive 1 (OSR1, Accession NP_005100.1) is another GAM3770 target gene, herein designated TARGET GENE. OSR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OSR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSR1 BINDING SITE, designated SEQ ID:8511, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47350] Another function of GAM3770 is therefore inhibition of Oxidative-stress responsive 1 (OSR1, Accession NP_005100.1), a gene which mediats stress- activated signals. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSR1.

[47351] The function of OSR1 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM133.1.OTOP3 (Accession XP_292588.2) is another GAM3770 target gene, herein designated TARGET GENE. OTOP3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by OTOP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OTOP3 BINDING SITE, designated SEQ ID:11275, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47352] Another function of GAM3770 is therefore inhibition of OTOP3 (Accession XP_292588.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OTOP3.

[47353] P21(cdkn1a)-activated kinase 6 (PAK6, Accession NP_064553.1) is another GAM3770 target gene, herein designated TARGET GENE. PAK6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PAK6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of PAK6 BINDING SITE, designated SEQ ID:10797, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47354] Another function of GAM3770 is therefore inhibition of P21(cdkn1a)-activated kinase 6 (PAK6, Accession NP_064553.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAK6.

[47355] Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) is another GAM3770 target gene, herein designated TARGET GENE. PASK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PASK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PASK BINDING SITE, designated SEQ ID:20147, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47356] Another function of GAM3770 is therefore inhibition of Pas domain containing serine/threonine kinase (PASK, Accession NP_055963.1) . Accordingly, utilities of GAM3770

include diagnosis, prevention and treatment of diseases and clinical conditions associated with PASK.

[47357] Procollagen (type iii) n-endopeptidase (PCOLN3, Accession NP_002759.1) is another GAM3770 target gene, herein designated TARGET GENE. PCOLN3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCOLN3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCOLN3 BINDING SITE, designated SEQ ID:2932, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47358] Another function of GAM3770 is therefore inhibition of Procollagen (type iii) n-endopeptidase (PCOLN3, Accession NP_002759.1), a gene which is a member of the zincin superfamily of zinc- dependent metalloproteases. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCOLN3.

[47359] The function of PCOLN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM38.1.Placental growth factor, vascular endothelial growth factor-related protein (PGF, Accession NP_002623.2) is another GAM3770 target gene, herein designated TARGET GENE. PGF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PGF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PGF BINDING SITE, designated SEQ ID:11465, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47360] Another function of GAM3770 is therefore inhibition of Placental growth factor, vascular endothelial growth factor-related protein (PGF, Accession NP_002623.2), a gene which is a growth factor active in angiogenesis, and endothelial cell growth, stimulating cell proliferation and migration. it binds to receptor vegfr- 1/fl. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGF.

[47361] The function of PGF and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM758.1.Phosphoglycerate kinase 1 (PGK1, Accession NP_000282.1) is another GAM3770 target gene, herein designated TARGET GENE. PGK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PGK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PGK1 BINDING SITE, designated SEQ ID:495, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47362] Another function of GAM3770 is therefore inhibition of Phosphoglycerate kinase 1 (PGK1, Accession NP_000282.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGK1.

[47363] Phosphotidylinositol transfer protein (PITPN, Accession NP_006215.1) is another GAM3770 target gene, herein designated TARGET GENE. PITPN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PITPN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of PITPN BINDING SITE, designated SEQ ID:423, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47364] Another function of GAM3770 is therefore inhibition of Phosphotidylinositol transfer protein (PITPN, Accession NP_006215.1), a gene which catalyzes the transfer of pt-dins and phosphatidylcholine between membranes. Ac-cordingly, utilities of GAM3770 include diagnosis, preven-tion and treatment of diseases and clinical conditions as-sociated with PITPN.

[47365] The function of PITPN and its association with various dis-eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_115288.1) is an-other GAM3770 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-mentarity of the nucleotide sequences of PPP1R12B BIND-ING SITE, designated SEQ ID:19376, to the nucleotide se-

quence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47366] Another function of GAM3770 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_115288.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[47367] Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) is another GAM3770 target gene, herein designated TARGET GENE. PPP1R12B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PPP1R12B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PPP1R12B BINDING SITE, designated SEQ ID:19376, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47368] Another function of GAM3770 is therefore inhibition of Protein phosphatase 1, regulatory (inhibitor) subunit 12b (PPP1R12B, Accession NP_002472.1) . Accordingly, utili-

ties of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R12B.

[47369] Protease, serine, 7 (enterokinase) (PRSS7, Accession NP_002763.1) is another GAM3770 target gene, herein designated TARGET GENE. PRSS7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PRSS7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRSS7 BINDING SITE, designated SEQ ID:4893, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47370] Another function of GAM3770 is therefore inhibition of Protease, serine, 7 (enterokinase) (PRSS7, Accession NP_002763.1), a gene which Some of the trypsinogen genes are expressed in nonpancreatic tissues where their function is unknown and therefore is associated with Enterokinase deficiency. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Enterokinase deficiency, and of other diseases and clinical conditions associated with PRSS7.

[47371] The function of PRSS7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1956.1.Protein tyrosine phosphatase, receptor type, r (PTPRR, Accession NP_002840.1) is another GAM3770 target gene, herein designated TARGET GENE. PTPRR BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PTPRR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTPRR BINDING SITE, designated SEQ ID:10961, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47372] Another function of GAM3770 is therefore inhibition of Protein tyrosine phosphatase, receptor type, r (PTPRR, Accession NP_002840.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRR.

[47373] Phosphorylase, glycogen; muscle (mcardle syndrome, glycogen storage disease type v) (PYGM, Accession NP_005600.1) is another GAM3770 target gene, herein

designated TARGET GENE. PYGM BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PYGM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PYGM BINDING SITE, designated SEQ ID:11354, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47374] Another function of GAM3770 is therefore inhibition of Phosphorylase, glycogen; muscle (mcardle syndrome, glycogen storage disease type v) (PYGM, Accession NP_005600.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PYGM.

[47375] Rab3a interacting protein (rabin3)-like 1 (RAB3IL1, Accession NP_037533.2) is another GAM3770 target gene, herein designated TARGET GENE. RAB3IL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB3IL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB3IL1 BIND-

ING SITE, designated SEQ ID:7921, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47376] Another function of GAM3770 is therefore inhibition of Rab3a interacting protein (rabin3)-like 1 (RAB3IL1, Accession NP_037533.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB3IL1.

[47377] Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602296.1) is another GAM3770 target gene, herein designated TARGET GENE. RAD52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAD52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE, designated SEQ ID:6948, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47378] Another function of GAM3770 is therefore inhibition of Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602296.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with RAD52.

[47379] Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602295.1) is another GAM3770 target gene, herein designated TARGET GENE. RAD52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAD52, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE, designated SEQ ID:6948, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47380] Another function of GAM3770 is therefore inhibition of Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602295.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52.

[47381] Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602294.1) is another GAM3770 target gene, herein designated TARGET GENE. RAD52 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RAD52, corresponding to a target binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE, designated SEQ ID:6948, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47382] Another function of GAM3770 is therefore inhibition of Rad52 homolog (s. cerevisiae) (RAD52, Accession NP_602294.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52.

[47383] RASSF4 (Accession NP_835281.1) is another GAM3770 target gene, herein designated TARGET GENE. RASSF4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF4 BINDING SITE, designated SEQ ID:725, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47384] Another function of GAM3770 is therefore inhibition of RASSF4 (Accession NP_835281.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with RASSF4.

[47385] RASSF4 (Accession NP_114412.2) is another GAM3770 target gene, herein designated TARGET GENE. RASSF4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RASSF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASSF4 BINDING SITE, designated SEQ ID:725, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47386] Another function of GAM3770 is therefore inhibition of RASSF4 (Accession NP_114412.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF4.

[47387] RE2 (Accession NP_722561.1) is another GAM3770 target gene, herein designated TARGET GENE. RE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by RE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RE2 BINDING SITE, designated SEQ ID:1602, to

the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47388] Another function of GAM3770 is therefore inhibition of RE2 (Accession NP_722561.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RE2.

[47389] RE2 (Accession NP_031395.1) is another GAM3770 target gene, herein designated TARGET GENE. RE2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by RE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RE2 BINDING SITE, designated SEQ ID:1602, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47390] Another function of GAM3770 is therefore inhibition of RE2 (Accession NP_031395.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RE2.

[47391] Replication factor c (activator 1) 1, 145kda (RFC1, Accession NP_002904.2) is another GAM3770 target gene, herein designated TARGET GENE. RFC1 BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by RFC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RFC1 BINDING SITE, designated SEQ ID:12616, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47392] Another function of GAM3770 is therefore inhibition of Replication factor c (activator 1) 1, 145kda (RFC1, Accession NP_002904.2), a gene which plays a role in dna transcription, replication and/or repair. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFC1.

[47393] The function of RFC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM195.2.Ribonuclease/angiogenin inhibitor (RNH, Accession NP_002930.2) is another GAM3770 target gene, herein designated TARGET GENE. RNH BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RNH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNH BINDING SITE, designated SEQ ID:8721, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47394] Another function of GAM3770 is therefore inhibition of Ribonuclease/angiogenin inhibitor (RNH, Accession NP_002930.2), a gene which is an inhibitor of pancreatic rnase and angiogenin. may also function in the modulation of cellular activities. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNH.

[47395] The function of RNH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM204.2.Ribonucleotide reductase m2 polypeptide (RRM2, Accession NP_001025.1) is another GAM3770 target gene, herein designated TARGET GENE. RRM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RRM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RRM2 BIND-

ING SITE, designated SEQ ID:17167, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47396] Another function of GAM3770 is therefore inhibition of Ribonucleotide reductase m2 polypeptide (RRM2, Accession NP_001025.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RRM2.

[47397] Runt-related transcription factor 3 (RUNX3, Accession NP_004341.1) is another GAM3770 target gene, herein designated TARGET GENE. RUNX3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RUNX3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RUNX3 BINDING SITE, designated SEQ ID:16681, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47398] Another function of GAM3770 is therefore inhibition of Runt-related transcription factor 3 (RUNX3, Accession NP_004341.1), a gene which binds to the core site, 5'-pygpyggt- 3', of a number of enhancers and promoters.

Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RUNX3.

[47399] The function of RUNX3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM69.2.Syndecan 3 (n-syndecan) (SDC3, Accession NP_055469.1) is another GAM3770 target gene, herein designated TARGET GENE. SDC3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SDC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SDC3 BINDING SITE, designated SEQ ID:5640, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47400] Another function of GAM3770 is therefore inhibition of Syndecan 3 (n-syndecan) (SDC3, Accession NP_055469.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDC3.

[47401] Spondyloepiphyseal dysplasia, late (SEDL, Accession

NP_055378.1) is another GAM3770 target gene, herein designated TARGET GENE. SEDL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SEDL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEDL BINDING SITE, designated SEQ ID:1404, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47402] Another function of GAM3770 is therefore inhibition of Spondyloepiphyseal dysplasia, late (SEDL, Accession NP_055378.1), a gene which may play role in vesicular transport from endoplasmic reticulum to golgi. and therefore may be associated with Spondyloepiphyseal dysplasia. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Spondyloepiphyseal dysplasia, and of other diseases and clinical conditions associated with SEDL.

[47403] The function of SEDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.SIT (Accession NP_055265.1) is another

GAM3770 target gene, herein designated TARGET GENE. SIT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SIT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIT BINDING SITE, designated SEQ ID:13417, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47404] Another function of GAM3770 is therefore inhibition of SIT (Accession NP_055265.1), a gene which recruits tyrosine phosphatase SHP2 to the cell membrane. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIT.

[47405] The function of SIT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM144.1.Solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10, Accession NP_110404.1) is another GAM3770 target gene, herein designated TARGET GENE. SLC2A10 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by SLC2A10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC2A10 BINDING SITE, designated SEQ ID:11011, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47406] Another function of GAM3770 is therefore inhibition of Solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10, Accession NP_110404.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC2A10.

[47407] Solute carrier family 2 (facilitated glucose transporter), member 6 (SLC2A6, Accession NP_060055.1) is another GAM3770 target gene, herein designated TARGET GENE. SLC2A6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC2A6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC2A6 BINDING SITE, designated SEQ ID:10319, to the nucleotide sequence of GAM3770 RNA, herein designated

GAM RNA, also designated SEQ ID:241.

[47408] Another function of GAM3770 is therefore inhibition of Solute carrier family 2 (facilitated glucose transporter), member 6 (SLC2A6, Accession NP_060055.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC2A6.

[47409] Smith-magenis syndrome chromosome region, candidate 5 (SMCR5, Accession NP_658987.1) is another GAM3770 target gene, herein designated TARGET GENE. SMCR5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SMCR5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMCR5 BINDING SITE, designated SEQ ID:20071, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47410] Another function of GAM3770 is therefore inhibition of Smith-magenis syndrome chromosome region, candidate 5 (SMCR5, Accession NP_658987.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMCR5.

[47411] Survival of motor neuron 1, telomeric (SMN1, Accession NP_000335.1) is another GAM3770 target gene, herein designated TARGET GENE. SMN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMN1 BINDING SITE, designated SEQ ID:3206, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47412] Another function of GAM3770 is therefore inhibition of Survival of motor neuron 1, telomeric (SMN1, Accession NP_000335.1), a gene which plays an essential role in spliceosomal snrnp assembly in the cytoplasm and therefore is associated with Spinal muscular atrophy, type i, ii,iii. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Spinal muscular atrophy, type i, ii,iii, and of other diseases and clinical conditions associated with SMN1.

[47413] The function of SMN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM148.2.Survival of motor neuron 1, telomeric (SMN1, Accession NP_075012.1) is another GAM3770 target gene, herein designated TARGET GENE. SMN1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMN1 BINDING SITE, designated SEQ ID:3206, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47414] Another function of GAM3770 is therefore inhibition of Survival of motor neuron 1, telomeric (SMN1, Accession NP_075012.1), a gene which plays an essential role in spliceosomal snrnp assembly in the cytoplasm and therefore is associated with Spinal muscular atrophy, type i, ii,iii. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Spinal muscular atrophy, type i, ii,iii, and of other diseases and clinical conditions associated with SMN1.

[47415] The function of SMN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM148.2.Survival of motor neuron 2, centromeric (SMN2, Accession NP_075013.1) is another GAM3770 target gene, herein designated TARGET GENE. SMN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMN2 BINDING SITE, designated SEQ ID:3206, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47416] Another function of GAM3770 is therefore inhibition of Survival of motor neuron 2, centromeric (SMN2, Accession NP_075013.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMN2.

[47417] Survival of motor neuron 2, centromeric (SMN2, Accession NP_059107.1) is another GAM3770 target gene, herein designated TARGET GENE. SMN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of SMN2 BINDING SITE, designated SEQ ID:3206, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47418] Another function of GAM3770 is therefore inhibition of Survival of motor neuron 2, centromeric (SMN2, Accession NP_059107.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMN2.

[47419] Survival of motor neuron 2, centromeric (SMN2, Accession NP_075015.1) is another GAM3770 target gene, herein designated TARGET GENE. SMN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMN2 BINDING SITE, designated SEQ ID:3206, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47420] Another function of GAM3770 is therefore inhibition of Survival of motor neuron 2, centromeric (SMN2, Accession NP_075015.1) . Accordingly, utilities of GAM3770 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with SMN2.

[47421] Survival of motor neuron 2, centromeric (SMN2, Accession NP_075014.1) is another GAM3770 target gene, herein designated TARGET GENE. SMN2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SMN2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SMN2 BINDING SITE, designated SEQ ID:3206, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47422] Another function of GAM3770 is therefore inhibition of Survival of motor neuron 2, centromeric (SMN2, Accession NP_075014.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMN2.

[47423] Serine protease inhibitor-like, with kunitz and wap domains 1 (eppin) (SPINLW1, Accession NP_852479.1) is another GAM3770 target gene, herein designated TARGET GENE. SPINLW1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of

mRNA encoded by SPINLW1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SPINLW1 BINDING SITE, designated SEQ ID:18980, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47424] Another function of GAM3770 is therefore inhibition of Serine protease inhibitor-like, with kunitz and wap domains 1 (eppin) (SPINLW1, Accession NP_852479.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPINLW1.

[47425] Sarcalumenin (SRL, Accession XP_064152.3) is another GAM3770 target gene, herein designated TARGET GENE. SRL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SRL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SRL BINDING SITE, designated SEQ ID:10846, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47426] Another function of GAM3770 is therefore inhibition of Sarcalumenin (SRL, Accession XP_064152.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRL.

[47427] Serine/threonine kinase 29 (STK29, Accession NP_003948.1) is another GAM3770 target gene, herein designated TARGET GENE. STK29 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by STK29, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of STK29 BINDING SITE, designated SEQ ID:19087, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47428] Another function of GAM3770 is therefore inhibition of Serine/threonine kinase 29 (STK29, Accession NP_003948.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK29.

[47429] SULF1 (Accession NP_055985.1) is another GAM3770 target gene, herein designated TARGET GENE. SULF1 BIND-

ING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SULF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SULF1 BINDING SITE, designated SEQ ID:12171, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47430] Another function of GAM3770 is therefore inhibition of SULF1 (Accession NP_055985.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SULF1.

[47431] Surfeit 4 (SURF4, Accession NP_149351.1) is another GAM3770 target gene, herein designated TARGET GENE. SURF4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SURF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SURF4 BINDING SITE, designated SEQ ID:547, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47432] Another function of GAM3770 is therefore inhibition of

Surfeit 4 (SURF4, Accession NP_149351.1), a gene which is a conserved integral membrane protein containing multiple putative transmembrane regions. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURF4.

[47433] The function of SURF4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM329.1.Transcription elongation factor a (sii), 1 (TCEA1, Accession NP_006747.1) is another GAM3770 target gene, herein designated TARGET GENE. TCEA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TCEA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCEA1 BINDING SITE, designated SEQ ID:10324, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47434] Another function of GAM3770 is therefore inhibition of Transcription elongation factor a (sii), 1 (TCEA1, Accession NP_006747.1), a gene which helps RNA polymerase II to transcribe past blockages. Accordingly, utilities of

GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCEA1.

[47435] The function of TCEA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM259.1.Thymidine kinase 1, soluble (TK1, Accession NP_003249.1) is another GAM3770 target gene, herein designated TARGET GENE. TK1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TK1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TK1 BINDING SITE, designated SEQ ID:11195, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47436] Another function of GAM3770 is therefore inhibition of Thymidine kinase 1, soluble (TK1, Accession NP_003249.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TK1.

[47437] TMPRSS6 (Accession NP_694564.2) is another GAM3770 target gene, herein designated TARGET GENE. TMPRSS6

BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TMPRSS6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS6 BINDING SITE, designated SEQ ID:18491, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47438] Another function of GAM3770 is therefore inhibition of TMPRSS6 (Accession NP_694564.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS6.

[47439] Tumor necrosis factor receptor superfamily, member 1b (TNFRSF1B, Accession NP_001057.1) is another GAM3770 target gene, herein designated TARGET GENE. TNFRSF1B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNFRSF1B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNFRSF1B BINDING SITE, designated SEQ ID:4544, to the

nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47440] Another function of GAM3770 is therefore inhibition of Tumor necrosis factor receptor superfamily, member 1b (TNFRSF1B, Accession NP_001057.1), a gene which mediates proinflammatory cellular responses. and therefore may be associated with Familial combined hyperlipidemia. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Familial combined hyperlipidemia., and of other diseases and clinical conditions associated with TNFRSF1B.

[47441] The function of TNFRSF1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.Topoisomerase (dna) i (TOP1, Accession NP_003277.1) is another GAM3770 target gene, herein designated TARGET GENE. TOP1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TOP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TOP1 BINDING SITE, designated SEQ ID:17569, to the nucleotide sequence of GAM3770

RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47442] Another function of GAM3770 is therefore inhibition of Topoisomerase (dna) i (TOP1, Accession NP_003277.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOP1.

[47443] Transient receptor potential cation channel, subfamily m, member 2 (TRPM2, Accession NP_003298.1) is another GAM3770 target gene, herein designated TARGET GENE. TRPM2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPM2 BINDING SITE, designated SEQ ID:16176, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47444] Another function of GAM3770 is therefore inhibition of Transient receptor potential cation channel, subfamily m, member 2 (TRPM2, Accession NP_003298.1), a gene which may be a calcium channel. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with TRPM2.

[47445] The function of TRPM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.1.TSAP6 (Accession NP_060704.1) is another GAM3770 target gene, herein designated TARGET GENE. TSAP6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSAP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TSAP6 BINDING SITE, designated SEQ ID:17391, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47446] Another function of GAM3770 is therefore inhibition of TSAP6 (Accession NP_060704.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSAP6.

[47447] TULP4 (Accession NP_064630.1) is another GAM3770 target gene, herein designated TARGET GENE. TULP4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TULP4, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TULP4 BINDING SITE, designated SEQ ID:5367, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47448] Another function of GAM3770 is therefore inhibition of TULP4 (Accession NP_064630.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TULP4.

[47449] Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) is another GAM3770 target gene, herein designated TARGET GENE. TXNL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TXNL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TXNL2 BINDING SITE, designated SEQ ID:13570, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47450] Another function of GAM3770 is therefore inhibition of Thioredoxin-like 2 (TXNL2, Accession NP_006532.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions as-

sociated with TXNL2.

[47451] Ubiquitin-conjugating enzyme e2g 1 (ubc7 homolog, c. elegans) (UBE2G1, Accession NP_003333.1) is another GAM3770 target gene, herein designated TARGET GENE. UBE2G1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBE2G1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBE2G1 BINDING SITE, designated SEQ ID:14637, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47452] Another function of GAM3770 is therefore inhibition of Ubiquitin-conjugating enzyme e2g 1 (ubc7 homolog, c. elegans) (UBE2G1, Accession NP_003333.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE2G1.

[47453] Ubiquitination factor e4a (ufd2 homolog, yeast) (UBE4A, Accession NP_004779.1) is another GAM3770 target gene, herein designated TARGET GENE. UBE4A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBE4A, corresponding to a target bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBE4A BINDING SITE, designated SEQ ID:5235, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47454] Another function of GAM3770 is therefore inhibition of Ubiquitination factor e4a (ufd2 homolog, yeast) (UBE4A, Accession NP_004779.1), a gene which binds to the ubiquitin moieties of preformed conjugates and catalyzes ubiquitin chain assembly in conjunction with E1, E2, and E3. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE4A.

[47455] The function of UBE4A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.2.Ubiquitin carboxyl-terminal esterase l1 (ubiquitin thiolesterase) (UCHL1, Accession NP_004172.2) is another GAM3770 target gene, herein designated TARGET GENE. UCHL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by UCHL1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UCHL1 BINDING SITE, designated SEQ ID:5541, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47456] Another function of GAM3770 is therefore inhibition of Ubiquitin carboxyl-terminal esterase l1 (ubiquitin thiolesterase) (UCHL1, Accession NP_004172.2), a gene which is involved both in the processing of ubiquitin precursors and of ubiquinated proteins. and therefore may be associated with Parkinson disease. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of Parkinson disease, and of other diseases and clinical conditions associated with UCHL1.

[47457] The function of UCHL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2745.2.UPLC1 (Accession NP_060177.2) is another GAM3770 target gene, herein designated TARGET GENE. UPLC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UPLC1, corresponding to a target binding site such as BINDING SITE

I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UPLC1 BINDING SITE, designated SEQ ID:10056, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47458] Another function of GAM3770 is therefore inhibition of UPLC1 (Accession NP_060177.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UPLC1.

[47459] Vasoactive intestinal peptide receptor 1 (VIPR1, Accession NP_004615.2) is another GAM3770 target gene, herein designated TARGET GENE. VIPR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VIPR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VIPR1 BINDING SITE, designated SEQ ID:12543, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47460] Another function of GAM3770 is therefore inhibition of Vasoactive intestinal peptide receptor 1 (VIPR1, Accession NP_004615.2), a gene which binds vip and is mediated by

g proteins which activate adenylyl cyclase. Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIPR1.

[47461] The function of VIPR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Von willebrand factor (VWF, Accession NP_000543.1) is another GAM3770 target gene, herein designated TARGET GENE. VWF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VWF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VWF BINDING SITE, designated SEQ ID:11547, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47462] Another function of GAM3770 is therefore inhibition of Von willebrand factor (VWF, Accession NP_000543.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VWF.

[47463] YAP (Accession NP_620830.1) is another GAM3770 target gene, herein designated TARGET GENE. YAP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by YAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of YAP BINDING SITE, designated SEQ ID:18388, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47464] Another function of GAM3770 is therefore inhibition of YAP (Accession NP_620830.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YAP.

[47465] YAP (Accession NP_620829.1) is another GAM3770 target gene, herein designated TARGET GENE. YAP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by YAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of YAP BINDING SITE, designated SEQ ID:18388, to the nucleotide sequence of GAM3770 RNA, herein des-

ignated GAM RNA, also designated SEQ ID:281.

[47466] Another function of GAM3770 is therefore inhibition of YAP (Accession NP_620829.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YAP.

[47467] YAP (Accession NP_620832.1) is another GAM3770 target gene, herein designated TARGET GENE. YAP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by YAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of YAP BINDING SITE, designated SEQ ID:18388, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47468] Another function of GAM3770 is therefore inhibition of YAP (Accession NP_620832.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YAP.

[47469] YAP (Accession NP_060723.2) is another GAM3770 target gene, herein designated TARGET GENE. YAP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by YAP,

corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of YAP BINDING SITE, designated SEQ ID:18388, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47470] Another function of GAM3770 is therefore inhibition of YAP (Accession NP_060723.2) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YAP.

[47471] YAP (Accession NP_620831.1) is another GAM3770 target gene, herein designated TARGET GENE. YAP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by YAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of YAP BINDING SITE, designated SEQ ID:18388, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:281.

[47472] Another function of GAM3770 is therefore inhibition of YAP (Accession NP_620831.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with YAP.

[47473] ZBED4 (Accession NP_055653.1) is another GAM3770 target gene, herein designated TARGET GENE. ZBED4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZBED4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZBED4 BINDING SITE, designated SEQ ID:2237, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47474] Another function of GAM3770 is therefore inhibition of ZBED4 (Accession NP_055653.1) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZBED4.

[47475] Zinc finger protein 36, c3h type-like 2 (ZFP36L2, Accession NP_008818.3) is another GAM3770 target gene, herein designated TARGET GENE. ZFP36L2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZFP36L2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZFP36L2 BIND-

ING SITE, designated SEQ ID:14047, to the nucleotide sequence of GAM3770 RNA, herein designated GAM RNA, also designated SEQ ID:241.

[47476] Another function of GAM3770 is therefore inhibition of Zinc finger protein 36, c3h type-like 2 (ZFP36L2, Accession NP_008818.3) . Accordingly, utilities of GAM3770 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP36L2.

[47477]

[47478] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 5227 (GAM5227), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[47479] GAM5227 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM5227 was detected is described hereinabove with reference to Figs. 8-15.

[47480] GAM5227 gene, herein designated GAM GENE, and GAM5227 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[47481] GAM5227 gene encodes a GAM5227 precursor RNA,

herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM5227 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5227 precursor RNA is designated SEQ ID:162, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:162 is located at position 200067225 relative to chromosome 1.

[47482] GAM5227 precursor RNA folds onto itself, forming GAM5227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[47483] GAM5227 precursor RNA folds onto itself, forming GAM5227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence

of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[47484] Nucleotide sequence of GAM5227 precursor RNA, designated SEQ-ID: 162, and a schematic representation of a predicted secondary folding of GAM5227 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[47485] An enzyme complex designated DICER COMPLEX, `dices` the GAM5227 folded precursor RNA into GAM5227 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: B) nucleotide sequence of GAM5227 RNA is designated SEQ ID:299, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[47486] GAM5227 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM5227 target RNA, herein designated GAM TARGET RNA. GAM5227

target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[47487] GAM5227 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5227 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5227 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM5227 RNA may have a different number of target binding sites in untranslated regions of a GAM5227 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[47488] The complementary binding of GAM5227 RNA, herein designated GAM RNA, to target binding sites on GAM5227 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5227 target RNA into GAM5227 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[47489] It is appreciated that GAM5227 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM5227 target genes. The mRNA of each one of this plurality of GAM5227 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5227 RNA, herein designated GAM RNA, and which when bound by GAM5227 RNA causes inhibition of translation of respective one or more GAM5227 target proteins.

[47490] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM5227 gene, herein designated GAM GENE, on one or more GAM5227 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[47491] It is appreciated that specific functions and accordingly utilities of GAM5227 correlate with, and may be deduced from, the identity of the target genes which GAM5227 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[47492]

[47493]

[47494] 3PAP (Accession NP_061934.2) is a GAM5227 target gene, herein designated TARGET GENE. 3PAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by 3PAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of 3PAP BINDING SITE, designated SEQ ID:18356, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47495] A function of GAM5227 is therefore inhibition of 3PAP (Accession NP_061934.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 3PAP.

[47496] Alpha-2-macroglobulin (A2M, Accession NP_000005.1) is another GAM5227 target gene, herein designated TARGET GENE. A2M BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by A2M, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A2M BINDING SITE, designated SEQ ID:1882, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47497] Another function of GAM5227 is therefore inhibition of Alpha-2-macroglobulin (A2M, Accession NP_000005.1), a gene which inhibit all four classes of proteinases and therefore may be associated with Alzheimer disease. Accordingly, utilities of GAM5227 include diagnosis, preven-

tion and treatment of Alzheimer disease, and of other diseases and clinical conditions associated with A2M.

[47498] The function of A2M and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1653.1.Acetyl-coenzyme a synthetase 2 (amp forming)-like (ACAS2L, Accession NP_115890.2) is another GAM5227 target gene, herein designated TARGET GENE. ACAS2L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACAS2L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACAS2L BINDING SITE, designated SEQ ID:4172, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47499] Another function of GAM5227 is therefore inhibition of Acetyl-coenzyme a synthetase 2 (amp forming)-like (ACAS2L, Accession NP_115890.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACAS2L.

[47500] Acrosomal vesicle protein 1 (ACRV1, Accession NP_064497.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47501] Another function of GAM5227 is therefore inhibition of Acrosomal vesicle protein 1 (ACRV1, Accession NP_064497.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47502] Acrosomal vesicle protein 1 (ACRV1, Accession NP_064495.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates

the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47503] Another function of GAM5227 is therefore inhibition of Acrosomal vesicle protein 1 (ACRV1, Accession NP_064495.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47504] Acrosomal vesicle protein 1 (ACRV1, Accession NP_064499.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47505] Another function of GAM5227 is therefore inhibition of Acrosomal vesicle protein 1 (ACRV1, Accession NP_064499.1) . Accordingly, utilities of GAM5227 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47506] Acrosomal vesicle protein 1 (ACRV1, Accession NP_064454.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47507] Another function of GAM5227 is therefore inhibition of Acrosomal vesicle protein 1 (ACRV1, Accession NP_064454.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47508] Acrosomal vesicle protein 1 (ACRV1, Accession NP_064496.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, correspond-

ing to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47509] Another function of GAM5227 is therefore inhibition of Acrosomal vesicle protein 1 (ACRV1, Accession NP_064496.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47510] Acrosomal vesicle protein 1 (ACRV1, Accession NP_064500.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47511] Another function of GAM5227 is therefore inhibition of

Acrosomal vesicle protein 1 (ACRV1, Accession NP_064500.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47512] Acrosomal vesicle protein 1 (ACRV1, Accession NP_064492.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47513] Another function of GAM5227 is therefore inhibition of Acrosomal vesicle protein 1 (ACRV1, Accession NP_064492.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47514] Acrosomal vesicle protein 1 (ACRV1, Accession NP_064494.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47515] Another function of GAM5227 is therefore inhibition of Acrosomal vesicle protein 1 (ACRV1, Accession NP_064494.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47516] Acrosomal vesicle protein 1 (ACRV1, Accession NP_064498.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated

GAM RNA, also designated SEQ ID:299.

[47517] Another function of GAM5227 is therefore inhibition of Acrosomal vesicle protein 1 (ACRV1, Accession NP_064498.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47518] Acrosomal vesicle protein 1 (ACRV1, Accession NP_064493.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47519] Another function of GAM5227 is therefore inhibition of Acrosomal vesicle protein 1 (ACRV1, Accession NP_064493.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47520] Acrosomal vesicle protein 1 (ACRV1, Accession

NP_001603.1) is another GAM5227 target gene, herein designated TARGET GENE. ACRV1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ACRV1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACRV1 BINDING SITE, designated SEQ ID:14126, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47521] Another function of GAM5227 is therefore inhibition of Acrosomal vesicle protein 1 (ACRV1, Accession NP_001603.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACRV1.

[47522] Arp1 actin-related protein 1 homolog a, centractin alpha (yeast) (ACTR1A, Accession NP_005727.1) is another GAM5227 target gene, herein designated TARGET GENE. ACTR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACTR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of ACTR1A BINDING SITE, designated SEQ ID:3042, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47523] Another function of GAM5227 is therefore inhibition of Arp1 actin-related protein 1 homolog a, centractin alpha (yeast) (ACTR1A, Accession NP_005727.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACTR1A.

[47524] Angiomotin like 1 (AMOTL1, Accession NP_570899.1) is another GAM5227 target gene, herein designated TARGET GENE. AMOTL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AMOTL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMOTL1 BINDING SITE, designated SEQ ID:11813, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47525] Another function of GAM5227 is therefore inhibition of Angiomotin like 1 (AMOTL1, Accession NP_570899.1) . Accordingly, utilities of GAM5227 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with AMOTL1.

[47526] Adenosine monophosphate deaminase 2 (isoform l) (AMPD2, Accession NP_004028.3) is another GAM5227 target gene, herein designated TARGET GENE. AMPD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AMPD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AMPD2 BINDING SITE, designated SEQ ID:6548, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47527] Another function of GAM5227 is therefore inhibition of Adenosine monophosphate deaminase 2 (isoform l) (AMPD2, Accession NP_004028.3), a gene which plays a critical role in energy metabolism. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMPD2.

[47528] The function of AMPD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM270.2.Annexin a5 (ANXA5, Accession

NP_001145.1) is another GAM5227 target gene, herein designated TARGET GENE. ANXA5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ANXA5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ANXA5 BINDING SITE, designated SEQ ID:2768, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47529] Another function of GAM5227 is therefore inhibition of Annexin a5 (ANXA5, Accession NP_001145.1), a gene which acts as an indirect inhibitor of the thromboplastin-specific complex. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANXA5.

[47530] The function of ANXA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1095.1.APA1 (Accession NP_067011.1) is another GAM5227 target gene, herein designated TARGET GENE. APA1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APA1, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APA1 BINDING SITE, designated SEQ ID:11175, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47531] Another function of GAM5227 is therefore inhibition of APA1 (Accession NP_067011.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APA1.

[47532] Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) is another GAM5227 target gene, herein designated TARGET GENE. ARHGAP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGAP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP1 BINDING SITE, designated SEQ ID:11478, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47533] Another function of GAM5227 is therefore inhibition of Rho gtpase activating protein 1 (ARHGAP1, Accession

NP_004299.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP1.

[47534] Rho gtpase activating protein 12 (ARHGAP12, Accession NP_060757.4) is another GAM5227 target gene, herein designated TARGET GENE. ARHGAP12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHGAP12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP12 BINDING SITE, designated SEQ ID:440, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47535] Another function of GAM5227 is therefore inhibition of Rho gtpase activating protein 12 (ARHGAP12, Accession NP_060757.4) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP12.

[47536] Atpase, na+/k+ transporting, alpha 2 (+) polypeptide (ATP1A2, Accession NP_000693.1) is another GAM5227 target gene, herein designated TARGET GENE. ATP1A2 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by ATP1A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP1A2 BINDING SITE, designated SEQ ID:14999, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47537] Another function of GAM5227 is therefore inhibition of Atpase, na+/k+ transporting, alpha 2 (+) polypeptide (ATP1A2, Accession NP_000693.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1A2.

[47538] Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 6 (B4GALT6, Accession NP_004766.1) is another GAM5227 target gene, herein designated TARGET GENE. B4GALT6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by B4GALT6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B4GALT6 BINDING SITE, designated SEQ ID:17518, to the nucleotide sequence of GAM5227

RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47539] Another function of GAM5227 is therefore inhibition of Udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 6 (B4GALT6, Accession NP_004766.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT6.

[47540] Bcl2-associated x protein (BAX, Accession NP_004315.1) is another GAM5227 target gene, herein designated TARGET GENE. BAX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BAX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAX BINDING SITE, designated SEQ ID:3053, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47541] Another function of GAM5227 is therefore inhibition of Bcl2-associated x protein (BAX, Accession NP_004315.1), a gene which accelerates programmed cell death and therefore may be associated with Colorectal cancer, t- cell

acute lymphoblastic leukemia. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Colorectal cancer, t- cell acute lymphoblastic leukemia, and of other diseases and clinical conditions associated with BAX.

[47542] The function of BAX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM960.1.Bone morphogenetic protein 8 (osteogenic protein 2) (BMP8, Accession NP_001711.2) is another GAM5227 target gene, herein designated TARGET GENE. BMP8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BMP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BMP8 BINDING SITE, designated SEQ ID:1565, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47543] Another function of GAM5227 is therefore inhibition of Bone morphogenetic protein 8 (osteogenic protein 2) (BMP8, Accession NP_001711.2), a gene which plays a role in calcium regulation and bone homeostasis. Accordingly,

utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMP8.

[47544] The function of BMP8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM347.1.BOP (Accession XP_097915.2) is another GAM5227 target gene, herein designated TARGET GENE. BOP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BOP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BOP BINDING SITE, designated SEQ ID:6088, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47545] Another function of GAM5227 is therefore inhibition of BOP (Accession XP_097915.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BOP.

[47546] Bernardinelli-seip congenital lipodystrophy 2 (seipin) (BSCL2, Accession NP_116056.2) is another GAM5227 target gene, herein designated TARGET GENE. BSCL2 BIND-

ING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by BSCL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BSCL2 BINDING SITE, designated SEQ ID:15949, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47547] Another function of GAM5227 is therefore inhibition of Bernardinelli-seip congenital lipodystrophy 2 (seipin) (BSCL2, Accession NP_116056.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BSCL2.

[47548] Chromosome 20 open reading frame 42 (C20orf42, Accession NP_060141.2) is another GAM5227 target gene, herein designated TARGET GENE. C20orf42 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf42, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf42 BINDING SITE, designated SEQ ID:16282, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA,

also designated SEQ ID:299.

[47549] Another function of GAM5227 is therefore inhibition of Chromosome 20 open reading frame 42 (C20orf42, Accession NP_060141.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf42.

[47550] Chromosome 21 open reading frame 90 (C21orf90, Accession NP_694936.1) is another GAM5227 target gene, herein designated TARGET GENE. C21orf90 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C21orf90, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C21orf90 BINDING SITE, designated SEQ ID:13507, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47551] Another function of GAM5227 is therefore inhibition of Chromosome 21 open reading frame 90 (C21orf90, Accession NP_694936.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf90.

[47552] C6orf151 (Accession NP_689764.1) is another GAM5227

target gene, herein designated TARGET GENE. C6orf151 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf151, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf151 BINDING SITE, designated SEQ ID:4598, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47553] Another function of GAM5227 is therefore inhibition of C6orf151 (Accession NP_689764.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf151.

[47554] Calcium channel, voltage-dependent, alpha 1h subunit (CACNA1H, Accession NP_066921.1) is another GAM5227 target gene, herein designated TARGET GENE. CACNA1H BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CACNA1H, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CACNA1H BINDING SITE, designated SEQ ID:4280, to the

nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47555] Another function of GAM5227 is therefore inhibition of Calcium channel, voltage-dependent, alpha 1h subunit (CACNA1H, Accession NP_066921.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNA1H.

[47556] Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) is another GAM5227 target gene, herein designated TARGET GENE. CCL22 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCL22, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL22 BINDING SITE, designated SEQ ID:5881, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47557] Another function of GAM5227 is therefore inhibition of Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with CCL22.

[47558] Cd209 antigen (CD209, Accession NP_066978.1) is another GAM5227 target gene, herein designated TARGET GENE. CD209 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD209, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD209 BINDING SITE, designated SEQ ID:14170, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47559] Another function of GAM5227 is therefore inhibition of Cd209 antigen (CD209, Accession NP_066978.1), a gene which may play an important role in the CD4- independent association of HIV with cells. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD209.

[47560] The function of CD209 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM96.1.Cd34 antigen (CD34, Accession NP_001764.1) is another GAM5227 target gene, herein

designated TARGET GENE. CD34 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD34, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD34 BINDING SITE, designated SEQ ID:8867, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47561] Another function of GAM5227 is therefore inhibition of Cd34 antigen (CD34, Accession NP_001764.1), a gene which is a monomeric cell surface antigen that is selectively expressed on human hematopoietic progenitor cells. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD34.

[47562] The function of CD34 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM38.1.Cadherin 16, ksp-cadherin (CDH16, Accession NP_004053.1) is another GAM5227 target gene, herein designated TARGET GENE. CDH16 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by CDH16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH16 BINDING SITE, designated SEQ ID:18186, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47563] Another function of GAM5227 is therefore inhibition of Cadherin 16, ksp-cadherin (CDH16, Accession NP_004053.1), a gene which is a calcium dependent cell adhesion protein. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH16.

[47564] The function of CDH16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM148.1.Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) is another GAM5227 target gene, herein designated TARGET GENE. CECR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CECR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE, designated SEQ ID:14307, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47565] Another function of GAM5227 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[47566] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) is another GAM5227 target gene, herein designated TARGET GENE. CECR1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CECR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE, designated SEQ ID:14307, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47567] Another function of GAM5227 is therefore inhibition of

Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[47568] Cyclin m4 (CNNM4, Accession NP_064569.1) is another GAM5227 target gene, herein designated TARGET GENE. CNNM4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CNNM4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNNM4 BINDING SITE, designated SEQ ID:14344, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47569] Another function of GAM5227 is therefore inhibition of Cyclin m4 (CNNM4, Accession NP_064569.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNNM4.

[47570] Collagen, type xi, alpha 1 (COL11A1, Accession NP_542197.1) is another GAM5227 target gene, herein designated TARGET GENE. COL11A1 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by COL11A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL11A1 BINDING SITE, designated SEQ ID:8352, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47571] Another function of GAM5227 is therefore inhibition of Collagen, type xi, alpha 1 (COL11A1, Accession NP_542197.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL11A1.

[47572] Collagen, type xi, alpha 1 (COL11A1, Accession NP_001845.2) is another GAM5227 target gene, herein designated TARGET GENE. COL11A1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COL11A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL11A1 BINDING SITE, designated SEQ ID:8352, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47573] Another function of GAM5227 is therefore inhibition of Collagen, type xi, alpha 1 (COL11A1, Accession NP_001845.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL11A1.

[47574] Collagen, type xi, alpha 1 (COL11A1, Accession NP_542196.1) is another GAM5227 target gene, herein designated TARGET GENE. COL11A1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COL11A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL11A1 BINDING SITE, designated SEQ ID:8352, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47575] Another function of GAM5227 is therefore inhibition of Collagen, type xi, alpha 1 (COL11A1, Accession NP_542196.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL11A1.

[47576] Collectin sub-family member 10 (c-type lectin) (COLEC10, Accession NP_006429.1) is another GAM5227 target gene,

herein designated TARGET GENE. COLEC10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by COLEC10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COLEC10 BINDING SITE, designated SEQ ID:13201, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47577] Another function of GAM5227 is therefore inhibition of Collectin sub-family member 10 (c-type lectin) (COLEC10, Accession NP_006429.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC10.

[47578] Carboxypeptidase d (CPD, Accession NP_001295.2) is another GAM5227 target gene, herein designated TARGET GENE. CPD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPD BINDING SITE, designated SEQ ID:3803, to the nucleotide sequence of GAM5227 RNA, herein designated

GAM RNA, also designated SEQ ID:299.

[47579] Another function of GAM5227 is therefore inhibition of Carboxypeptidase d (CPD, Accession NP_001295.2), a gene which is a membrane- bound metalloprotease. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPD.

[47580] The function of CPD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Casein kinase 1, alpha 1 (CSNK1A1, Accession NP_001883.3) is another GAM5227 target gene, herein designated TARGET GENE. CSNK1A1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CSNK1A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSNK1A1 BINDING SITE, designated SEQ ID:8360, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47581] Another function of GAM5227 is therefore inhibition of Casein kinase 1, alpha 1 (CSNK1A1, Accession

NP_001883.3) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK1A1.

[47582] Catenin (cadherin-associated protein), delta 1 (CTNND1, Accession NP_001322.1) is another GAM5227 target gene, herein designated TARGET GENE. CTNND1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTNND1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTNND1 BINDING SITE, designated SEQ ID:15067, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47583] Another function of GAM5227 is therefore inhibition of Catenin (cadherin-associated protein), delta 1 (CTNND1, Accession NP_001322.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTNND1.

[47584] Cathepsin b (CTSB, Accession NP_680090.1) is another GAM5227 target gene, herein designated TARGET GENE. CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA en-

coded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSB BINDING SITE, designated SEQ ID:12008, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47585] Another function of GAM5227 is therefore inhibition of Cathepsin b (CTSB, Accession NP_680090.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSB.

[47586] Cathepsin b (CTSB, Accession NP_001899.1) is another GAM5227 target gene, herein designated TARGET GENE. CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSB BINDING SITE, designated SEQ ID:12008, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47587] Another function of GAM5227 is therefore inhibition of Cathepsin b (CTSB, Accession NP_001899.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSB.

[47588] Cathepsin b (CTSB, Accession NP_680092.1) is another GAM5227 target gene, herein designated TARGET GENE. CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSB BINDING SITE, designated SEQ ID:12008, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47589] Another function of GAM5227 is therefore inhibition of Cathepsin b (CTSB, Accession NP_680092.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSB.

[47590] Cathepsin b (CTSB, Accession NP_680093.1) is another GAM5227 target gene, herein designated TARGET GENE.

CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSB BINDING SITE, designated SEQ ID:12008, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47591] Another function of GAM5227 is therefore inhibition of Cathepsin b (CTSB, Accession NP_680093.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSB.

[47592] Cathepsin b (CTSB, Accession NP_680091.1) is another GAM5227 target gene, herein designated TARGET GENE. CTSB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CTSB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTSB BINDING SITE, designated SEQ ID:12008, to the nucleotide sequence of GAM5227

RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47593] Another function of GAM5227 is therefore inhibition of Cathepsin b (CTSB, Accession NP_680091.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSB.

[47594] Coxsackie virus and adenovirus receptor (CXADR, Accession NP_001329.1) is another GAM5227 target gene, herein designated TARGET GENE. CXADR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CXADR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CXADR BINDING SITE, designated SEQ ID:8611, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47595] Another function of GAM5227 is therefore inhibition of Coxsackie virus and adenovirus receptor (CXADR, Accession NP_001329.1), a gene which is a member of the immunoglobulin superfamily. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with CXADR.

[47596] The function of CXADR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM378.2.Dystroglycan 1 (dystrophin-associated glycoprotein 1) (DAG1, Accession NP_004384.1) is another GAM5227 target gene, herein designated TARGET GENE. DAG1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DAG1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DAG1 BINDING SITE, designated SEQ ID:16633, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47597] Another function of GAM5227 is therefore inhibition of Dystroglycan 1 (dystrophin-associated glycoprotein 1) (DAG1, Accession NP_004384.1), a gene which may provide linkage between the sarcolemma and extracellular matrix (ECM) and therefore may be associated with Fukuyama- type congenital muscular dystrophy. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Fukuyama- type congenital muscular

dystrophy., and of other diseases and clinical conditions associated with DAG1.

[47598] The function of DAG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Defensin, theta 1 (DEFT1, Accession NP_624312.1) is another GAM5227 target gene, herein designated TARGET GENE. DEFT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DEFT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DEFT1 BINDING SITE, designated SEQ ID:863, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47599] Another function of GAM5227 is therefore inhibition of Defensin, theta 1 (DEFT1, Accession NP_624312.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DEFT1.

[47600] Digeorge syndrome critical region gene 2 (DGCR2, Accession NP_005128.1) is another GAM5227 target gene, herein designated TARGET GENE. DGCR2 BINDING SITE is a

target binding site found in the 3` untranslated region of mRNA encoded by DGCR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DGCR2 BINDING SITE, designated SEQ ID:7719, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47601] Another function of GAM5227 is therefore inhibition of Digeorge syndrome critical region gene 2 (DGCR2, Accession NP_005128.1), a gene which is putative adhesion receptor and intervenes in cell- cell or cell- matrix interactions and therefore may be associated with Digeorge syndrome . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Digeorge syndrome ., and of other diseases and clinical conditions associated with DGCR2.

[47602] The function of DGCR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM84.1.Dicer1, dcr-1 homolog (drosophila) (DICER1, Accession NP_085124.2) is another GAM5227 target gene, herein designated TARGET GENE. DICER1 BINDING SITE is

a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DICER1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DICER1 BINDING SITE, designated SEQ ID:13841, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47603] Another function of GAM5227 is therefore inhibition of Dicer1, dcr-1 homolog (drosophila) (DICER1, Accession NP_085124.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DICER1.

[47604] Dicer1, dcr-1 homolog (drosophila) (DICER1, Accession NP_803187.1) is another GAM5227 target gene, herein designated TARGET GENE. DICER1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DICER1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DICER1 BINDING SITE, designated SEQ ID:13841, to the nucleotide sequence of GAM5227 RNA, herein designated

GAM RNA, also designated SEQ ID:299.

[47605] Another function of GAM5227 is therefore inhibition of Dicer1, dcr-1 homolog (drosophila) (DICER1, Accession NP_803187.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DICER1.

[47606] DKFZP434P0714 (Accession NP_115507.2) is another GAM5227 target gene, herein designated TARGET GENE. DKFZP434P0714 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP434P0714, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434P0714 BINDING SITE, designated SEQ ID:17734, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47607] Another function of GAM5227 is therefore inhibition of DKFZP434P0714 (Accession NP_115507.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434P0714.

[47608] DKFZp547A023 (Accession NP_061174.1) is another

GAM5227 target gene, herein designated TARGET GENE. DKFZp547A023 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547A023, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547A023 BINDING SITE, designated SEQ ID:18504, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47609] Another function of GAM5227 is therefore inhibition of DKFZp547A023 (Accession NP_061174.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547A023.

[47610] DKFZP586B1621 (Accession NP_056348.2) is another GAM5227 target gene, herein designated TARGET GENE. DKFZP586B1621 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP586B1621, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586B1621 BINDING SITE,

designated SEQ ID:1196, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47611] Another function of GAM5227 is therefore inhibition of DKFZP586B1621 (Accession NP_056348.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586B1621.

[47612] DKFZp667G2110 (Accession NP_705833.1) is another GAM5227 target gene, herein designated TARGET GENE. DKFZp667G2110 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp667G2110, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667G2110 BINDING SITE, designated SEQ ID:20018, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47613] Another function of GAM5227 is therefore inhibition of DKFZp667G2110 (Accession NP_705833.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZp667G2110.

[47614] DKFZp761H0421 (Accession NP_775102.1) is another GAM5227 target gene, herein designated TARGET GENE. DKFZp761H0421 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761H0421, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761H0421 BINDING SITE, designated SEQ ID:3514, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47615] Another function of GAM5227 is therefore inhibition of DKFZp761H0421 (Accession NP_775102.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761H0421.

[47616] E2f transcription factor 3 (E2F3, Accession NP_001940.1) is another GAM5227 target gene, herein designated TARGET GENE. E2F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by E2F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of E2F3 BINDING SITE, designated SEQ ID:16017, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47617] Another function of GAM5227 is therefore inhibition of E2f transcription factor 3 (E2F3, Accession NP_001940.1), a gene which binds dna and controls cell- cycle progression from g1 to s phase. and therefore may be associated with Hereditary autosomal dominant myoclonus dystonia. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Hereditary autosomal dominant myoclonus dystonia, and of other diseases and clinical conditions associated with E2F3.

[47618] The function of E2F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.Endothelial differentiation-related factor 1 (EDF1, Accession NP_003783.1) is another GAM5227 target gene, herein designated TARGET GENE. EDF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by EDF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of EDF1 BINDING SITE, designated SEQ ID:535, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47619] Another function of GAM5227 is therefore inhibition of Endothelial differentiation-related factor 1 (EDF1, Accession NP_003783.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDF1.

[47620] Epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR, Accession NP_005219.2) is another GAM5227 target gene, herein designated TARGET GENE. EGFR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EGFR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EGFR BINDING SITE, designated SEQ ID:7441, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47621] Another function of GAM5227 is therefore inhibition of Epidermal growth factor receptor (erythroblastic leukemia

viral (v-erb-b) oncogene homolog, avian) (EGFR, Accession NP_005219.2), a gene which is a receptor for egf, but also for other members of the egf family. and therefore may be associated with Colon cancer, silver- russell syndrome. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Colon cancer, silver- russell syndrome, and of other diseases and clinical conditions associated with EGFR.

[47622] The function of EGFR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM148.2.Engulfment and cell motility 2 (ced-12 homolog, c. elegans) (ELMO2, Accession NP_071369.4) is another GAM5227 target gene, herein designated TARGET GENE. ELMO2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ELMO2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ELMO2 BINDING SITE, designated SEQ ID:15621, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47623] Another function of GAM5227 is therefore inhibition of Engulfment and cell motility 2 (ced-12 homolog, c. elegans) (ELMO2, Accession NP_071369.4) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELMO2.

[47624] Engulfment and cell motility 2 (ced-12 homolog, c. elegans) (ELMO2, Accession NP_573403.1) is another GAM5227 target gene, herein designated TARGET GENE. ELMO2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ELMO2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ELMO2 BINDING SITE, designated SEQ ID:15621, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47625] Another function of GAM5227 is therefore inhibition of Engulfment and cell motility 2 (ced-12 homolog, c. elegans) (ELMO2, Accession NP_573403.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with ELMO2.

[47626] ENT4 (Accession NP_694979.1) is another GAM5227 target gene, herein designated TARGET GENE. ENT4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ENT4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ENT4 BINDING SITE, designated SEQ ID:8473, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47627] Another function of GAM5227 is therefore inhibition of ENT4 (Accession NP_694979.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENT4.

[47628] FAD104 (Accession NP_073600.2) is another GAM5227 target gene, herein designated TARGET GENE. FAD104 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FAD104, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FAD104 BINDING SITE, designated SEQ ID:19708, to the

nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47629] Another function of GAM5227 is therefore inhibition of FAD104 (Accession NP_073600.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAD104.

[47630] FAT3 (Accession XP_061871.5) is another GAM5227 target gene, herein designated TARGET GENE. FAT3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FAT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FAT3 BINDING SITE, designated SEQ ID:7573, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47631] Another function of GAM5227 is therefore inhibition of FAT3 (Accession XP_061871.5) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAT3.

[47632] FBXW8 (Accession NP_036306.1) is another GAM5227 target gene, herein designated TARGET GENE. FBXW8 BIND-

ING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXW8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXW8 BINDING SITE, designated SEQ ID:11502, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47633] Another function of GAM5227 is therefore inhibition of FBXW8 (Accession NP_036306.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW8.

[47634] FBXW8 (Accession NP_699179.2) is another GAM5227 target gene, herein designated TARGET GENE. FBXW8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXW8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXW8 BINDING SITE, designated SEQ ID:11502, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ

ID:299.

[47635] Another function of GAM5227 is therefore inhibition of FBXW8 (Accession NP_699179.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW8.

[47636] FLJ00026 (Accession XP_036307.7) is another GAM5227 target gene, herein designated TARGET GENE. FLJ00026 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ00026, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ00026 BINDING SITE, designated SEQ ID:10221, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47637] Another function of GAM5227 is therefore inhibition of FLJ00026 (Accession XP_036307.7) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00026.

[47638] FLJ00225 (Accession XP_084552.3) is another GAM5227 target gene, herein designated TARGET GENE. FLJ00225 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ00225, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ00225 BINDING SITE, designated SEQ ID:13481, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47639] Another function of GAM5227 is therefore inhibition of FLJ00225 (Accession XP_084552.3) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00225.

[47640] FLJ10074 (Accession NP_060458.2) is another GAM5227 target gene, herein designated TARGET GENE. FLJ10074 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10074, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10074 BINDING SITE, designated SEQ ID:18487, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47641] Another function of GAM5227 is therefore inhibition of

FLJ10074 (Accession NP_060458.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10074.

[47642] FLJ10097 (Accession XP_043653.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ10097 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10097, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10097 BINDING SITE, designated SEQ ID:10680, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47643] Another function of GAM5227 is therefore inhibition of FLJ10097 (Accession XP_043653.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10097.

[47644] FLJ10260 (Accession NP_060512.2) is another GAM5227 target gene, herein designated TARGET GENE. FLJ10260 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10260, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10260 BINDING SITE, designated SEQ ID:2454, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47645] Another function of GAM5227 is therefore inhibition of FLJ10260 (Accession NP_060512.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10260.

[47646] FLJ10420 (Accession NP_060560.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ10420 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10420, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10420 BINDING SITE, designated SEQ ID:1979, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47647] Another function of GAM5227 is therefore inhibition of FLJ10420 (Accession NP_060560.1) . Accordingly, utilities

of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10420.

[47648] FLJ12505 (Accession NP_079025.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ12505 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12505, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12505 BINDING SITE, designated SEQ ID:8025, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47649] Another function of GAM5227 is therefore inhibition of FLJ12505 (Accession NP_079025.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12505.

[47650] FLJ12975 (Accession NP_079085.2) is another GAM5227 target gene, herein designated TARGET GENE. FLJ12975 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12975, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12975 BINDING SITE, designated SEQ ID:11304, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47651] Another function of GAM5227 is therefore inhibition of FLJ12975 (Accession NP_079085.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12975.

[47652] FLJ13114 (Accession NP_078817.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ13114 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13114, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13114 BINDING SITE, designated SEQ ID:5150, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47653] Another function of GAM5227 is therefore inhibition of FLJ13114 (Accession NP_078817.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13114.

[47654] FLJ20254 (Accession NP_060197.2) is another GAM5227 target gene, herein designated TARGET GENE. FLJ20254 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20254, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20254 BINDING SITE, designated SEQ ID:9250, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47655] Another function of GAM5227 is therefore inhibition of FLJ20254 (Accession NP_060197.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20254.

[47656] FLJ23510 (Accession NP_078996.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ23510 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ23510, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ23510 BINDING SITE, designated SEQ ID:10450, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47657] Another function of GAM5227 is therefore inhibition of FLJ23510 (Accession NP_078996.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23510.

[47658] FLJ31713 (Accession NP_689788.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ31713 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31713, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31713 BINDING SITE, designated SEQ ID:8441, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47659] Another function of GAM5227 is therefore inhibition of FLJ31713 (Accession NP_689788.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ31713.

[47660] FLJ37478 (Accession NP_848652.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ37478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37478, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37478 BINDING SITE, designated SEQ ID:11160, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47661] Another function of GAM5227 is therefore inhibition of FLJ37478 (Accession NP_848652.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37478.

[47662] FLJ38608 (Accession NP_694947.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ38608 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38608, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ38608 BINDING SITE, designated SEQ ID:8113, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47663] Another function of GAM5227 is therefore inhibition of FLJ38608 (Accession NP_694947.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38608.

[47664] FLJ38690 (Accession NP_848608.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ38690 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38690, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38690 BINDING SITE, designated SEQ ID:5440, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47665] Another function of GAM5227 is therefore inhibition of FLJ38690 (Accession NP_848608.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38690.

[47666] FLJ39116 (Accession NP_689848.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ39116 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ39116, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39116 BINDING SITE, designated SEQ ID:19608, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47667] Another function of GAM5227 is therefore inhibition of FLJ39116 (Accession NP_689848.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39116.

[47668] FLJ39599 (Accession NP_776164.1) is another GAM5227 target gene, herein designated TARGET GENE. FLJ39599 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39599, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39599 BINDING SITE, designated SEQ ID:11751, to the

nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47669] Another function of GAM5227 is therefore inhibition of FLJ39599 (Accession NP_776164.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39599.

[47670] FLJ39647 (Accession NP_775896.2) is another GAM5227 target gene, herein designated TARGET GENE. FLJ39647 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39647, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39647 BINDING SITE, designated SEQ ID:14874, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47671] Another function of GAM5227 is therefore inhibition of FLJ39647 (Accession NP_775896.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39647.

[47672] Frequently rearranged in advanced t-cell lymphomas

(FRAT1, Accession NP_005470.2) is another GAM5227 target gene, herein designated TARGET GENE. FRAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FRAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FRAT1 BINDING SITE, designated SEQ ID:11515, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47673] Another function of GAM5227 is therefore inhibition of Frequently rearranged in advanced t-cell lymphomas (FRAT1, Accession NP_005470.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FRAT1.

[47674] Frequently rearranged in advanced t-cell lymphomas (FRAT1, Accession NP_852000.1) is another GAM5227 target gene, herein designated TARGET GENE. FRAT1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FRAT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FRAT1 BINDING SITE, designated SEQ ID:11515, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47675] Another function of GAM5227 is therefore inhibition of Frequently rearranged in advanced t-cell lymphomas (FRAT1, Accession NP_852000.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FRAT1.

[47676] Fyve and coiled-coil domain containing 1 (FYCO1, Accession NP_078789.1) is another GAM5227 target gene, herein designated TARGET GENE. FYCO1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FYCO1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FYCO1 BINDING SITE, designated SEQ ID:653, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47677] Another function of GAM5227 is therefore inhibition of Fyve and coiled-coil domain containing 1 (FYCO1, Acces-

sion NP_078789.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FYCO1.

[47678] Frizzled homolog 4 (drosophila) (FZD4, Accession NP_036325.2) is another GAM5227 target gene, herein designated TARGET GENE. FZD4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FZD4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FZD4 BINDING SITE, designated SEQ ID:19026, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47679] Another function of GAM5227 is therefore inhibition of Frizzled homolog 4 (drosophila) (FZD4, Accession NP_036325.2), a gene which may function in cell polarity, cell fate specification and cancer; similar to frizzled receptor family, has seven transmembrane domains and therefore may be associated with Familial exudative vitreoretinopathy. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Familial exudative vitreoretinopathy., and of other diseases and clinical con-

ditions associated with FZD4.

[47680] The function of FZD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.1.Glutamate-cysteine ligase, modifier subunit (GCLM, Accession NP_002052.1) is another GAM5227 target gene, herein designated TARGET GENE. GCLM BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GCLM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GCLM BINDING SITE, designated SEQ ID:4027, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47681] Another function of GAM5227 is therefore inhibition of Glutamate-cysteine ligase, modifier subunit (GCLM, Accession NP_002052.1), a gene which is GLUTAMATE- CYSTEINE LIGASE. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GCLM.

[47682] The function of GCLM and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM879.1.G protein-coupled receptor 4 (GPR4, Accession NP_005273.1) is another GAM5227 target gene, herein designated TARGET GENE. GPR4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR4 BINDING SITE, designated SEQ ID:13775, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47683] Another function of GAM5227 is therefore inhibition of G protein-coupled receptor 4 (GPR4, Accession NP_005273.1), a gene which stimulates to produce increased calcium by both SPC and LPC . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR4.

[47684] The function of GPR4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.G1 to s phase transition 1 (GSPT1, Accession

NP_002085.1) is another GAM5227 target gene, herein designated TARGET GENE. GSPT1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GSPT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GSPT1 BINDING SITE, designated SEQ ID:10693, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47685] Another function of GAM5227 is therefore inhibition of G1 to s phase transition 1 (GSPT1, Accession NP_002085.1), a gene which involves in regulation of mammalian cell growth. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSPT1.

[47686] The function of GSPT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM229.1.H41 (Accession NP_060018.1) is another GAM5227 target gene, herein designated TARGET GENE. H41 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by H41, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H41 BINDING SITE, designated SEQ ID:15147, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47687] Another function of GAM5227 is therefore inhibition of H41 (Accession NP_060018.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H41.

[47688] Hyaluronan synthase 2 (HAS2, Accession NP_005319.1) is another GAM5227 target gene, herein designated TARGET GENE. HAS2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HAS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HAS2 BINDING SITE, designated SEQ ID:15347, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47689] Another function of GAM5227 is therefore inhibition of Hyaluronan synthase 2 (HAS2, Accession NP_005319.1), a gene which plays a role in hyaluronan/hyaluronic acid (ha)

synthesis and transport . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAS2.

[47690] The function of HAS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM715.1.Hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN, Accession NP_060372.1) is another GAM5227 target gene, herein designated TARGET GENE. HIF1AN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HIF1AN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIF1AN BINDING SITE, designated SEQ ID:8091, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47691] Another function of GAM5227 is therefore inhibition of Hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN, Accession NP_060372.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIF1AN.

[47692] HN1L (Accession NP_653171.1) is another GAM5227 target gene, herein designated TARGET GENE. HN1L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HN1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HN1L BINDING SITE, designated SEQ ID:6999, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47693] Another function of GAM5227 is therefore inhibition of HN1L (Accession NP_653171.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HN1L.

[47694] Heparan sulfate (glucosamine) 3-o-sulfotransferase 2 (HS3ST2, Accession NP_006034.1) is another GAM5227 target gene, herein designated TARGET GENE. HS3ST2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HS3ST2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HS3ST2 BINDING SITE, designated SEQ ID:10566, to the

nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47695] Another function of GAM5227 is therefore inhibition of Heparan sulfate (glucosamine) 3-o-sulfotransferase 2 (HS3ST2, Accession NP_006034.1), a gene which plays a role in the generation of heparan sulfate proteoglycan. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HS3ST2.

[47696] The function of HS3ST2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM767.1.Indian hedgehog homolog (drosophila) (IHH, Accession XP_050846.3) is another GAM5227 target gene, herein designated TARGET GENE. IHH BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IHH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IHH BINDING SITE, designated SEQ ID:762, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47697] Another function of GAM5227 is therefore inhibition of

Indian hedgehog homolog (drosophila) (IHH, Accession XP_050846.3), a gene which intercellular signal essential for a variety of patterning events during development. binds to the patched (ptc) receptor, which functions in association with smoothened (smo), to activate the transcription of target genes. implicated in endochondral ossification: may regulate the balance between growth and ossification of the developing bones. induces the expression of parathyroid hormone- related protein (pthrp) (by similarity). and therefore is associated with Brachydactyly type a1. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Brachydactyly type a1, and of other diseases and clinical conditions associated with IHH.

[47698] The function of IHH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM206.1.Interleukin 1 family, member 8 (eta) (IL1F8, Accession NP_055253.2) is another GAM5227 target gene, herein designated TARGET GENE. IL1F8 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by IL1F8, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL1F8 BINDING SITE, designated SEQ ID:2378, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47699] Another function of GAM5227 is therefore inhibition of Interleukin 1 family, member 8 (eta) (IL1F8, Accession NP_055253.2), a gene which initiates and promotes the host response to injury or infection by activating a set of transcription factors. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1F8.

[47700] The function of IL1F8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM488.1.Interleukin 1 family, member 8 (eta) (IL1F8, Accession NP_775270.1) is another GAM5227 target gene, herein designated TARGET GENE. IL1F8 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by IL1F8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

IL1F8 BINDING SITE, designated SEQ ID:2378, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47701] Another function of GAM5227 is therefore inhibition of Interleukin 1 family, member 8 (eta) (IL1F8, Accession NP_775270.1), a gene which initiates and promotes the host response to injury or infection by activating a set of transcription factors. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1F8.

[47702] The function of IL1F8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM488.1.Interleukin 1 receptor, type i (IL1R1, Accession NP_000868.1) is another GAM5227 target gene, herein designated TARGET GENE. IL1R1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IL1R1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL1R1 BINDING SITE, designated SEQ ID:7235, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:299.

[47703] Another function of GAM5227 is therefore inhibition of Interleukin 1 receptor, type i (IL1R1, Accession NP_000868.1), a gene which is a receptor for interleukin-1 alpha (il- 1a), beta (il- 1b), and interleukin- 1 receptor antagonist protein (il- 1ra). Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1R1.

[47704] The function of IL1R1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM40.1.Interleukin 1 receptor accessory protein (IL1RAP, Accession NP_002173.1) is another GAM5227 target gene, herein designated TARGET GENE. IL1RAP BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL1RAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL1RAP BINDING SITE, designated SEQ ID:19607, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47705] Another function of GAM5227 is therefore inhibition of Interleukin 1 receptor accessory protein (IL1RAP, Accession NP_002173.1), a gene which may function as a membrane receptor. promotes heterophilic cellular adhesion. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1RAP.

[47706] The function of IL1RAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.2.IMP-2 (Accession NP_006539.2) is another GAM5227 target gene, herein designated TARGET GENE. IMP-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IMP-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IMP-2 BINDING SITE, designated SEQ ID:9919, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47707] Another function of GAM5227 is therefore inhibition of IMP-2 (Accession NP_006539.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with IMP-2.

[47708] KIAA0140 (Accession NP_055476.1) is another GAM5227 target gene, herein designated TARGET GENE. KIAA0140 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0140, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0140 BINDING SITE, designated SEQ ID:9212, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47709] Another function of GAM5227 is therefore inhibition of KIAA0140 (Accession NP_055476.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0140.

[47710] KIAA0157 (Accession NP_115558.2) is another GAM5227 target gene, herein designated TARGET GENE. KIAA0157 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0157, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA0157 BINDING SITE, designated SEQ ID:13266, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47711] Another function of GAM5227 is therefore inhibition of KIAA0157 (Accession NP_115558.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0157.

[47712] KIAA0232 (Accession XP_291106.1) is another GAM5227 target gene, herein designated TARGET GENE. KIAA0232 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0232, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0232 BINDING SITE, designated SEQ ID:17412, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47713] Another function of GAM5227 is therefore inhibition of KIAA0232 (Accession XP_291106.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0232.

[47714] KIAA0268 (Accession XP_300768.1) is another GAM5227 target gene, herein designated TARGET GENE. KIAA0268 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0268 BINDING SITE, designated SEQ ID:9788, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47715] Another function of GAM5227 is therefore inhibition of KIAA0268 (Accession XP_300768.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0268.

[47716] KIAA0295 (Accession XP_042833.2) is another GAM5227 target gene, herein designated TARGET GENE. KIAA0295 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0295, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0295 BINDING SITE, designated SEQ ID:19557, to the

nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47717] Another function of GAM5227 is therefore inhibition of KIAA0295 (Accession XP_042833.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0295.

[47718] KIAA0367 (Accession XP_041018.2) is another GAM5227 target gene, herein designated TARGET GENE. KIAA0367 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0367, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0367 BINDING SITE, designated SEQ ID:10082, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47719] Another function of GAM5227 is therefore inhibition of KIAA0367 (Accession XP_041018.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0367.

[47720] KIAA0514 (Accession NP_055511.1) is another GAM5227

target gene, herein designated TARGET GENE. KIAA0514 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0514, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0514 BINDING SITE, designated SEQ ID:15950, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47721] Another function of GAM5227 is therefore inhibition of KIAA0514 (Accession NP_055511.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0514.

[47722] KIAA0721 (Accession NP_067680.2) is another GAM5227 target gene, herein designated TARGET GENE. KIAA0721 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0721, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0721 BINDING SITE, designated SEQ ID:19760, to the nucleotide sequence of GAM5227 RNA, herein designated

GAM RNA, also designated SEQ ID:299.

[47723] Another function of GAM5227 is therefore inhibition of KIAA0721 (Accession NP_067680.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0721.

[47724] KIAA1136 (Accession XP_166110.3) is another GAM5227 target gene, herein designated TARGET GENE. KIAA1136 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1136 BINDING SITE, designated SEQ ID:12332, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47725] Another function of GAM5227 is therefore inhibition of KIAA1136 (Accession XP_166110.3) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1136.

[47726] KIAA1157 (Accession XP_051093.2) is another GAM5227 target gene, herein designated TARGET GENE. KIAA1157

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1157, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1157 BINDING SITE, designated SEQ ID:7957, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47727] Another function of GAM5227 is therefore inhibition of KIAA1157 (Accession XP_051093.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1157.

[47728] KIAA1446 (Accession NP_065887.1) is another GAM5227 target gene, herein designated TARGET GENE. KIAA1446 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1446, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1446 BINDING SITE, designated SEQ ID:6089, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47729] Another function of GAM5227 is therefore inhibition of KIAA1446 (Accession NP_065887.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1446.

[47730] KIAA1822 (Accession XP_041566.2) is another GAM5227 target gene, herein designated TARGET GENE. KIAA1822 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1822 BINDING SITE, designated SEQ ID:17711, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47731] Another function of GAM5227 is therefore inhibition of KIAA1822 (Accession XP_041566.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1822.

[47732] KIAA1854 (Accession XP_049884.1) is another GAM5227 target gene, herein designated TARGET GENE. KIAA1854 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1854, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1854 BINDING SITE, designated SEQ ID:9010, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47733] Another function of GAM5227 is therefore inhibition of KIAA1854 (Accession XP_049884.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1854.

[47734] KIAA1879 (Accession XP_056635.1) is another GAM5227 target gene, herein designated TARGET GENE. KIAA1879 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1879, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1879 BINDING SITE, designated SEQ ID:15546, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47735] Another function of GAM5227 is therefore inhibition of

KIAA1879 (Accession XP_056635.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1879.

[47736] Kruppel-like factor 12 (KLF12, Accession NP_009180.3) is another GAM5227 target gene, herein designated TARGET GENE. KLF12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KLF12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLF12 BINDING SITE, designated SEQ ID:5272, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47737] Another function of GAM5227 is therefore inhibition of Kruppel-like factor 12 (KLF12, Accession NP_009180.3) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF12.

[47738] Low density lipoprotein receptor (familial hypercholesterolemia) (LDLR, Accession NP_000518.1) is another GAM5227 target gene, herein designated TARGET GENE.

LDLR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LDLR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LDLR BINDING SITE, designated SEQ ID:9706, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47739] Another function of GAM5227 is therefore inhibition of Low density lipoprotein receptor (familial hypercholesterolemia) (LDLR, Accession NP_000518.1), a gene which also acts as a tumor suppressor. and therefore is associated with Familial hypercholesterolemia. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Familial hypercholesterolemia, and of other diseases and clinical conditions associated with LDLR.

[47740] The function of LDLR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM99.1.Lim homeobox 9 (LHX9, Accession NP_064589.1) is another GAM5227 target gene, herein designated TARGET GENE. LHX9 BINDING SITE is a target binding site found in the 5` untranslated region of multi-

ple transcripts of mRNA encoded by LHX9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LHX9 BINDING SITE, designated SEQ ID:7190, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47741] Another function of GAM5227 is therefore inhibition of Lim homeobox 9 (LHX9, Accession NP_064589.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHX9.

[47742] LOC115131 (Accession NP_660285.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC115131 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC115131, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115131 BINDING SITE, designated SEQ ID:9407, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47743] Another function of GAM5227 is therefore inhibition of LOC115131 (Accession NP_660285.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115131.

[47744] LOC143310 (Accession XP_084485.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC143310 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC143310, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143310 BINDING SITE, designated SEQ ID:1541, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47745] Another function of GAM5227 is therefore inhibition of LOC143310 (Accession XP_084485.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143310.

[47746] LOC145453 (Accession XP_085120.1) is another GAM5227 target gene, herein designated TARGET GENE.

LOC145453 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145453, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145453 BINDING SITE, designated SEQ ID:1961, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47747] Another function of GAM5227 is therefore inhibition of LOC145453 (Accession XP_085120.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145453.

[47748] LOC145601 (Accession XP_096816.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC145601 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145601, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145601 BINDING SITE, designated SEQ ID:1398, to the nucleotide sequence of

GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47749] Another function of GAM5227 is therefore inhibition of LOC145601 (Accession XP_096816.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145601.

[47750] LOC145725 (Accession XP_085211.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC145725 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145725 BINDING SITE, designated SEQ ID:17221, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47751] Another function of GAM5227 is therefore inhibition of LOC145725 (Accession XP_085211.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145725.

[47752] LOC145845 (Accession XP_096884.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC145845 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145845, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145845 BINDING SITE, designated SEQ ID:19334, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47753] Another function of GAM5227 is therefore inhibition of LOC145845 (Accession XP_096884.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145845.

[47754] LOC146272 (Accession XP_085396.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC146272 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146272, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC146272 BINDING SITE, designated SEQ ID:10066, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47755] Another function of GAM5227 is therefore inhibition of LOC146272 (Accession XP_085396.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146272.

[47756] LOC151234 (Accession XP_087136.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC151234 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151234, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151234 BINDING SITE, designated SEQ ID:16533, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47757] Another function of GAM5227 is therefore inhibition of LOC151234 (Accession XP_087136.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC151234.

[47758] LOC152078 (Accession XP_087376.2) is another GAM5227 target gene, herein designated TARGET GENE. LOC152078 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152078 BINDING SITE, designated SEQ ID:16522, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47759] Another function of GAM5227 is therefore inhibition of LOC152078 (Accession XP_087376.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152078.

[47760] LOC153577 (Accession XP_098394.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC153577 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153577, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153577 BINDING SITE, designated SEQ ID:10222, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47761] Another function of GAM5227 is therefore inhibition of LOC153577 (Accession XP_098394.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153577.

[47762] LOC154834 (Accession XP_098621.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC154834 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC154834, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154834 BINDING SITE, designated SEQ ID:7900, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47763] Another function of GAM5227 is therefore inhibition of

LOC154834 (Accession XP_098621.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154834.

[47764] LOC154877 (Accession XP_098626.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC154877 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC154877, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE, designated SEQ ID:17668, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47765] Another function of GAM5227 is therefore inhibition of LOC154877 (Accession XP_098626.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877.

[47766] LOC161635 (Accession XP_172921.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC161635 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC161635, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC161635 BINDING SITE, designated SEQ ID:11973, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47767] Another function of GAM5227 is therefore inhibition of LOC161635 (Accession XP_172921.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161635.

[47768] LOC164580 (Accession XP_104562.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC164580 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC164580, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC164580 BINDING SITE, designated SEQ ID:1232, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:299.

[47769] Another function of GAM5227 is therefore inhibition of LOC164580 (Accession XP_104562.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164580.

[47770] LOC199692 (Accession NP_660338.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC199692 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC199692, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199692 BINDING SITE, designated SEQ ID:17021, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47771] Another function of GAM5227 is therefore inhibition of LOC199692 (Accession NP_660338.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199692.

[47772] LOC200574 (Accession XP_114264.1) is another

GAM5227 target gene, herein designated TARGET GENE. LOC200574 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200574, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200574 BINDING SITE, designated SEQ ID:5245, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47773] Another function of GAM5227 is therefore inhibition of LOC200574 (Accession XP_114264.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200574.

[47774] LOC200681 (Accession XP_117260.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC200681 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC200681, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200681 BINDING SITE, desig-

nated SEQ ID:15034, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47775] Another function of GAM5227 is therefore inhibition of LOC200681 (Accession XP_117260.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200681.

[47776] LOC201194 (Accession XP_117061.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC201194 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC201194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201194 BINDING SITE, designated SEQ ID:2742, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47777] Another function of GAM5227 is therefore inhibition of LOC201194 (Accession XP_117061.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC201194.

[47778] LOC222252 (Accession XP_168640.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC222252 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222252, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222252 BINDING SITE, designated SEQ ID:13169, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47779] Another function of GAM5227 is therefore inhibition of LOC222252 (Accession XP_168640.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222252.

[47780] LOC254128 (Accession XP_171004.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC254128 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC254128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254128 BINDING SITE, designated SEQ ID:2157, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47781] Another function of GAM5227 is therefore inhibition of LOC254128 (Accession XP_171004.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254128.

[47782] LOC254544 (Accession XP_172947.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC254544 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC254544, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254544 BINDING SITE, designated SEQ ID:3693, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47783] Another function of GAM5227 is therefore inhibition of LOC254544 (Accession XP_172947.1) . Accordingly, utili-

ties of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254544.

[47784] LOC254556 (Accession XP_170588.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC254556 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC254556, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254556 BINDING SITE, designated SEQ ID:13871, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47785] Another function of GAM5227 is therefore inhibition of LOC254556 (Accession XP_170588.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254556.

[47786] LOC283018 (Accession XP_208026.2) is another GAM5227 target gene, herein designated TARGET GENE. LOC283018 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC283018, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283018 BINDING SITE, designated SEQ ID:9893, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47787] Another function of GAM5227 is therefore inhibition of LOC283018 (Accession XP_208026.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283018.

[47788] LOC283107 (Accession XP_210889.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283107 BINDING SITE1 and LOC283107 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283107, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283107 BINDING SITE1 and LOC283107 BINDING SITE2, designated SEQ ID:10191 and SEQ ID:13094 respectively, to the nucleotide sequence of GAM5227 RNA, herein designated

GAM RNA, also designated SEQ ID:299.

[47789] Another function of GAM5227 is therefore inhibition of LOC283107 (Accession XP_210889.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283107.

[47790] LOC283153 (Accession XP_208532.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283153 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283153, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283153 BINDING SITE, designated SEQ ID:13811, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47791] Another function of GAM5227 is therefore inhibition of LOC283153 (Accession XP_208532.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283153.

[47792] LOC283332 (Accession XP_210976.1) is another

GAM5227 target gene, herein designated TARGET GENE. LOC283332 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283332, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283332 BINDING SITE, designated SEQ ID:19526, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47793] Another function of GAM5227 is therefore inhibition of LOC283332 (Accession XP_210976.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283332.

[47794] LOC283385 (Accession NP_776254.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283385 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283385, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283385 BINDING SITE, desig-

nated SEQ ID:2089, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47795] Another function of GAM5227 is therefore inhibition of LOC283385 (Accession NP_776254.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283385.

[47796] LOC283460 (Accession XP_208682.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283460 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283460, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283460 BINDING SITE, designated SEQ ID:5440, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47797] Another function of GAM5227 is therefore inhibition of LOC283460 (Accession XP_208682.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283460.

[47798] LOC283534 (Accession XP_211083.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283534 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283534, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283534 BINDING SITE, designated SEQ ID:19940, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47799] Another function of GAM5227 is therefore inhibition of LOC283534 (Accession XP_211083.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283534.

[47800] LOC283551 (Accession XP_211110.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283551 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283551, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283551 BINDING SITE, designated SEQ ID:10476, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47801] Another function of GAM5227 is therefore inhibition of LOC283551 (Accession XP_211110.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283551.

[47802] LOC283738 (Accession XP_211186.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283738 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283738, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283738 BINDING SITE, designated SEQ ID:9445, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47803] Another function of GAM5227 is therefore inhibition of LOC283738 (Accession XP_211186.1) . Accordingly, utili-

ties of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283738.

[47804] LOC283806 (Accession XP_208846.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283806 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283806, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283806 BINDING SITE, designated SEQ ID:17351, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47805] Another function of GAM5227 is therefore inhibition of LOC283806 (Accession XP_208846.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283806.

[47806] LOC283849 (Accession NP_848611.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283849 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of

mRNA encoded by LOC283849, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283849 BINDING SITE, designated SEQ ID:5876, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47807] Another function of GAM5227 is therefore inhibition of LOC283849 (Accession NP_848611.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283849.

[47808] LOC283924 (Accession XP_208906.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283924 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283924, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283924 BINDING SITE, designated SEQ ID:6869, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47809] Another function of GAM5227 is therefore inhibition of LOC283924 (Accession XP_208906.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283924.

[47810] LOC283949 (Accession XP_208928.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC283949 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283949, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283949 BINDING SITE, designated SEQ ID:1669, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47811] Another function of GAM5227 is therefore inhibition of LOC283949 (Accession XP_208928.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283949.

[47812] LOC284082 (Accession XP_211323.1) is another GAM5227 target gene, herein designated TARGET GENE.

LOC284082 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284082, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284082 BINDING SITE, designated SEQ ID:15264, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47813] Another function of GAM5227 is therefore inhibition of LOC284082 (Accession XP_211323.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284082.

[47814] LOC284118 (Accession XP_211336.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC284118 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284118, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284118 BINDING SITE, designated SEQ ID:12184, to the nucleotide sequence of

GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47815] Another function of GAM5227 is therefore inhibition of LOC284118 (Accession XP_211336.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284118.

[47816] LOC284178 (Accession XP_211365.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC284178 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284178, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284178 BINDING SITE, designated SEQ ID:8059, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47817] Another function of GAM5227 is therefore inhibition of LOC284178 (Accession XP_211365.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284178.

[47818] LOC284281 (Accession XP_211415.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC284281 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284281, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284281 BINDING SITE, designated SEQ ID:15205, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47819] Another function of GAM5227 is therefore inhibition of LOC284281 (Accession XP_211415.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284281.

[47820] LOC284325 (Accession XP_209143.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC284325 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284325, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284325 BINDING SITE, designated SEQ ID:6963, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47821] Another function of GAM5227 is therefore inhibition of LOC284325 (Accession XP_209143.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284325.

[47822] LOC284375 (Accession XP_209154.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC284375 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284375, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284375 BINDING SITE, designated SEQ ID:6814, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47823] Another function of GAM5227 is therefore inhibition of LOC284375 (Accession XP_209154.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284375.

[47824] LOC284402 (Accession XP_211453.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC284402 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284402, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284402 BINDING SITE, designated SEQ ID:13078, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47825] Another function of GAM5227 is therefore inhibition of LOC284402 (Accession XP_211453.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284402.

[47826] LOC284459 (Accession XP_290826.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC284459 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284459, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284459 BINDING SITE, designated SEQ ID:1608, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47827] Another function of GAM5227 is therefore inhibition of LOC284459 (Accession XP_290826.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284459.

[47828] LOC284650 (Accession XP_211571.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC284650 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284650, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284650 BINDING SITE, designated SEQ ID:9610, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47829] Another function of GAM5227 is therefore inhibition of

LOC284650 (Accession XP_211571.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284650.

[47830] LOC285117 (Accession XP_209482.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC285117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285117 BINDING SITE, designated SEQ ID:13418, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47831] Another function of GAM5227 is therefore inhibition of LOC285117 (Accession XP_209482.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285117.

[47832] LOC285127 (Accession XP_211771.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC285127 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC285127, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285127 BINDING SITE, designated SEQ ID:7199, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47833] Another function of GAM5227 is therefore inhibition of LOC285127 (Accession XP_211771.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285127.

[47834] LOC285194 (Accession XP_211803.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC285194 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285194, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285194 BINDING SITE, designated SEQ ID:16102, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:299.

[47835] Another function of GAM5227 is therefore inhibition of LOC285194 (Accession XP_211803.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285194.

[47836] LOC285284 (Accession XP_211836.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC285284 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285284, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285284 BINDING SITE, designated SEQ ID:567, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47837] Another function of GAM5227 is therefore inhibition of LOC285284 (Accession XP_211836.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285284.

[47838] LOC285587 (Accession XP_211947.1) is another

GAM5227 target gene, herein designated TARGET GENE. LOC285587 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285587 BINDING SITE, designated SEQ ID:1779, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47839] Another function of GAM5227 is therefore inhibition of LOC285587 (Accession XP_211947.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285587.

[47840] LOC285673 (Accession XP_209720.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC285673 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285673, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285673 BINDING SITE, desig-

nated SEQ ID:4976, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47841] Another function of GAM5227 is therefore inhibition of LOC285673 (Accession XP_209720.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285673.

[47842] LOC285799 (Accession XP_209764.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC285799 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285799, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285799 BINDING SITE, designated SEQ ID:3655, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47843] Another function of GAM5227 is therefore inhibition of LOC285799 (Accession XP_209764.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC285799.

[47844] LOC285806 (Accession XP_212028.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC285806 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285806, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285806 BINDING SITE, designated SEQ ID:17117, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47845] Another function of GAM5227 is therefore inhibition of LOC285806 (Accession XP_212028.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285806.

[47846] LOC285827 (Accession XP_212645.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC285827 BINDING SITE1 and LOC285827 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC285827, corresponding to target binding sites such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285827 BINDING SITE1 and LOC285827 BINDING SITE2, designated SEQ ID:13212 and SEQ ID:13212 respectively, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47847] Another function of GAM5227 is therefore inhibition of LOC285827 (Accession XP_212645.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285827.

[47848] LOC285827 (Accession XP_212604.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC285827 BINDING SITE1 and LOC285827 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by LOC285827, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285827 BINDING SITE1 and LOC285827 BINDING SITE2, designated SEQ ID:4842 and SEQ ID:5526 respectively, to the nucleotide sequence of

GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47849] Another function of GAM5227 is therefore inhibition of LOC285827 (Accession XP_212604.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285827.

[47850] LOC286045 (Accession XP_212151.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC286045 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286045 BINDING SITE, designated SEQ ID:17966, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47851] Another function of GAM5227 is therefore inhibition of LOC286045 (Accession XP_212151.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286045.

[47852] LOC286208 (Accession XP_212230.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC286208 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC286208, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286208 BINDING SITE, designated SEQ ID:8321, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47853] Another function of GAM5227 is therefore inhibition of LOC286208 (Accession XP_212230.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286208.

[47854] LOC286255 (Accession XP_209977.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC286255 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286255, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC286255 BINDING SITE, designated SEQ ID:13323, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47855] Another function of GAM5227 is therefore inhibition of LOC286255 (Accession XP_209977.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC286255.

[47856] LOC286354 (Accession XP_212286.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC286354 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC286354, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC286354 BINDING SITE, designated SEQ ID:1632, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47857] Another function of GAM5227 is therefore inhibition of LOC286354 (Accession XP_212286.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC286354.

[47858] LOC338653 (Accession XP_294673.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC338653 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC338653, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338653 BINDING SITE, designated SEQ ID:10990, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47859] Another function of GAM5227 is therefore inhibition of LOC338653 (Accession XP_294673.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338653.

[47860] LOC339679 (Accession XP_295029.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC339679 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339679, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339679 BINDING SITE, designated SEQ ID:2642, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47861] Another function of GAM5227 is therefore inhibition of LOC339679 (Accession XP_295029.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339679.

[47862] LOC339983 (Accession XP_291101.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC339983 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339983, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339983 BINDING SITE, designated SEQ ID:11160, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47863] Another function of GAM5227 is therefore inhibition of

LOC339983 (Accession XP_291101.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339983.

[47864] LOC340504 (Accession XP_295260.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC340504 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340504, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340504 BINDING SITE, designated SEQ ID:1223, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47865] Another function of GAM5227 is therefore inhibition of LOC340504 (Accession XP_295260.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340504.

[47866] LOC348399 (Accession XP_302744.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC348399 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC348399, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348399 BINDING SITE, designated SEQ ID:12324, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47867] Another function of GAM5227 is therefore inhibition of LOC348399 (Accession XP_302744.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348399.

[47868] LOC348428 (Accession XP_302753.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC348428 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348428, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348428 BINDING SITE, designated SEQ ID:6112, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:299.

[47869] Another function of GAM5227 is therefore inhibition of LOC348428 (Accession XP_302753.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348428.

[47870] LOC348477 (Accession XP_046126.4) is another GAM5227 target gene, herein designated TARGET GENE. LOC348477 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348477, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348477 BINDING SITE, designated SEQ ID:9788, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47871] Another function of GAM5227 is therefore inhibition of LOC348477 (Accession XP_046126.4) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348477.

[47872] LOC348928 (Accession XP_209688.1) is another

GAM5227 target gene, herein designated TARGET GENE. LOC348928 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348928, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348928 BINDING SITE, designated SEQ ID:8901, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47873] Another function of GAM5227 is therefore inhibition of LOC348928 (Accession XP_209688.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348928.

[47874] LOC349289 (Accession XP_300477.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC349289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC349289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349289 BINDING SITE, desig-

nated SEQ ID:8287, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47875] Another function of GAM5227 is therefore inhibition of LOC349289 (Accession XP_300477.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349289.

[47876] LOC352027 (Accession XP_302245.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC352027 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC352027, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC352027 BINDING SITE, designated SEQ ID:13440, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47877] Another function of GAM5227 is therefore inhibition of LOC352027 (Accession XP_302245.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC352027.

[47878] LOC56920 (Accession NP_064548.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC56920 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC56920, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC56920 BINDING SITE, designated SEQ ID:14103, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47879] Another function of GAM5227 is therefore inhibition of LOC56920 (Accession NP_064548.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56920.

[47880] LOC90408 (Accession XP_031517.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC90408 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90408, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

LOC90408 BINDING SITE, designated SEQ ID:6783, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47881] Another function of GAM5227 is therefore inhibition of LOC90408 (Accession XP_031517.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90408.

[47882] LOC90529 (Accession NP_835223.1) is another GAM5227 target gene, herein designated TARGET GENE. LOC90529 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90529, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90529 BINDING SITE, designated SEQ ID:13508, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47883] Another function of GAM5227 is therefore inhibition of LOC90529 (Accession NP_835223.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90529.

[47884] Lymphotoxin alpha (tnf superfamily, member 1) (LTA, Accession NP_000586.2) is another GAM5227 target gene, herein designated TARGET GENE. LTA BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LTA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LTA BINDING SITE, designated SEQ ID:16521, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47885] Another function of GAM5227 is therefore inhibition of Lymphotoxin alpha (tnf superfamily, member 1) (LTA, Accession NP_000586.2), a gene which is a cytokine that in its homotrimeric form binds to tnfrsf1a/tnfr1, tnfrsf1b/tnfbr and tnfrsf14/hvem. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LTA.

[47886] The function of LTA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM44.1.Leukotriene b4 receptor (LTB4R, Accession NP_000743.1) is another GAM5227 target gene, herein

designated TARGET GENE. LTB4R BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LTB4R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LTB4R BINDING SITE, designated SEQ ID:19312, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47887] Another function of GAM5227 is therefore inhibition of Leukotriene b4 receptor (LTB4R, Accession NP_000743.1), a gene which may be the cardiac p2y receptor involved in the regulation of cardiac muscle contraction through modulation of l- type calcium currents. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LTB4R.

[47888] The function of LTB4R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Mitogen-activated protein kinase kinase kinase kinase 2 (MAP4K2, Accession NP_004570.2) is another GAM5227 target gene, herein designated TARGET

GENE. MAP4K2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MAP4K2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAP4K2 BINDING SITE, designated SEQ ID:12350, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47889] Another function of GAM5227 is therefore inhibition of Mitogen-activated protein kinase kinase kinase kinase 2 (MAP4K2, Accession NP_004570.2), a gene which serine/threonine protein kinase required for spore wall development. activates Jun N- terminal kinase; member of the STE20 kinase family. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP4K2.

[47890] The function of MAP4K2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1849.1.MCFP (Accession NP_061331.1) is another GAM5227 target gene, herein designated TARGET GENE. MCFP BINDING SITE is a target binding site found in the 5`

untranslated region of mRNA encoded by MCFP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCFP BINDING SITE, designated SEQ ID:906, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47891] Another function of GAM5227 is therefore inhibition of MCFP (Accession NP_061331.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCFP.

[47892] MDS018 (Accession NP_068595.2) is another GAM5227 target gene, herein designated TARGET GENE. MDS018 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MDS018, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MDS018 BINDING SITE, designated SEQ ID:3171, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47893] Another function of GAM5227 is therefore inhibition of MDS018 (Accession NP_068595.2) . Accordingly, utilities

of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDS018.

[47894] MGC14161 (Accession NP_116281.1) is another GAM5227 target gene, herein designated TARGET GENE. MGC14161 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC14161, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC14161 BINDING SITE, designated SEQ ID:11439, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47895] Another function of GAM5227 is therefore inhibition of MGC14161 (Accession NP_116281.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14161.

[47896] MGC15730 (Accession NP_116269.2) is another GAM5227 target gene, herein designated TARGET GENE. MGC15730 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC15730, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC15730 BINDING SITE, designated SEQ ID:10025, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47897] Another function of GAM5227 is therefore inhibition of MGC15730 (Accession NP_116269.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15730.

[47898] MGC17515 (Accession NP_689684.1) is another GAM5227 target gene, herein designated TARGET GENE. MGC17515 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC17515, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC17515 BINDING SITE, designated SEQ ID:4222, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47899] Another function of GAM5227 is therefore inhibition of MGC17515 (Accession NP_689684.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC17515.

[47900] MGC3020 (Accession NP_076953.2) is another GAM5227 target gene, herein designated TARGET GENE. MGC3020 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC3020, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC3020 BINDING SITE, designated SEQ ID:3360, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47901] Another function of GAM5227 is therefore inhibition of MGC3020 (Accession NP_076953.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3020.

[47902] MGC3113 (Accession NP_076940.1) is another GAM5227 target gene, herein designated TARGET GENE. MGC3113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC3113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of MGC3113 BINDING SITE, designated SEQ ID:1375, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47903] Another function of GAM5227 is therefore inhibition of MGC3113 (Accession NP_076940.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3113.

[47904] MGC39633 (Accession NP_689762.1) is another GAM5227 target gene, herein designated TARGET GENE. MGC39633 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC39633, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC39633 BINDING SITE, designated SEQ ID:1566, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47905] Another function of GAM5227 is therefore inhibition of MGC39633 (Accession NP_689762.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC39633.

[47906] MI-ER1 (Accession NP_065999.1) is another GAM5227 target gene, herein designated TARGET GENE. MI-ER1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MI-ER1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MI-ER1 BINDING SITE, designated SEQ ID:2832, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47907] Another function of GAM5227 is therefore inhibition of MI-ER1 (Accession NP_065999.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MI-ER1.

[47908] Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, drosophila); translocated to, 3 (MLLT3, Accession NP_004520.1) is another GAM5227 target gene, herein designated TARGET GENE. MLLT3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MLLT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of MLLT3 BINDING SITE, designated SEQ ID:16801, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47909] Another function of GAM5227 is therefore inhibition of Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, drosophila); translocated to, 3 (MLLT3, Accession NP_004520.1), a gene which is Serine and proline rich protein and therefore is associated with Acute leukemias. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Acute leukemias, and of other diseases and clinical conditions associated with MLLT3.

[47910] The function of MLLT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM233.1.Myeloproliferative leukemia virus oncogene (MPL, Accession NP_005364.1) is another GAM5227 target gene, herein designated TARGET GENE. MPL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of MPL BINDING SITE, designated SEQ ID:8412, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47911] Another function of GAM5227 is therefore inhibition of Myeloproliferative leukemia virus oncogene (MPL, Accession NP_005364.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPL.

[47912] MPRG (Accession NP_060175.2) is another GAM5227 target gene, herein designated TARGET GENE. MPRG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MPRG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MPRG BINDING SITE, designated SEQ ID:19256, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47913] Another function of GAM5227 is therefore inhibition of MPRG (Accession NP_060175.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPRG.

[47914] Max interacting protein 1 (MXI1, Accession NP_005953.2) is another GAM5227 target gene, herein designated TARGET GENE. MXI1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MXI1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MXI1 BINDING SITE, designated SEQ ID:10235, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47915] Another function of GAM5227 is therefore inhibition of Max interacting protein 1 (MXI1, Accession NP_005953.2), a gene which acts as a tumor suppressor in vivo, engages the MYC network in a functionally relevant manner and therefore may be associated with Prostate cancer, neurofibrosarcoma. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Prostate cancer, neurofibrosarcoma, and of other diseases and clinical conditions associated with MXI1.

[47916] The function of MXI1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM94.1.Max interacting protein 1 (MXI1, Accession NP_569157.1) is another GAM5227 target gene, herein designated TARGET GENE. MXI1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MXI1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MXI1 BINDING SITE, designated SEQ ID:10235, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47917] Another function of GAM5227 is therefore inhibition of Max interacting protein 1 (MXI1, Accession NP_569157.1), a gene which acts as a tumor suppressor in vivo, engages the MYC network in a functionally relevant manner and therefore may be associated with Prostate cancer, neurofibrosarcoma. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Prostate cancer, neurofibrosarcoma, and of other diseases and clinical conditions associated with MXI1.

[47918] The function of MXI1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM94.1.Myosin light chain kinase 2, skeletal muscle (MYLK2, Accession NP_149109.1) is another GAM5227 target gene, herein designated TARGET GENE. MYLK2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MYLK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYLK2 BINDING SITE, designated SEQ ID:8353, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47919] Another function of GAM5227 is therefore inhibition of Myosin light chain kinase 2, skeletal muscle (MYLK2, Accession NP_149109.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLK2.

[47920] Nuclear receptor co-repressor 2 (NCOR2, Accession NP_006303.1) is another GAM5227 target gene, herein designated TARGET GENE. NCOR2 BINDING SITE1 and NCOR2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by NCOR2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of NCOR2 BINDING SITE1 and NCOR2 BINDING SITE2, designated SEQ ID:19433 and SEQ ID:18576 respectively, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47921] Another function of GAM5227 is therefore inhibition of Nuclear receptor co-repressor 2 (NCOR2, Accession NP_006303.1), a gene which mediates the transcriptional repression activity of some nuclear receptors by promoting chromatin condensation, thus preventing access of the basal transcription. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOR2.

[47922] The function of NCOR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1065.1.NDEL1 (Accession NP_110435.1) is another GAM5227 target gene, herein designated TARGET GENE. NDEL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NDEL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of NDEL1 BINDING SITE, designated SEQ ID:4770, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47923] Another function of GAM5227 is therefore inhibition of NDEL1 (Accession NP_110435.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDEL1.

[47924] Neuroglobin (NGB, Accession NP_067080.1) is another GAM5227 target gene, herein designated TARGET GENE. NGB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NGB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NGB BINDING SITE, designated SEQ ID:16217, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47925] Another function of GAM5227 is therefore inhibition of Neuroglobin (NGB, Accession NP_067080.1), a gene which has function in oxygen transport and storage in humans. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NGB.

[47926] The function of NGB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM404.2.Non-metastatic cells 2, protein (nm23b) expressed in (NME2, Accession NP_002503.1) is another GAM5227 target gene, herein designated TARGET GENE. NME2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NME2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NME2 BINDING SITE, designated SEQ ID:1264, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47927] Another function of GAM5227 is therefore inhibition of Non-metastatic cells 2, protein (nm23b) expressed in (NME2, Accession NP_002503.1), a gene which has a major role in the synthesis of nucleoside triphosphates other than atp and acts as a transcriptional activator of the c-myc gene. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NME2.

[47928] The function of NME2 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM762.1.Nsfl1 (p97) cofactor (p47) (NSFL1C, Accession NP_061327.2) is another GAM5227 target gene, herein designated TARGET GENE. NSFL1C BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NSFL1C, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NSFL1C BINDING SITE, designated SEQ ID:15237, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47929] Another function of GAM5227 is therefore inhibition of Nsfl1 (p97) cofactor (p47) (NSFL1C, Accession NP_061327.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NSFL1C.

[47930] Purinergic receptor p2x, ligand-gated ion channel, 1 (P2RX1, Accession NP_002549.1) is another GAM5227 target gene, herein designated TARGET GENE. P2RX1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P2RX1, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P2RX1 BINDING SITE, designated SEQ ID:8598, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47931] Another function of GAM5227 is therefore inhibition of Purinergic receptor p2x, ligand-gated ion channel, 1 (P2RX1, Accession NP_002549.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RX1.

[47932] P53AIP1 (Accession NP_071395.1) is another GAM5227 target gene, herein designated TARGET GENE. P53AIP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by P53AIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of P53AIP1 BINDING SITE, designated SEQ ID:17485, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47933] Another function of GAM5227 is therefore inhibition of P53AIP1 (Accession NP_071395.1) . Accordingly, utilities

of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P53AIP1.

[47934] Protocadherin beta 12 (PCDHB12, Accession NP_061755.1) is another GAM5227 target gene, herein designated TARGET GENE. PCDHB12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCDHB12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCDHB12 BINDING SITE, designated SEQ ID:7917, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47935] Another function of GAM5227 is therefore inhibition of Protocadherin beta 12 (PCDHB12, Accession NP_061755.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB12.

[47936] PCMF (Accession NP_064507.2) is another GAM5227 target gene, herein designated TARGET GENE. PCMF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCMF, corresponding to a

target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCMF BINDING SITE, designated SEQ ID:11762, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47937] Another function of GAM5227 is therefore inhibition of PCMF (Accession NP_064507.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCMF.

[47938] Proprotein convertase subtilisin/kexin type 7 (PCSK7, Accession NP_004707.2) is another GAM5227 target gene, herein designated TARGET GENE. PCSK7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PCSK7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PCSK7 BINDING SITE, designated SEQ ID:11321, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47939] Another function of GAM5227 is therefore inhibition of Proprotein convertase subtilisin/kexin type 7 (PCSK7, Ac-

cession NP_004707.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCSK7.

[47940] Pyruvate dehydrogenase kinase, isoenzyme 4 (PDK4, Accession NP_002603.1) is another GAM5227 target gene, herein designated TARGET GENE. PDK4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PDK4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PDK4 BINDING SITE, designated SEQ ID:2181, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47941] Another function of GAM5227 is therefore inhibition of Pyruvate dehydrogenase kinase, isoenzyme 4 (PDK4, Accession NP_002603.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDK4.

[47942] Paternally expressed 10 (PEG10, Accession NP_055883.1) is another GAM5227 target gene, herein designated TARGET GENE. PEG10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

PEG10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PEG10 BINDING SITE, designated SEQ ID:10949, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47943] Another function of GAM5227 is therefore inhibition of Paternally expressed 10 (PEG10, Accession NP_055883.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEG10.

[47944] 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3, Accession NP_004557.1) is another GAM5227 target gene, herein designated TARGET GENE. PFKFB3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PFKFB3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PFKFB3 BINDING SITE, designated SEQ ID:2796, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47945] Another function of GAM5227 is therefore inhibition of 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3, Accession NP_004557.1), a gene which catalizes synthesis and degradation of fructose 2,6- bisphosphate. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFKFB3.

[47946] The function of PFKFB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.PI4KII (Accession NP_060895.1) is another GAM5227 target gene, herein designated TARGET GENE. PI4KII BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PI4KII, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PI4KII BINDING SITE, designated SEQ ID:11397, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47947] Another function of GAM5227 is therefore inhibition of PI4KII (Accession NP_060895.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with PI4KII.

[47948] Plexin a2 (PLXNA2, Accession NP_079455.1) is another GAM5227 target gene, herein designated TARGET GENE. PLXNA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PLXNA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PLXNA2 BINDING SITE, designated SEQ ID:6296, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47949] Another function of GAM5227 is therefore inhibition of Plexin a2 (PLXNA2, Accession NP_079455.1), a gene which is a transmembrane protein. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLXNA2.

[47950] The function of PLXNA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM65.1.Podocalyxin-like (PODXL, Accession NP_005388.1) is another GAM5227 target gene, herein designated TARGET GENE. PODXL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by PODXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PODXL BINDING SITE, designated SEQ ID:15111, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47951] Another function of GAM5227 is therefore inhibition of Podocalyxin-like (PODXL, Accession NP_005388.1), a gene which is an antiadhesin. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PODXL.

[47952] The function of PODXL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM335.1.Polymerase (dna directed), epsilon 3 (p17 subunit) (POLE3, Accession NP_059139.2) is another GAM5227 target gene, herein designated TARGET GENE. POLE3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POLE3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of POLE3 BINDING SITE, designated SEQ ID:18239, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47953] Another function of GAM5227 is therefore inhibition of Polymerase (dna directed), epsilon 3 (p17 subunit) (POLE3, Accession NP_059139.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLE3.

[47954] Pou domain, class 2, transcription factor 2 (POU2F2, Accession NP_002689.1) is another GAM5227 target gene, herein designated TARGET GENE. POU2F2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by POU2F2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of POU2F2 BINDING SITE, designated SEQ ID:13248, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47955] Another function of GAM5227 is therefore inhibition of Pou domain, class 2, transcription factor 2 (POU2F2, Accession NP_002689.1), a gene which activates immunoglobulin gene expression. Accordingly, utilities of

GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU2F2.

[47956] The function of POU2F2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM148.2.Protein kinase, interferon-inducible double stranded rna dependent (PRKR, Accession NP_002750.1) is another GAM5227 target gene, herein designated TARGET GENE. PRKR BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRKR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRKR BINDING SITE, designated SEQ ID:1023, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47957] Another function of GAM5227 is therefore inhibition of Protein kinase, interferon-inducible double stranded rna dependent (PRKR, Accession NP_002750.1), a gene which catalyze the phosphorylation of the alpha subunit of eif2. and therefore may be associated with Huntington's disease. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Huntington's disease, and of

other diseases and clinical conditions associated with PRKR.

[47958] The function of PRKR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.PRO2435 (Accession NP_060997.1) is another GAM5227 target gene, herein designated TARGET GENE. PRO2435 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PRO2435, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PRO2435 BINDING SITE, designated SEQ ID:18921, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47959] Another function of GAM5227 is therefore inhibition of PRO2435 (Accession NP_060997.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2435.

[47960] PROM2 (Accession NP_653308.1) is another GAM5227 target gene, herein designated TARGET GENE. PROM2

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PROM2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PROM2 BINDING SITE, designated SEQ ID:11956, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47961] Another function of GAM5227 is therefore inhibition of PROM2 (Accession NP_653308.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROM2.

[47962] Pregnancy specific beta-1-glycoprotein 7 (PSG7, Accession NP_002774.1) is another GAM5227 target gene, herein designated TARGET GENE. PSG7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PSG7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSG7 BINDING SITE, designated SEQ ID:3072, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47963] Another function of GAM5227 is therefore inhibition of Pregnancy specific beta-1-glycoprotein 7 (PSG7, Accession NP_002774.1), a gene which function still unknown. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSG7.

[47964] The function of PSG7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Quiescin q6 (QSCN6, Accession NP_002817.2) is another GAM5227 target gene, herein designated TARGET GENE. QSCN6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by QSCN6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of QSCN6 BINDING SITE, designated SEQ ID:11516, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47965] Another function of GAM5227 is therefore inhibition of Quiescin q6 (QSCN6, Accession NP_002817.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with QSCN6.

[47966] Rab17, member ras oncogene family (RAB17, Accession NP_071894.1) is another GAM5227 target gene, herein designated TARGET GENE. RAB17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAB17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAB17 BINDING SITE, designated SEQ ID:18385, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47967] Another function of GAM5227 is therefore inhibition of Rab17, member ras oncogene family (RAB17, Accession NP_071894.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB17.

[47968] Receptor (calcitonin) activity modifying protein 3 (RAMP3, Accession NP_005847.1) is another GAM5227 target gene, herein designated TARGET GENE. RAMP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RAMP3, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RAMP3 BINDING SITE, designated SEQ ID:7834, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47969] Another function of GAM5227 is therefore inhibition of Receptor (calcitonin) activity modifying protein 3 (RAMP3, Accession NP_005847.1), a gene which is required to transport calcitonin- receptor- like receptor (crlr) to the plasma membrane. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAMP3.

[47970] The function of RAMP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM625.1.Reelin (RELN, Accession NP_774959.1) is another GAM5227 target gene, herein designated TARGET GENE. RELN BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RELN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementar-

ity of the nucleotide sequences of RELN BINDING SITE, designated SEQ ID:16254, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47971] Another function of GAM5227 is therefore inhibition of Reelin (RELN, Accession NP_774959.1), a gene which regulates microtubule function in neurons and neuronal migration. and therefore is associated with Norman- roberts syndrome. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Norman- roberts syndrome, and of other diseases and clinical conditions associated with RELN.

[47972] The function of RELN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM700.2.Reelin (RELN, Accession NP_005036.2) is another GAM5227 target gene, herein designated TARGET GENE. RELN BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by RELN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RELN BINDING SITE,

designated SEQ ID:16254, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47973] Another function of GAM5227 is therefore inhibition of Reelin (RELN, Accession NP_005036.2), a gene which regulates microtubule function in neurons and neuronal migration. and therefore is associated with Norman- roberts syndrome. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Norman- roberts syndrome, and of other diseases and clinical conditions associated with RELN.

[47974] The function of RELN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM700.2.RETNLB (Accession NP_115968.1) is another GAM5227 target gene, herein designated TARGET GENE. RETNLB BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by RETNLB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RETNLB BINDING SITE, designated SEQ ID:1728, to the nucleotide sequence of GAM5227 RNA, herein designated

GAM RNA, also designated SEQ ID:299.

[47975] Another function of GAM5227 is therefore inhibition of RETNLB (Accession NP_115968.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RETNLB.

[47976] Regulator of g-protein signalling 7 (RGS7, Accession NP_002915.2) is another GAM5227 target gene, herein designated TARGET GENE. RGS7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RGS7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RGS7 BINDING SITE, designated SEQ ID:20171, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47977] Another function of GAM5227 is therefore inhibition of Regulator of g-protein signalling 7 (RGS7, Accession NP_002915.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS7.

[47978] Ring finger protein 24 (RNF24, Accession NP_009150.1) is another GAM5227 target gene, herein designated TARGET

GENE. RNF24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RNF24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RNF24 BINDING SITE, designated SEQ ID:16047, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47979] Another function of GAM5227 is therefore inhibition of Ring finger protein 24 (RNF24, Accession NP_009150.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF24.

[47980] Sodium channel, voltage-gated, type iv, alpha polypeptide (SCN4A, Accession NP_000325.1) is another GAM5227 target gene, herein designated TARGET GENE. SCN4A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SCN4A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCN4A BINDING SITE, designated SEQ ID:3212, to the nucleotide sequence of GAM5227 RNA, herein designated

GAM RNA, also designated SEQ ID:299.

[47981] Another function of GAM5227 is therefore inhibition of Sodium channel, voltage-gated, type iv, alpha polypeptide (SCN4A, Accession NP_000325.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN4A.

[47982] SETDB2 (Accession NP_114121.1) is another GAM5227 target gene, herein designated TARGET GENE. SETDB2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SETDB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SETDB2 BINDING SITE, designated SEQ ID:9368, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47983] Another function of GAM5227 is therefore inhibition of SETDB2 (Accession NP_114121.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SETDB2.

[47984] Solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (SLC13A3, Accession NP_073740.2) is another GAM5227 target gene, herein

designated TARGET GENE. SLC13A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC13A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC13A3 BINDING SITE, designated SEQ ID:18351, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47985] Another function of GAM5227 is therefore inhibition of Solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (SLC13A3, Accession NP_073740.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC13A3.

[47986] Solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7 (SLC17A7, Accession NP_064705.1) is another GAM5227 target gene, herein designated TARGET GENE. SLC17A7 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC17A7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of SLC17A7 BINDING SITE, designated SEQ ID:4723, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47987] Another function of GAM5227 is therefore inhibition of Solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7 (SLC17A7, Accession NP_064705.1), a gene which is a brain- specific Na- dependent inorganic phosphate cotransporter. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC17A7.

[47988] The function of SLC17A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM500.2.SLC9A8 (Accession XP_030524.2) is another GAM5227 target gene, herein designated TARGET GENE. SLC9A8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC9A8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC9A8 BINDING SITE, designated SEQ ID:13104, to the

nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47989] Another function of GAM5227 is therefore inhibition of SLC9A8 (Accession XP_030524.2) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC9A8.

[47990] Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1) is another GAM5227 target gene, herein designated TARGET GENE. SS18 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SS18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SS18 BINDING SITE, designated SEQ ID:5489, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47991] Another function of GAM5227 is therefore inhibition of Synovial sarcoma translocation, chromosome 18 (SS18, Accession NP_005628.1), a gene which is a putative transcriptional activator. and therefore is associated with Human synovial sarcomas. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Human

synovial sarcomas., and of other diseases and clinical conditions associated with SS18.

[47992] The function of SS18 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.T-cell leukemia/lymphoma 6 (TCL6, Accession NP_055233.1) is another GAM5227 target gene, herein designated TARGET GENE. TCL6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TCL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE, designated SEQ ID:13727, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47993] Another function of GAM5227 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_055233.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[47994] T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065575.1) is another GAM5227 target gene, herein

designated TARGET GENE. TCL6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TCL6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TCL6 BINDING SITE, designated SEQ ID:13727, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47995] Another function of GAM5227 is therefore inhibition of T-cell leukemia/lymphoma 6 (TCL6, Accession NP_065575.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCL6.

[47996] Thioesterase, adipose associated (THEA, Accession NP_671517.1) is another GAM5227 target gene, herein designated TARGET GENE. THEA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by THEA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of THEA BINDING SITE, designated SEQ ID:7538, to the nucleotide

sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47997] Another function of GAM5227 is therefore inhibition of Thioesterase, adipose associated (THEA, Accession NP_671517.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THEA.

[47998] Transducin-like enhancer of split 2 (e(sp1) homolog, drosophila) (TLE2, Accession NP_003251.2) is another GAM5227 target gene, herein designated TARGET GENE. TLE2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by TLE2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLE2 BINDING SITE, designated SEQ ID:642, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[47999] Another function of GAM5227 is therefore inhibition of Transducin-like enhancer of split 2 (e(sp1) homolog, drosophila) (TLE2, Accession NP_003251.2), a gene which involves in epithelial differentiation. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with TLE2.

[48000] The function of TLE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM223.1.Transmembrane protease, serine 3 (TMPRSS3, Accession NP_076927.1) is another GAM5227 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE1 and TMPRSS3 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE1 and TMPRSS3 BINDING SITE2, designated SEQ ID:19374 and SEQ ID:17983 respectively, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[48001] Another function of GAM5227 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_076927.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[48002] Transmembrane protease, serine 3 (TMPRSS3, Accession

NP_076927.1) is another GAM5227 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE1 and TMPRSS3 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE1 and TMPRSS3 BINDING SITE2, designated SEQ ID:17983 and SEQ ID:17983 respectively, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[48003] Another function of GAM5227 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_076927.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[48004] Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115777.1) is another GAM5227 target gene, herein designated TARGET GENE. TMPRSS3 BINDING SITE1 and TMPRSS3 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by TMPRSS3, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TMPRSS3 BINDING SITE1 and TMPRSS3 BINDING SITE2, designated SEQ ID:19374 and SEQ ID:19374 respectively, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[48005] Another function of GAM5227 is therefore inhibition of Transmembrane protease, serine 3 (TMPRSS3, Accession NP_115777.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS3.

[48006] Troponin c, slow (TNNC1, Accession NP_003271.1) is another GAM5227 target gene, herein designated TARGET GENE. TNNC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TNNC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TNNC1 BINDING SITE, designated SEQ ID:12996, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[48007] Another function of GAM5227 is therefore inhibition of Troponin c, slow (TNNC1, Accession NP_003271.1), a gene which Troponin C; calcium- binding subunit of troponin, a regulatory protein, prevents actin and myosin interaction in resting muscle tissue. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNNC1.

[48008] The function of TNNC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM3099.2.Trichorhinophalangeal syndrome i (TRPS1, Accession NP_054831.1) is another GAM5227 target gene, herein designated TARGET GENE. TRPS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRPS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRPS1 BINDING SITE, designated SEQ ID:5417, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[48009] Another function of GAM5227 is therefore inhibition of Trichorhinophalangeal syndrome i (TRPS1, Accession

NP_054831.1), a gene which may function as a transcriptional activator protein and therefore is associated with Trichorhinophalangeal syndrome type i, type iii. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Trichorhinophalangeal syndrome type i, type iii, and of other diseases and clinical conditions associated with TRPS1.

[48010] The function of TRPS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM139.1.Tissue specific transplantation antigen p35b (TSTA3, Accession NP_003304.1) is another GAM5227 target gene, herein designated TARGET GENE. TSTA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TSTA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TSTA3 BINDING SITE, designated SEQ ID:19224, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[48011] Another function of GAM5227 is therefore inhibition of Tissue specific transplantation antigen p35b (TSTA3, Ac-

cession NP_003304.1), a gene which converts gdp- 4- dehydro- 6- deoxy- d- mannose to gdp- fucose. and therefore may be associated with Leukocyte adhesion deficiency, type ii. Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of Leukocyte adhesion deficiency, type ii, and of other diseases and clinical conditions associated with TSTA3.

[48012] The function of TSTA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2012.2.VCIP135 (Accession NP_079330.1) is another GAM5227 target gene, herein designated TARGET GENE. VCIP135 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by VCIP135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of VCIP135 BINDING SITE, designated SEQ ID:16563, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[48013] Another function of GAM5227 is therefore inhibition of VCIP135 (Accession NP_079330.1) . Accordingly, utilities

of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VCIP135.

[48014] Zinc finger, dhhc domain containing 2 (ZDHHC2, Accession NP_057437.1) is another GAM5227 target gene, herein designated TARGET GENE. ZDHHC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZDHHC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZDHHC2 BINDING SITE, designated SEQ ID:8860, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[48015] Another function of GAM5227 is therefore inhibition of Zinc finger, dhhc domain containing 2 (ZDHHC2, Accession NP_057437.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZDHHC2.

[48016] Zinc finger protein 297b (ZNF297B, Accession NP_054726.1) is another GAM5227 target gene, herein designated TARGET GENE. ZNF297B BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by ZNF297B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF297B BINDING SITE, designated SEQ ID:14345, to the nucleotide sequence of GAM5227 RNA, herein designated GAM RNA, also designated SEQ ID:299.

[48017] Another function of GAM5227 is therefore inhibition of Zinc finger protein 297b (ZNF297B, Accession NP_054726.1) . Accordingly, utilities of GAM5227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF297B.

[48018]

[48019] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 5346 (GAM5346), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[48020] GAM5346 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM5346 was detected is described hereinabove with reference to Figs. 8-15.

[48021] GAM5346 gene, herein designated GAM GENE, and GAM5346 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[48022] GAM5346 gene encodes a GAM5346 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM5346 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5346 precursor RNA is designated SEQ ID:152, and is provided hereinbelow with reference to the sequence listing part.

[48023] GAM5346 precursor RNA folds onto itself, forming GAM5346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[48024] GAM5346 precursor RNA folds onto itself, forming GAM5346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional

`hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[48025] Nucleotide sequence of GAM5346 precursor RNA, designated SEQ-ID: 152, and a schematic representation of a predicted secondary folding of GAM5346 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[48026] An enzyme complex designated DICER COMPLEX, `dices` the GAM5346 folded precursor RNA into GAM5346 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: B) nucleotide sequence of GAM5346 RNA is designated SEQ ID:319, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[48027] GAM5346 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM5346 target RNA, herein designated GAM TARGET RNA. GAM5346 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[48028] GAM5346 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5346 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5346 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM5346 RNA may have a different number of target binding sites in untranslated regions of a GAM5346 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an

example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[48029] The complementary binding of GAM5346 RNA, herein designated GAM RNA, to target binding sites on GAM5346 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5346 target RNA into GAM5346 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[48030] It is appreciated that GAM5346 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM5346 target genes. The mRNA of each one of this plurality of GAM5346 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5346 RNA, herein designated GAM RNA, and which when bound by GAM5346 RNA causes inhibition of translation of respective one or more GAM5346 target proteins.

[48031] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM5346 gene, herein designated GAM GENE, on one or

more GAM5346 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[48032] It is appreciated that specific functions and accordingly utilities of GAM5346 correlate with, and may be deduced from, the identity of the target genes which GAM5346 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[48033]

[48034]

[48035] A kinase (prka) anchor protein 11 (AKAP11, Accession NP_652761.1) is a GAM5346 target gene, herein designated TARGET GENE. AKAP11 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AKAP11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKAP11 BINDING SITE, designated SEQ ID:11814, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48036] A function of GAM5346 is therefore inhibition of A kinase (prka) anchor protein 11 (AKAP11, Accession NP_652761.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP11.

[48037] Aquaporin 10 (AQP10, Accession NP_536354.2) is another GAM5346 target gene, herein designated TARGET GENE. AQP10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AQP10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP10 BINDING SITE, designated SEQ ID:3157, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48038] Another function of GAM5346 is therefore inhibition of Aquaporin 10 (AQP10, Accession NP_536354.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP10.

[48039] Adp-ribosylation factor-like 6 interacting protein (ARL6IP, Accession NP_055976.1) is another GAM5346 target gene, herein designated TARGET GENE. ARL6IP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARL6IP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARL6IP BINDING SITE, designated SEQ ID:422, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48040] Another function of GAM5346 is therefore inhibition of Adp-ribosylation factor-like 6 interacting protein (ARL6IP, Accession NP_055976.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARL6IP.

[48041] Aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2, Accession NP_055677.1) is another GAM5346 target gene,

herein designated TARGET GENE. ARNT2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARNT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARNT2 BINDING SITE, designated SEQ ID:12943, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48042] Another function of GAM5346 is therefore inhibition of Aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2, Accession NP_055677.1), a gene which specifically recognizes the xenobiotic response element (xre). Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARNT2.

[48043] The function of ARNT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.1.Alpha thalassemia/mental retardation syndrome x-linked (rad54 homolog, s. cerevisiae) (ATRX, Accession NP_612115.1) is another GAM5346 target gene, herein designated TARGET GENE. ATRX BINDING SITE is a

target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ATRX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATRX BINDING SITE, designated SEQ ID:13943, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48044] Another function of GAM5346 is therefore inhibition of Alpha thalassemia/mental retardation syndrome x-linked (rad54 homolog, s. cerevisiae) (ATRX, Accession NP_612115.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATRX.

[48045] Butyrophilin, subfamily 2, member a2 (BTN2A2, Accession NP_008926.2) is another GAM5346 target gene, herein designated TARGET GENE. BTN2A2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BTN2A2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BTN2A2 BINDING SITE, designated SEQ ID:2449, to the nucleotide sequence

of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48046] Another function of GAM5346 is therefore inhibition of Butyrophilin, subfamily 2, member a2 (BTN2A2, Accession NP_008926.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN2A2.

[48047] Blood vessel epicardial substance (BVES, Accession NP_009004.2) is another GAM5346 target gene, herein designated TARGET GENE. BVES BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BVES, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BVES BINDING SITE, designated SEQ ID:7200, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48048] Another function of GAM5346 is therefore inhibition of Blood vessel epicardial substance (BVES, Accession NP_009004.2), a gene which plays an important role in vertebrate heart development. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with BVES.

[48049] The function of BVES and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM180.1.Chromosome 1 open reading frame 17 (C1orf17, Accession NP_055916.1) is another GAM5346 target gene, herein designated TARGET GENE. C1orf17 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1orf17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf17 BINDING SITE, designated SEQ ID:9464, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48050] Another function of GAM5346 is therefore inhibition of Chromosome 1 open reading frame 17 (C1orf17, Accession NP_055916.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf17.

[48051] Chromosome 1 open reading frame 21 (C1orf21, Accession NP_110433.1) is another GAM5346 target gene, herein designated TARGET GENE. C1orf21 BINDING SITE is

a target binding site found in the 3` untranslated region of mRNA encoded by C1orf21, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1orf21 BINDING SITE, designated SEQ ID:2690, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48052] Another function of GAM5346 is therefore inhibition of Chromosome 1 open reading frame 21 (C1orf21, Accession NP_110433.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf21.

[48053] C1QDC1 (Accession NP_115532.1) is another GAM5346 target gene, herein designated TARGET GENE. C1QDC1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C1QDC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1QDC1 BINDING SITE, designated SEQ ID:6143, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ

ID:319.

[48054] Another function of GAM5346 is therefore inhibition of C1QDC1 (Accession NP_115532.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QDC1.

[48055] Chromosome 20 open reading frame 38 (C20orf38, Accession NP_060797.1) is another GAM5346 target gene, herein designated TARGET GENE. C20orf38 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf38, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf38 BINDING SITE, designated SEQ ID:9565, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48056] Another function of GAM5346 is therefore inhibition of Chromosome 20 open reading frame 38 (C20orf38, Accession NP_060797.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf38.

[48057] Chromosome 21 open reading frame 109 (C21orf109, Ac-

cession NP_620418.1) is another GAM5346 target gene, herein designated TARGET GENE. C21orf109 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C21orf109, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C21orf109 BINDING SITE, designated SEQ ID:13650, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48058] Another function of GAM5346 is therefore inhibition of Chromosome 21 open reading frame 109 (C21orf109, Accession NP_620418.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf109.

[48059] Chromosome 5 open reading frame 6 (C5orf6, Accession NP_057689.1) is another GAM5346 target gene, herein designated TARGET GENE. C5orf6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C5orf6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C5orf6 BINDING SITE, designated

SEQ ID:4877, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48060] Another function of GAM5346 is therefore inhibition of Chromosome 5 open reading frame 6 (C5orf6, Accession NP_057689.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf6.

[48061] Carbonic anhydrase viii (CA8, Accession NP_004047.3) is another GAM5346 target gene, herein designated TARGET GENE. CA8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CA8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CA8 BINDING SITE, designated SEQ ID:2246, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48062] Another function of GAM5346 is therefore inhibition of Carbonic anhydrase viii (CA8, Accession NP_004047.3) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CA8.

[48063] Calcium/calmodulin-dependent protein kinase (cam kinase) ii alpha (CAMK2A, Accession NP_057065.2) is another GAM5346 target gene, herein designated TARGET GENE. CAMK2A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CAMK2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMK2A BINDING SITE, designated SEQ ID:12760, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48064] Another function of GAM5346 is therefore inhibition of Calcium/calmodulin-dependent protein kinase (cam kinase) ii alpha (CAMK2A, Accession NP_057065.2), a gene which may modulate the synaptic events required for the consolidation of memory traces in cortical networks. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMK2A.

[48065] The function of CAMK2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM223.1.Calcium/calmodulin-dependent protein kinase (cam kinase) ii alpha (CAMK2A, Accession NP_741960.1) is another GAM5346 target gene, herein designated TARGET GENE. CAMK2A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CAMK2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMK2A BINDING SITE, designated SEQ ID:12760, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48066] Another function of GAM5346 is therefore inhibition of Calcium/calmodulin-dependent protein kinase (cam kinase) ii alpha (CAMK2A, Accession NP_741960.1), a gene which may modulate the synaptic events required for the consolidation of memory traces in cortical networks. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMK2A.

[48067] The function of CAMK2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM223.1.CARF (Accession NP_060102.1) is another GAM5346 target gene, herein designated TARGET GENE. CARF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CARF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CARF BINDING SITE, designated SEQ ID:11378, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48068] Another function of GAM5346 is therefore inhibition of CARF (Accession NP_060102.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARF.

[48069] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) is another GAM5346 target gene, herein designated TARGET GENE. CECR1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CECR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE, designated

SEQ ID:12603, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48070] Another function of GAM5346 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_803124.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[48071] CGI-141 (Accession NP_057156.1) is another GAM5346 target gene, herein designated TARGET GENE. CGI-141 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CGI-141, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-141 BINDING SITE, designated SEQ ID:6784, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48072] Another function of GAM5346 is therefore inhibition of CGI-141 (Accession NP_057156.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-141.

[48073] Chondrolectin (CHODL, Accession NP_079220.2) is another GAM5346 target gene, herein designated TARGET GENE. CHODL BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHODL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHODL BINDING SITE, designated SEQ ID:3700, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48074] Another function of GAM5346 is therefore inhibition of Chondrolectin (CHODL, Accession NP_079220.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHODL.

[48075] Cholinergic receptor, nicotinic, alpha polypeptide 3 (CHRNA3, Accession NP_000734.2) is another GAM5346 target gene, herein designated TARGET GENE. CHRNA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHRNA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of CHRNA3 BINDING SITE, designated SEQ ID:15387, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48076] Another function of GAM5346 is therefore inhibition of Cholinergic receptor, nicotinic, alpha polypeptide 3 (CHRNA3, Accession NP_000734.2), a gene which binds acetylcholine and opens an ion- conducting channel across the plasma membrane. and therefore may be associated with Myasthenia gravis. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of Myasthenia gravis, and of other diseases and clinical conditions associated with CHRNA3.

[48077] The function of CHRNA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM404.2.CHST10 (Accession NP_004845.1) is another GAM5346 target gene, herein designated TARGET GENE. CHST10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHST10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences

of CHST10 BINDING SITE, designated SEQ ID:14727, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48078] Another function of GAM5346 is therefore inhibition of CHST10 (Accession NP_004845.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST10.

[48079] Clock homolog (mouse) (CLOCK, Accession NP_004889.1) is another GAM5346 target gene, herein designated TARGET GENE. CLOCK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLOCK, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLOCK BINDING SITE, designated SEQ ID:6844, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48080] Another function of GAM5346 is therefore inhibition of Clock homolog (mouse) (CLOCK, Accession NP_004889.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with CLOCK.

[48081] Ccr4-not transcription complex, subunit 7 (CNOT7, Accession NP_473367.1) is another GAM5346 target gene, herein designated TARGET GENE. CNOT7 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CNOT7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CNOT7 BINDING SITE, designated SEQ ID:12054, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48082] Another function of GAM5346 is therefore inhibition of Ccr4-not transcription complex, subunit 7 (CNOT7, Accession NP_473367.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNOT7.

[48083] Collagen, type iv, alpha 3 (goodpasture antigen) binding protein (COL4A3BP, Accession NP_112729.1) is another GAM5346 target gene, herein designated TARGET GENE. COL4A3BP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by COL4A3BP, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL4A3BP BINDING SITE, designated SEQ ID:13701, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48084] Another function of GAM5346 is therefore inhibition of Collagen, type iv, alpha 3 (goodpasture antigen) binding protein (COL4A3BP, Accession NP_112729.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A3BP.

[48085] Collagen, type iv, alpha 3 (goodpasture antigen) binding protein (COL4A3BP, Accession NP_005704.1) is another GAM5346 target gene, herein designated TARGET GENE. COL4A3BP BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by COL4A3BP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COL4A3BP BINDING SITE, designated SEQ ID:13701, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA,

also designated SEQ ID:319.

[48086] Another function of GAM5346 is therefore inhibition of Collagen, type iv, alpha 3 (goodpasture antigen) binding protein (COL4A3BP, Accession NP_005704.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A3BP.

[48087] Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) is another GAM5346 target gene, herein designated TARGET GENE. COLEC12 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by COLEC12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COLEC12 BINDING SITE, designated SEQ ID:1211, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48088] Another function of GAM5346 is therefore inhibition of Collectin sub-family member 12 (COLEC12, Accession NP_110408.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC12.

[48089] Cytochrome c oxidase subunit vb (COX5B, Accession NP_001853.2) is another GAM5346 target gene, herein designated TARGET GENE. COX5B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by COX5B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of COX5B BINDING SITE, designated SEQ ID:15248, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48090] Another function of GAM5346 is therefore inhibition of Cytochrome c oxidase subunit vb (COX5B, Accession NP_001853.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COX5B.

[48091] Cytochrome c oxidase subunit viia polypeptide 2 like (COX7A2L, Accession NP_004709.2) is another GAM5346 target gene, herein designated TARGET GENE. COX7A2L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by COX7A2L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of COX7A2L BINDING SITE, designated SEQ ID:14171, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48092] Another function of GAM5346 is therefore inhibition of Cytochrome c oxidase subunit viia polypeptide 2 like (COX7A2L, Accession NP_004709.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COX7A2L.

[48093] Cofactor required for sp1 transcriptional activation, subunit 3, 130kda (CRSP3, Accession NP_004821.2) is another GAM5346 target gene, herein designated TARGET GENE. CRSP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CRSP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRSP3 BINDING SITE, designated SEQ ID:19755, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48094] Another function of GAM5346 is therefore inhibition of

Cofactor required for sp1 transcriptional activation, subunit 3, 130kda (CRSP3, Accession NP_004821.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRSP3.

[48095] Crystallin, lambda 1 (CRYL1, Accession NP_057058.1) is another GAM5346 target gene, herein designated TARGET GENE. CRYL1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CRYL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRYL1 BINDING SITE, designated SEQ ID:18424, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48096] Another function of GAM5346 is therefore inhibition of Crystallin, lambda 1 (CRYL1, Accession NP_057058.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRYL1.

[48097] Dead/h (asp-glu-ala-asp/his) box polypeptide 11 (chl1-like helicase homolog, s. cerevisiae) (DDX11, Accession NP_085911.1) is another GAM5346 target gene,

herein designated TARGET GENE. DDX11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DDX11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX11 BINDING SITE, designated SEQ ID:13852, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48098] Another function of GAM5346 is therefore inhibition of Dead/h (asp-glu-ala-asp/his) box polypeptide 11 (chl1-like helicase homolog, s. cerevisiae) (DDX11, Accession NP_085911.1), a gene which could be an ATP- dependent DNA- binding helicase and may intervene in cell cycle regulation. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX11.

[48099] The function of DDX11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Dead/h (asp-glu-ala-asp/his) box polypeptide 11 (chl1-like helicase homolog, s. cerevisiae) (DDX11, Accession NP_004390.2) is another GAM5346 target gene,

herein designated TARGET GENE. DDX11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DDX11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX11 BINDING SITE, designated SEQ ID:13852, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48100] Another function of GAM5346 is therefore inhibition of Dead/h (asp-glu-ala-asp/his) box polypeptide 11 (chl1-like helicase homolog, s. cerevisiae) (DDX11, Accession NP_004390.2), a gene which could be an ATP- dependent DNA- binding helicase and may intervene in cell cycle regulation. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX11.

[48101] The function of DDX11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Dead/h (asp-glu-ala-asp/his) box polypeptide 11 (chl1-like helicase homolog, s. cerevisiae) (DDX11, Accession NP_085913.1) is another GAM5346 target gene,

herein designated TARGET GENE. DDX11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DDX11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX11 BINDING SITE, designated SEQ ID:13852, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48102] Another function of GAM5346 is therefore inhibition of Dead/h (asp-glu-ala-asp/his) box polypeptide 11 (chl1-like helicase homolog, s. cerevisiae) (DDX11, Accession NP_085913.1), a gene which could be an ATP- dependent DNA- binding helicase and may intervene in cell cycle regulation. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX11.

[48103] The function of DDX11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.DDX56 (Accession NP_061955.1) is another GAM5346 target gene, herein designated TARGET GENE. DDX56 BINDING SITE is a target binding site found in the

3` untranslated region of mRNA encoded by DDX56, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDX56 BINDING SITE, designated SEQ ID:13267, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48104] Another function of GAM5346 is therefore inhibition of DDX56 (Accession NP_061955.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX56.

[48105] DKFZp434E1119 (Accession XP_210937.1) is another GAM5346 target gene, herein designated TARGET GENE. DKFZp434E1119 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434E1119, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434E1119 BINDING SITE, designated SEQ ID:3872, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48106] Another function of GAM5346 is therefore inhibition of

DKFZp434E1119 (Accession XP_210937.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E1119.

[48107] DKFZP564D166 (Accession NP_056438.1) is another GAM5346 target gene, herein designated TARGET GENE. DKFZP564D166 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DKFZP564D166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564D166 BINDING SITE, designated SEQ ID:14703, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48108] Another function of GAM5346 is therefore inhibition of DKFZP564D166 (Accession NP_056438.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D166.

[48109] DKFZp761O17121 (Accession NP_115663.1) is another GAM5346 target gene, herein designated TARGET GENE. DKFZp761O17121 BINDING SITE is a target binding site

found in the 5` untranslated region of mRNA encoded by DKFZp761O17121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761O17121 BINDING SITE, designated SEQ ID:15142, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48110] Another function of GAM5346 is therefore inhibition of DKFZp761O17121 (Accession NP_115663.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761O17121.

[48111] Doublesex and mab-3 related transcription factor 1 (DMRT1, Accession NP_068770.1) is another GAM5346 target gene, herein designated TARGET GENE. DMRT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DMRT1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DMRT1 BINDING SITE, designated SEQ ID:12585, to the nucleotide sequence of GAM5346 RNA, herein designated

GAM RNA, also designated SEQ ID:319.

[48112] Another function of GAM5346 is therefore inhibition of Doublesex and mab-3 related transcription factor 1 (DMRT1, Accession NP_068770.1), a gene which May be involved in male sexual development. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMRT1.

[48113] The function of DMRT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM505.1.Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D, Accession NP_001951.2) is another GAM5346 target gene, herein designated TARGET GENE. EEF1D BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by EEF1D, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EEF1D BINDING SITE, designated SEQ ID:10991, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48114] Another function of GAM5346 is therefore inhibition of

Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D, Accession NP_001951.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EEF1D.

[48115] Eukaryotic translation initiation factor 4e-like 3 (EIF4EL3, Accession NP_004837.1) is another GAM5346 target gene, herein designated TARGET GENE. EIF4EL3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by EIF4EL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EIF4EL3 BINDING SITE, designated SEQ ID:14958, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48116] Another function of GAM5346 is therefore inhibition of Eukaryotic translation initiation factor 4e-like 3 (EIF4EL3, Accession NP_004837.1), a gene which is a cap- binding protein. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF4EL3.

[48117] The function of EIF4EL3 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1713.2.FLJ10204 (Accession NP_060494.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ10204 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10204, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10204 BINDING SITE, designated SEQ ID:19088, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48118] Another function of GAM5346 is therefore inhibition of FLJ10204 (Accession NP_060494.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10204.

[48119] FLJ11267 (Accession NP_062553.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ11267 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11267, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11267 BINDING SITE, designated SEQ ID:5853, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48120] Another function of GAM5346 is therefore inhibition of FLJ11267 (Accession NP_062553.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11267.

[48121] FLJ11724 (Accession XP_044426.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ11724 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11724, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11724 BINDING SITE, designated SEQ ID:11865, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48122] Another function of GAM5346 is therefore inhibition of FLJ11724 (Accession XP_044426.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ11724.

[48123] FLJ11806 (Accession NP_079100.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ11806 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ11806, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11806 BINDING SITE, designated SEQ ID:12794, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48124] Another function of GAM5346 is therefore inhibition of FLJ11806 (Accession NP_079100.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11806.

[48125] FLJ12294 (Accession NP_079376.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ12294 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12294, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ12294 BINDING SITE, designated SEQ ID:7539, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48126] Another function of GAM5346 is therefore inhibition of FLJ12294 (Accession NP_079376.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12294.

[48127] FLJ12891 (Accession NP_079226.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ12891 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12891, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12891 BINDING SITE, designated SEQ ID:2301, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48128] Another function of GAM5346 is therefore inhibition of FLJ12891 (Accession NP_079226.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ12891.

[48129] FLJ14001 (Accession NP_078953.2) is another GAM5346 target gene, herein designated TARGET GENE. FLJ14001 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14001 BINDING SITE, designated SEQ ID:9178, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48130] Another function of GAM5346 is therefore inhibition of FLJ14001 (Accession NP_078953.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14001.

[48131] FLJ14816 (Accession NP_116234.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ14816 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14816, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ14816 BINDING SITE, designated SEQ ID:10584, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48132] Another function of GAM5346 is therefore inhibition of FLJ14816 (Accession NP_116234.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14816.

[48133] FLJ20209 (Accession XP_098142.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ20209 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20209, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20209 BINDING SITE, designated SEQ ID:2433, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48134] Another function of GAM5346 is therefore inhibition of FLJ20209 (Accession XP_098142.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20209.

[48135] FLJ20300 (Accession NP_060223.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ20300 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20300, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20300 BINDING SITE, designated SEQ ID:6291, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48136] Another function of GAM5346 is therefore inhibition of FLJ20300 (Accession NP_060223.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20300.

[48137] FLJ21272 (Accession NP_079308.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ21272 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21272, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21272 BINDING SITE, designated SEQ ID:15440, to the

nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48138] Another function of GAM5346 is therefore inhibition of FLJ21272 (Accession NP_079308.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21272.

[48139] FLJ23259 (Accession NP_079003.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ23259 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ23259, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23259 BINDING SITE, designated SEQ ID:19128, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48140] Another function of GAM5346 is therefore inhibition of FLJ23259 (Accession NP_079003.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23259.

[48141] FLJ23861 (Accession NP_689732.1) is another GAM5346

target gene, herein designated TARGET GENE. FLJ23861 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ23861, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23861 BINDING SITE, designated SEQ ID:11394, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48142] Another function of GAM5346 is therefore inhibition of FLJ23861 (Accession NP_689732.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23861.

[48143] FLJ25359 (Accession NP_653188.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ25359 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ25359, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25359 BINDING SITE, designated SEQ ID:16387, to the nucleotide sequence of GAM5346 RNA, herein designated

GAM RNA, also designated SEQ ID:319.

[48144] Another function of GAM5346 is therefore inhibition of FLJ25359 (Accession NP_653188.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25359.

[48145] FLJ32028 (Accession NP_689893.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ32028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32028 BINDING SITE, designated SEQ ID:5186, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48146] Another function of GAM5346 is therefore inhibition of FLJ32028 (Accession NP_689893.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32028.

[48147] FLJ32940 (Accession NP_653220.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ32940

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ32940, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32940 BINDING SITE, designated SEQ ID:9834, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48148] Another function of GAM5346 is therefore inhibition of FLJ32940 (Accession NP_653220.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32940.

[48149] FLJ35728 (Accession NP_689823.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ35728 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ35728, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35728 BINDING SITE, designated SEQ ID:14579, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48150] Another function of GAM5346 is therefore inhibition of FLJ35728 (Accession NP_689823.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35728.

[48151] FLJ35801 (Accession NP_694589.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ35801 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ35801, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35801 BINDING SITE, designated SEQ ID:3807, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48152] Another function of GAM5346 is therefore inhibition of FLJ35801 (Accession NP_694589.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35801.

[48153] FLJ36576 (Accession NP_775793.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ36576 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ36576, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36576 BINDING SITE, designated SEQ ID:11409, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48154] Another function of GAM5346 is therefore inhibition of FLJ36576 (Accession NP_775793.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36576.

[48155] FLJ37228 (Accession NP_787113.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ37228 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37228, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37228 BINDING SITE, designated SEQ ID:11241, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48156] Another function of GAM5346 is therefore inhibition of

FLJ37228 (Accession NP_787113.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37228.

[48157] FLJ37307 (Accession NP_848610.1) is another GAM5346 target gene, herein designated TARGET GENE. FLJ37307 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37307, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37307 BINDING SITE, designated SEQ ID:12590, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48158] Another function of GAM5346 is therefore inhibition of FLJ37307 (Accession NP_848610.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37307.

[48159] Fibronectin leucine rich transmembrane protein 2 (FLRT2, Accession NP_037363.1) is another GAM5346 target gene, herein designated TARGET GENE. FLRT2 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by FLRT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLRT2 BINDING SITE, designated SEQ ID:11704, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48160] Another function of GAM5346 is therefore inhibition of Fibronectin leucine rich transmembrane protein 2 (FLRT2, Accession NP_037363.1), a gene which may have a function in cell adhesion and/or receptor signaling. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLRT2.

[48161] The function of FLRT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM72.1.G2 (Accession XP_039515.8) is another GAM5346 target gene, herein designated TARGET GENE. G2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates

the complementarity of the nucleotide sequences of G2 BINDING SITE, designated SEQ ID:13665, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48162] Another function of GAM5346 is therefore inhibition of G2 (Accession XP_039515.8) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G2.

[48163] GPR124 (Accession NP_116166.6) is another GAM5346 target gene, herein designated TARGET GENE. GPR124 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPR124, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR124 BINDING SITE, designated SEQ ID:6815, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48164] Another function of GAM5346 is therefore inhibition of GPR124 (Accession NP_116166.6) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR124.

[48165] G-rich rna sequence binding factor 1 (GRSF1, Accession NP_002083.1) is another GAM5346 target gene, herein designated TARGET GENE. GRSF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRSF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRSF1 BINDING SITE, designated SEQ ID:17530, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48166] Another function of GAM5346 is therefore inhibition of G-rich rna sequence binding factor 1 (GRSF1, Accession NP_002083.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRSF1.

[48167] High-mobility group 20a (HMG20A, Accession NP_060670.1) is another GAM5346 target gene, herein designated TARGET GENE. HMG20A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HMG20A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of HMG20A BINDING SITE, designated SEQ ID:1619, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48168] Another function of GAM5346 is therefore inhibition of High-mobility group 20a (HMG20A, Accession NP_060670.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMG20A.

[48169] Isoleucine-trna synthetase (IARS, Accession NP_002152.1) is another GAM5346 target gene, herein designated TARGET GENE. IARS BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IARS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IARS BINDING SITE, designated SEQ ID:8969, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48170] Another function of GAM5346 is therefore inhibition of Isoleucine-trna synthetase (IARS, Accession NP_002152.1), a gene which functions in protein biosyn-

thesis. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IARS.

[48171] The function of IARS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM291.1.Isoleucine-trna synthetase (IARS, Accession NP_038203.1) is another GAM5346 target gene, herein designated TARGET GENE. IARS BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IARS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IARS BINDING SITE, designated SEQ ID:8969, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48172] Another function of GAM5346 is therefore inhibition of Isoleucine-trna synthetase (IARS, Accession NP_038203.1), a gene which functions in protein biosynthesis. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IARS.

[48173] The function of IARS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM291.1.Interleukin 23, alpha subunit p19 (IL23A, Accession NP_057668.1) is another GAM5346 target gene, herein designated TARGET GENE. IL23A BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by IL23A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL23A BINDING SITE, designated SEQ ID:15401, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48174] Another function of GAM5346 is therefore inhibition of Interleukin 23, alpha subunit p19 (IL23A, Accession NP_057668.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL23A.

[48175] Inositol 1,4,5-trisphosphate 3-kinase b (ITPKB, Accession NP_002212.1) is another GAM5346 target gene, herein designated TARGET GENE. ITPKB BINDING SITE is a target binding site found in the 3` untranslated region of mRNA

encoded by ITPKB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITPKB BINDING SITE, designated SEQ ID:8612, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48176] Another function of GAM5346 is therefore inhibition of Inositol 1,4,5-trisphosphate 3-kinase b (ITPKB, Accession NP_002212.1), a gene which is a type B inositol 1,4,5-triphosphate 3 kinase. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPKB.

[48177] The function of ITPKB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.JMJD1 (Accession NP_060903.2) is another GAM5346 target gene, herein designated TARGET GENE. JMJD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JMJD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

JMJD1 BINDING SITE, designated SEQ ID:1010, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48178] Another function of GAM5346 is therefore inhibition of JMJD1 (Accession NP_060903.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JMJD1.

[48179] Potassium voltage-gated channel, shaker-related subfamily, member 3 (KCNA3, Accession NP_002223.2) is another GAM5346 target gene, herein designated TARGET GENE. KCNA3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KCNA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNA3 BINDING SITE, designated SEQ ID:9276, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48180] Another function of GAM5346 is therefore inhibition of Potassium voltage-gated channel, shaker-related subfamily, member 3 (KCNA3, Accession NP_002223.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with KCNA3.

[48181] KIAA0218 (Accession NP_055575.1) is another GAM5346 target gene, herein designated TARGET GENE. KIAA0218 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0218, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0218 BINDING SITE, designated SEQ ID:15087, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48182] Another function of GAM5346 is therefore inhibition of KIAA0218 (Accession NP_055575.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0218.

[48183] KIAA0962 (Accession XP_290942.1) is another GAM5346 target gene, herein designated TARGET GENE. KIAA0962 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0962, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA0962 BINDING SITE, designated SEQ ID:5013, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48184] Another function of GAM5346 is therefore inhibition of KIAA0962 (Accession XP_290942.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0962.

[48185] KIAA1554 (Accession XP_290768.1) is another GAM5346 target gene, herein designated TARGET GENE. KIAA1554 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1554, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1554 BINDING SITE, designated SEQ ID:19516, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48186] Another function of GAM5346 is therefore inhibition of KIAA1554 (Accession XP_290768.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1554.

[48187] KIAA1673 (Accession XP_047672.4) is another GAM5346 target gene, herein designated TARGET GENE. KIAA1673 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1673, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1673 BINDING SITE, designated SEQ ID:13140, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48188] Another function of GAM5346 is therefore inhibition of KIAA1673 (Accession XP_047672.4) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1673.

[48189] KIAA1998 (Accession XP_068710.3) is another GAM5346 target gene, herein designated TARGET GENE. KIAA1998 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1998, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1998 BINDING SITE, designated SEQ ID:1079, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48190] Another function of GAM5346 is therefore inhibition of KIAA1998 (Accession XP_068710.3) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1998.

[48191] LOC115442 (Accession XP_052510.3) is another GAM5346 target gene, herein designated TARGET GENE. LOC115442 BINDING SITE1 and LOC115442 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC115442, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115442 BINDING SITE1 and LOC115442 BINDING SITE2, designated SEQ ID:14698 and SEQ ID:16018 respectively, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48192] Another function of GAM5346 is therefore inhibition of LOC115442 (Accession XP_052510.3) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC115442.

[48193] LOC126037 (Accession XP_058967.6) is another GAM5346 target gene, herein designated TARGET GENE. LOC126037 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC126037, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126037 BINDING SITE, designated SEQ ID:10991, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48194] Another function of GAM5346 is therefore inhibition of LOC126037 (Accession XP_058967.6) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126037.

[48195] LOC130985 (Accession XP_059490.3) is another GAM5346 target gene, herein designated TARGET GENE. LOC130985 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC130985, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130985 BINDING SITE, designated SEQ ID:3929, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48196] Another function of GAM5346 is therefore inhibition of LOC130985 (Accession XP_059490.3) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130985.

[48197] LOC144866 (Accession XP_096699.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC144866 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144866, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144866 BINDING SITE, designated SEQ ID:780, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48198] Another function of GAM5346 is therefore inhibition of

LOC144866 (Accession XP_096699.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144866.

[48199] LOC145644 (Accession XP_035608.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC145644 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145644, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145644 BINDING SITE, designated SEQ ID:16433, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48200] Another function of GAM5346 is therefore inhibition of LOC145644 (Accession XP_035608.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145644.

[48201] LOC145786 (Accession XP_096860.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC145786 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC145786, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145786 BINDING SITE, designated SEQ ID:2737, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48202] Another function of GAM5346 is therefore inhibition of LOC145786 (Accession XP_096860.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145786.

[48203] LOC145957 (Accession NP_612640.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC145957 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC145957, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145957 BINDING SITE, designated SEQ ID:11305, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:319.

[48204] Another function of GAM5346 is therefore inhibition of LOC145957 (Accession NP_612640.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145957.

[48205] LOC148918 (Accession XP_086361.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC148918 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148918, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148918 BINDING SITE, designated SEQ ID:8659, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48206] Another function of GAM5346 is therefore inhibition of LOC148918 (Accession XP_086361.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148918.

[48207] LOC149127 (Accession XP_097584.1) is another

GAM5346 target gene, herein designated TARGET GENE. LOC149127 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC149127, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149127 BINDING SITE, designated SEQ ID:11810, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48208] Another function of GAM5346 is therefore inhibition of LOC149127 (Accession XP_097584.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149127.

[48209] LOC149372 (Accession XP_086509.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC149372 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149372, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149372 BINDING SITE, desig-

nated SEQ ID:16788, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48210] Another function of GAM5346 is therefore inhibition of LOC149372 (Accession XP_086509.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149372.

[48211] LOC155060 (Accession XP_098650.3) is another GAM5346 target gene, herein designated TARGET GENE. LOC155060 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC155060, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC155060 BINDING SITE, designated SEQ ID:10054, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48212] Another function of GAM5346 is therefore inhibition of LOC155060 (Accession XP_098650.3) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC155060.

[48213] LOC158450 (Accession XP_088580.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC158450 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158450, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158450 BINDING SITE, designated SEQ ID:1358, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48214] Another function of GAM5346 is therefore inhibition of LOC158450 (Accession XP_088580.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158450.

[48215] LOC196337 (Accession XP_113696.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC196337 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC196337, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196337 BINDING SITE, designated SEQ ID:3387, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48216] Another function of GAM5346 is therefore inhibition of LOC196337 (Accession XP_113696.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196337.

[48217] LOC200008 (Accession XP_114089.3) is another GAM5346 target gene, herein designated TARGET GENE. LOC200008 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200008, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200008 BINDING SITE, designated SEQ ID:11957, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48218] Another function of GAM5346 is therefore inhibition of LOC200008 (Accession XP_114089.3) . Accordingly, utili-

ties of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200008.

[48219] LOC202451 (Accession XP_117401.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC202451 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC202451, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202451 BINDING SITE, designated SEQ ID:2543, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48220] Another function of GAM5346 is therefore inhibition of LOC202451 (Accession XP_117401.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202451.

[48221] LOC220477 (Accession XP_071675.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC220477 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC220477, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220477 BINDING SITE, designated SEQ ID:17554, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48222] Another function of GAM5346 is therefore inhibition of LOC220477 (Accession XP_071675.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220477.

[48223] LOC254719 (Accession XP_171166.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC254719 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC254719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254719 BINDING SITE, designated SEQ ID:17345, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48224] Another function of GAM5346 is therefore inhibition of LOC254719 (Accession XP_171166.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254719.

[48225] LOC283119 (Accession XP_210895.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC283119 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283119, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283119 BINDING SITE, designated SEQ ID:18560, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48226] Another function of GAM5346 is therefore inhibition of LOC283119 (Accession XP_210895.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283119.

[48227] LOC283387 (Accession XP_211007.1) is another GAM5346 target gene, herein designated TARGET GENE.

LOC283387 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283387, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283387 BINDING SITE, designated SEQ ID:884, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48228] Another function of GAM5346 is therefore inhibition of LOC283387 (Accession XP_211007.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283387.

[48229] LOC283516 (Accession XP_211072.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC283516 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283516, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283516 BINDING SITE, designated SEQ ID:763, to the nucleotide sequence of

GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48230] Another function of GAM5346 is therefore inhibition of LOC283516 (Accession XP_211072.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283516.

[48231] LOC283521 (Accession XP_208705.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC283521 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283521, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283521 BINDING SITE, designated SEQ ID:12590, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48232] Another function of GAM5346 is therefore inhibition of LOC283521 (Accession XP_208705.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283521.

[48233] LOC283887 (Accession XP_211248.2) is another GAM5346 target gene, herein designated TARGET GENE. LOC283887 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283887, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283887 BINDING SITE, designated SEQ ID:6494, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48234] Another function of GAM5346 is therefore inhibition of LOC283887 (Accession XP_211248.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283887.

[48235] LOC283925 (Accession XP_208907.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC283925 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283925, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC283925 BINDING SITE, designated SEQ ID:1883, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48236] Another function of GAM5346 is therefore inhibition of LOC283925 (Accession XP_208907.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283925.

[48237] LOC284019 (Accession XP_211302.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC284019 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284019, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284019 BINDING SITE, designated SEQ ID:8913, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48238] Another function of GAM5346 is therefore inhibition of LOC284019 (Accession XP_211302.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284019.

[48239] LOC284135 (Accession XP_209032.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC284135 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284135 BINDING SITE, designated SEQ ID:1642, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48240] Another function of GAM5346 is therefore inhibition of LOC284135 (Accession XP_209032.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284135.

[48241] LOC284221 (Accession XP_211392.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC284221 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284221, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284221 BINDING SITE, designated SEQ ID:1752, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48242] Another function of GAM5346 is therefore inhibition of LOC284221 (Accession XP_211392.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284221.

[48243] LOC284262 (Accession XP_211402.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC284262 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284262 BINDING SITE, designated SEQ ID:1292, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48244] Another function of GAM5346 is therefore inhibition of

LOC284262 (Accession XP_211402.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284262.

[48245] LOC284506 (Accession XP_211498.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC284506 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284506, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284506 BINDING SITE, designated SEQ ID:417, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48246] Another function of GAM5346 is therefore inhibition of LOC284506 (Accession XP_211498.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284506.

[48247] LOC284542 (Accession XP_209254.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC284542 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC284542, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284542 BINDING SITE, designated SEQ ID:15471, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48248] Another function of GAM5346 is therefore inhibition of LOC284542 (Accession XP_209254.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284542.

[48249] LOC284561 (Accession XP_211519.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC284561 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284561, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284561 BINDING SITE, designated SEQ ID:9611, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:319.

[48250] Another function of GAM5346 is therefore inhibition of LOC284561 (Accession XP_211519.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284561.

[48251] LOC284751 (Accession XP_211622.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC284751 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284751, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284751 BINDING SITE, designated SEQ ID:10156, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48252] Another function of GAM5346 is therefore inhibition of LOC284751 (Accession XP_211622.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284751.

[48253] LOC284796 (Accession XP_208248.1) is another

GAM5346 target gene, herein designated TARGET GENE. LOC284796 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284796, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284796 BINDING SITE, designated SEQ ID:16414, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48254] Another function of GAM5346 is therefore inhibition of LOC284796 (Accession XP_208248.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284796.

[48255] LOC284899 (Accession XP_211680.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC284899 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284899 BINDING SITE, desig-

nated SEQ ID:7326, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48256] Another function of GAM5346 is therefore inhibition of LOC284899 (Accession XP_211680.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284899.

[48257] LOC284925 (Accession XP_209414.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC284925 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284925, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284925 BINDING SITE, designated SEQ ID:15142, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48258] Another function of GAM5346 is therefore inhibition of LOC284925 (Accession XP_209414.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC284925.

[48259] LOC285192 (Accession XP_209508.3) is another GAM5346 target gene, herein designated TARGET GENE. LOC285192 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285192, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285192 BINDING SITE, designated SEQ ID:3929, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48260] Another function of GAM5346 is therefore inhibition of LOC285192 (Accession XP_209508.3) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285192.

[48261] LOC285535 (Accession XP_211930.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC285535 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285535, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285535 BINDING SITE, designated SEQ ID:5061, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48262] Another function of GAM5346 is therefore inhibition of LOC285535 (Accession XP_211930.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285535.

[48263] LOC285822 (Accession XP_209777.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC285822 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC285822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285822 BINDING SITE, designated SEQ ID:8268, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48264] Another function of GAM5346 is therefore inhibition of LOC285822 (Accession XP_209777.1) . Accordingly, utili-

ties of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285822.

[48265] LOC285857 (Accession XP_212054.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC285857 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC285857, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC285857 BINDING SITE, designated SEQ ID:1533, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48266] Another function of GAM5346 is therefore inhibition of LOC285857 (Accession XP_212054.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC285857.

[48267] LOC338558 (Accession XP_290465.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC338558 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC338558, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338558 BINDING SITE, designated SEQ ID:17259, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48268] Another function of GAM5346 is therefore inhibition of LOC338558 (Accession XP_290465.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338558.

[48269] LOC339232 (Accession XP_294874.2) is another GAM5346 target gene, herein designated TARGET GENE. LOC339232 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339232, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339232 BINDING SITE, designated SEQ ID:11810, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48270] Another function of GAM5346 is therefore inhibition of LOC339232 (Accession XP_294874.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339232.

[48271] LOC339829 (Accession XP_291028.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC339829 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC339829, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339829 BINDING SITE, designated SEQ ID:6647, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48272] Another function of GAM5346 is therefore inhibition of LOC339829 (Accession XP_291028.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339829.

[48273] LOC340074 (Accession XP_295148.1) is another GAM5346 target gene, herein designated TARGET GENE.

LOC340074 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340074, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340074 BINDING SITE, designated SEQ ID:15029, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48274] Another function of GAM5346 is therefore inhibition of LOC340074 (Accession XP_295148.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340074.

[48275] LOC340113 (Accession XP_295157.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC340113 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC340113, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340113 BINDING SITE, designated SEQ ID:16181, to the nucleotide sequence of

GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48276] Another function of GAM5346 is therefore inhibition of LOC340113 (Accession XP_295157.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340113.

[48277] LOC343699 (Accession XP_293153.2) is another GAM5346 target gene, herein designated TARGET GENE. LOC343699 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC343699, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC343699 BINDING SITE, designated SEQ ID:11126, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48278] Another function of GAM5346 is therefore inhibition of LOC343699 (Accession XP_293153.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC343699.

[48279] LOC346178 (Accession XP_294100.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC346178 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC346178, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC346178 BINDING SITE, designated SEQ ID:11727, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48280] Another function of GAM5346 is therefore inhibition of LOC346178 (Accession XP_294100.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC346178.

[48281] LOC347926 (Accession XP_302628.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC347926 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC347926, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC347926 BINDING SITE, designated SEQ ID:17961, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48282] Another function of GAM5346 is therefore inhibition of LOC347926 (Accession XP_302628.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC347926.

[48283] LOC348174 (Accession XP_300648.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC348174 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348174, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348174 BINDING SITE, designated SEQ ID:1883, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48284] Another function of GAM5346 is therefore inhibition of LOC348174 (Accession XP_300648.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC348174.

[48285] LOC348798 (Accession XP_300845.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC348798 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348798, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348798 BINDING SITE, designated SEQ ID:10026, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48286] Another function of GAM5346 is therefore inhibition of LOC348798 (Accession XP_300845.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348798.

[48287] LOC349288 (Accession XP_300476.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC349288 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC349288, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC349288 BINDING SITE, designated SEQ ID:6413, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48288] Another function of GAM5346 is therefore inhibition of LOC349288 (Accession XP_300476.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC349288.

[48289] LOC93273 (Accession XP_050184.1) is another GAM5346 target gene, herein designated TARGET GENE. LOC93273 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC93273, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC93273 BINDING SITE, designated SEQ ID:4336, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48290] Another function of GAM5346 is therefore inhibition of LOC93273 (Accession XP_050184.1) . Accordingly, utili-

ties of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93273.

[48291] MAGEC3 (Accession NP_803251.1) is another GAM5346 target gene, herein designated TARGET GENE. MAGEC3 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MAGEC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAGEC3 BINDING SITE, designated SEQ ID:17747, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48292] Another function of GAM5346 is therefore inhibition of MAGEC3 (Accession NP_803251.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGEC3.

[48293] Mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (MAP3K7IP2, Accession NP_055908.1) is another GAM5346 target gene, herein designated TARGET GENE. MAP3K7IP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts

of mRNA encoded by MAP3K7IP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAP3K7IP2 BINDING SITE, designated SEQ ID:1518, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48294] Another function of GAM5346 is therefore inhibition of Mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (MAP3K7IP2, Accession NP_055908.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K7IP2.

[48295] Mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (MAP3K7IP2, Accession NP_663317.1) is another GAM5346 target gene, herein designated TARGET GENE. MAP3K7IP2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MAP3K7IP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MAP3K7IP2 BINDING SITE, designated SEQ ID:1518, to the nucleotide

sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48296] Another function of GAM5346 is therefore inhibition of Mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (MAP3K7IP2, Accession NP_663317.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K7IP2.

[48297] Mcm6 minichromosome maintenance deficient 6 (mis5 homolog, s. pombe) (s. cerevisiae) (MCM6, Accession NP_005906.2) is another GAM5346 target gene, herein designated TARGET GENE. MCM6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MCM6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MCM6 BINDING SITE, designated SEQ ID:7000, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48298] Another function of GAM5346 is therefore inhibition of Mcm6 minichromosome maintenance deficient 6 (mis5 homolog, s. pombe) (s. cerevisiae) (MCM6, Accession

NP_005906.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCM6.

[48299] Methyl cpg binding protein 2 (rett syndrome) (MECP2, Accession NP_004983.1) is another GAM5346 target gene, herein designated TARGET GENE. MECP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MECP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MECP2 BINDING SITE, designated SEQ ID:17727, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48300] Another function of GAM5346 is therefore inhibition of Methyl cpg binding protein 2 (rett syndrome) (MECP2, Accession NP_004983.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MECP2.

[48301] MGC13198 (Accession NP_116079.1) is another GAM5346 target gene, herein designated TARGET GENE. MGC13198 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC13198, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC13198 BINDING SITE, designated SEQ ID:14308, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48302] Another function of GAM5346 is therefore inhibition of MGC13198 (Accession NP_116079.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13198.

[48303] MGC16385 (Accession NP_659476.1) is another GAM5346 target gene, herein designated TARGET GENE. MGC16385 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC16385, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC16385 BINDING SITE, designated SEQ ID:14308, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48304] Another function of GAM5346 is therefore inhibition of MGC16385 (Accession NP_659476.1) . Accordingly, utili-

ties of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16385.

[48305] MGC34761 (Accession NP_775890.1) is another GAM5346 target gene, herein designated TARGET GENE. MGC34761 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC34761, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34761 BINDING SITE, designated SEQ ID:1883, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48306] Another function of GAM5346 is therefore inhibition of MGC34761 (Accession NP_775890.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34761.

[48307] MGC45726 (Accession NP_689777.1) is another GAM5346 target gene, herein designated TARGET GENE. MGC45726 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC45726, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC45726 BINDING SITE, designated SEQ ID:10845, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48308] Another function of GAM5346 is therefore inhibition of MGC45726 (Accession NP_689777.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC45726.

[48309] MGC5528 (Accession NP_076999.1) is another GAM5346 target gene, herein designated TARGET GENE. MGC5528 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC5528, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC5528 BINDING SITE, designated SEQ ID:600, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48310] Another function of GAM5346 is therefore inhibition of MGC5528 (Accession NP_076999.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MGC5528.

[48311] MI-ER1 (Accession NP_065999.1) is another GAM5346 target gene, herein designated TARGET GENE. MI-ER1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MI-ER1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MI-ER1 BINDING SITE, designated SEQ ID:3518, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48312] Another function of GAM5346 is therefore inhibition of MI-ER1 (Accession NP_065999.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MI-ER1.

[48313] Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, calla, cd10) (MME, Accession NP_009219.1) is another GAM5346 target gene, herein designated TARGET GENE. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MME BINDING SITE, designated SEQ ID:4799, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48314] Another function of GAM5346 is therefore inhibition of Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, calla, cd10) (MME, Accession NP_009219.1), a gene which is thermolysin- like specificity. and therefore is associated with Acute lymphocytic leukemia. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of Acute lymphocytic leukemia, and of other diseases and clinical conditions associated with MME.

[48315] The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, calla, cd10) (MME, Accession NP_009220.1) is another GAM5346 target gene, herein designated TARGET GENE. MME BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MME BINDING SITE, designated SEQ ID:4799, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48316] Another function of GAM5346 is therefore inhibition of Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, calla, cd10) (MME, Accession NP_009220.1), a gene which is thermolysin- like specificity. and therefore is associated with Acute lymphocytic leukemia. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of Acute lymphocytic leukemia, and of other diseases and clinical conditions associated with MME.

[48317] The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, calla, cd10) (MME, Accession NP_009218.1) is another GAM5346 target gene, herein designated TARGET GENE. MME BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MME BINDING SITE, designated SEQ ID:4799, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48318] Another function of GAM5346 is therefore inhibition of Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, calla, cd10) (MME, Accession NP_009218.1), a gene which is thermolysin- like specificity. and therefore is associated with Acute lymphocytic leukemia. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of Acute lymphocytic leukemia, and of other diseases and clinical conditions associated with MME.

[48319] The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, calla, cd10) (MME, Accession NP_000893.1) is another GAM5346 target gene, herein designated TARGET GENE. MME BINDING SITE is a

target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by MME, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MME BINDING SITE, designated SEQ ID:4799, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48320] Another function of GAM5346 is therefore inhibition of Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, calla, cd10) (MME, Accession NP_000893.1), a gene which is thermolysin- like specificity. and therefore is associated with Acute lymphocytic leukemia. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of Acute lymphocytic leukemia, and of other diseases and clinical conditions associated with MME.

[48321] The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Myogenic factor 5 (MYF5, Accession NP_005584.1) is another GAM5346 target gene, herein designated TARGET GENE. MYF5 BINDING SITE is a target

binding site found in the 3` untranslated region of mRNA encoded by MYF5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MYF5 BINDING SITE, designated SEQ ID:4931, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48322] Another function of GAM5346 is therefore inhibition of Myogenic factor 5 (MYF5, Accession NP_005584.1), a gene which is involved in muscle differentiation and induces fibroblasts to differentiate into myoblasts. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYF5.

[48323] The function of MYF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM1906.1.Notch homolog 2 (drosophila) (NOTCH2, Accession NP_077719.2) is another GAM5346 target gene, herein designated TARGET GENE. NOTCH2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NOTCH2, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NOTCH2 BINDING SITE, designated SEQ ID:5941, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48324] Another function of GAM5346 is therefore inhibition of Notch homolog 2 (drosophila) (NOTCH2, Accession NP_077719.2), a gene which is moderately similar to a region of murine Notch1 and contains an ankyrin repeat. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOTCH2.

[48325] The function of NOTCH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.NSE1 (Accession NP_660158.1) is another GAM5346 target gene, herein designated TARGET GENE. NSE1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by NSE1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of NSE1 BINDING SITE, designated SEQ ID:7984, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48326] Another function of GAM5346 is therefore inhibition of NSE1 (Accession NP_660158.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NSE1.

[48327] NYD-SP14 (Accession NP_114162.1) is another GAM5346 target gene, herein designated TARGET GENE. NYD-SP14 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by NYD-SP14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NYD-SP14 BINDING SITE, designated SEQ ID:17669, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48328] Another function of GAM5346 is therefore inhibition of NYD-SP14 (Accession NP_114162.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NYD-SP14.

[48329] Orthodenticle homolog 3 (drosophila) (OTX3, Accession NP_757379.1) is another GAM5346 target gene, herein designated TARGET GENE. OTX3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OTX3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OTX3 BINDING SITE, designated SEQ ID:7260, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48330] Another function of GAM5346 is therefore inhibition of Orthodenticle homolog 3 (drosophila) (OTX3, Accession NP_757379.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OTX3.

[48331] Orthodenticle homolog 3 (drosophila) (OTX3, Accession NP_671725.1) is another GAM5346 target gene, herein designated TARGET GENE. OTX3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by OTX3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the

complementarity of the nucleotide sequences of OTX3 BINDING SITE, designated SEQ ID:7260, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48332] Another function of GAM5346 is therefore inhibition of Orthodenticle homolog 3 (drosophila) (OTX3, Accession NP_671725.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OTX3.

[48333] Pantothenate kinase 2 (hallervorden-spatz syndrome) (PANK2, Accession NP_705903.1) is another GAM5346 target gene, herein designated TARGET GENE. PANK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PANK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PANK2 BINDING SITE, designated SEQ ID:15989, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48334] Another function of GAM5346 is therefore inhibition of Pantothenate kinase 2 (hallervorden-spatz syndrome)

(PANK2, Accession NP_705903.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PANK2.

[48335] Proteasome (prosome, macropain) 26s subunit, non-atpase, 8 (PSMD8, Accession NP_002803.1) is another GAM5346 target gene, herein designated TARGET GENE. PSMD8 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PSMD8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PSMD8 BINDING SITE, designated SEQ ID:19154, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48336] Another function of GAM5346 is therefore inhibition of Proteasome (prosome, macropain) 26s subunit, non-atpase, 8 (PSMD8, Accession NP_002803.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSMD8.

[48337] Polypyrimidine tract binding protein 1 (PTBP1, Accession NP_002810.1) is another GAM5346 target gene, herein designated TARGET GENE. PTBP1 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTBP1 BINDING SITE, designated SEQ ID:18181, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48338] Another function of GAM5346 is therefore inhibition of Polypyrimidine tract binding protein 1 (PTBP1, Accession NP_002810.1), a gene which is required for pre- mRNA splicing, and acts via the protein degradation ubiquitin-proteasome pathway. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTBP1.

[48339] The function of PTBP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.1.Polypyrimidine tract binding protein 1 (PTBP1, Accession NP_114367.1) is another GAM5346 target gene, herein designated TARGET GENE. PTBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by

PTBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTBP1 BINDING SITE, designated SEQ ID:18181, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48340] Another function of GAM5346 is therefore inhibition of Polypyrimidine tract binding protein 1 (PTBP1, Accession NP_114367.1), a gene which is required for pre- mRNA splicing, and acts via the protein degradation ubiquitin-proteasome pathway. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTBP1.

[48341] The function of PTBP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.1.Polypyrimidine tract binding protein 1 (PTBP1, Accession NP_114368.1) is another GAM5346 target gene, herein designated TARGET GENE. PTBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTBP1, corresponding to a target binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTBP1 BINDING SITE, designated SEQ ID:18181, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48342] Another function of GAM5346 is therefore inhibition of Polypyrimidine tract binding protein 1 (PTBP1, Accession NP_114368.1), a gene which is required for pre- mRNA splicing, and acts via the protein degradation ubiquitin-proteasome pathway. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTBP1.

[48343] The function of PTBP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.1.Polypyrimidine tract binding protein 1 (PTBP1, Accession NP_787041.1) is another GAM5346 target gene, herein designated TARGET GENE. PTBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by PTBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTBP1 BINDING SITE, designated SEQ ID:18181, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48344] Another function of GAM5346 is therefore inhibition of Polypyrimidine tract binding protein 1 (PTBP1, Accession NP_787041.1), a gene which is required for pre- mRNA splicing, and acts via the protein degradation ubiquitin-proteasome pathway. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTBP1.

[48345] The function of PTBP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM354.1.Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1) is another GAM5346 target gene, herein designated TARGET GENE. PTGIS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTGIS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PTGIS BIND-

ING SITE, designated SEQ ID:9392, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48346] Another function of GAM5346 is therefore inhibition of Prostaglandin i2 (prostacyclin) synthase (PTGIS, Accession NP_000952.1), a gene which catalyzes the isomerization of prostaglandin h2 to prostacyclin (= prostaglandin i2). Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGIS.

[48347] The function of PTGIS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.SH3YL1 (Accession NP_056492.1) is another GAM5346 target gene, herein designated TARGET GENE. SH3YL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SH3YL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SH3YL1 BINDING SITE, designated SEQ ID:16719, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48348] Another function of GAM5346 is therefore inhibition of SH3YL1 (Accession NP_056492.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3YL1.

[48349] Signal-regulatory protein beta 2 (SIRPB2, Accession NP_061026.1) is another GAM5346 target gene, herein designated TARGET GENE. SIRPB2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SIRPB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIRPB2 BINDING SITE, designated SEQ ID:17134, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48350] Another function of GAM5346 is therefore inhibition of Signal-regulatory protein beta 2 (SIRPB2, Accession NP_061026.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIRPB2.

[48351] Signal-regulatory protein beta 2 (SIRPB2, Accession NP_543006.1) is another GAM5346 target gene, herein designated TARGET GENE. SIRPB2 BINDING SITE is a target

binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by SIRPB2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SIRPB2 BINDING SITE, designated SEQ ID:17134, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48352] Another function of GAM5346 is therefore inhibition of Signal-regulatory protein beta 2 (SIRPB2, Accession NP_543006.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIRPB2.

[48353] Telomeric repeat binding factor 2 (TERF2, Accession NP_005643.1) is another GAM5346 target gene, herein designated TARGET GENE. TERF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TERF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TERF2 BINDING SITE, designated SEQ ID:2418, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ

ID:319.

[48354] Another function of GAM5346 is therefore inhibition of Telomeric repeat binding factor 2 (TERF2, Accession NP_005643.1), a gene which plays a key role in the protective activity of telomeres. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF2.

[48355] The function of TERF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM133.2.TRAD (Accession NP_008995.1) is another GAM5346 target gene, herein designated TARGET GENE. TRAD BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRAD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRAD BINDING SITE, designated SEQ ID:2049, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48356] Another function of GAM5346 is therefore inhibition of TRAD (Accession NP_008995.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with TRAD.

[48357] Ubiquitin specific protease 24 (USP24, Accession XP_165973.3) is another GAM5346 target gene, herein designated TARGET GENE. USP24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by USP24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of USP24 BINDING SITE, designated SEQ ID:17338, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48358] Another function of GAM5346 is therefore inhibition of Ubiquitin specific protease 24 (USP24, Accession XP_165973.3) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP24.

[48359] Zinc finger protein 254 (ZNF254, Accession NP_004867.1) is another GAM5346 target gene, herein designated TARGET GENE. ZNF254 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF254, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF254 BINDING SITE, designated SEQ ID:9378, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48360] Another function of GAM5346 is therefore inhibition of Zinc finger protein 254 (ZNF254, Accession NP_004867.1) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF254.

[48361] Zinc finger protein 255 (ZNF255, Accession NP_005765.1) is another GAM5346 target gene, herein designated TARGET GENE. ZNF255 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZNF255, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF255 BINDING SITE, designated SEQ ID:2601, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48362] Another function of GAM5346 is therefore inhibition of Zinc finger protein 255 (ZNF255, Accession NP_005765.1)

. Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF255.

[48363] ZNF431 (Accession XP_086098.2) is another GAM5346 target gene, herein designated TARGET GENE. ZNF431 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF431, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF431 BINDING SITE, designated SEQ ID:9162, to the nucleotide sequence of GAM5346 RNA, herein designated GAM RNA, also designated SEQ ID:319.

[48364] Another function of GAM5346 is therefore inhibition of ZNF431 (Accession XP_086098.2) . Accordingly, utilities of GAM5346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF431.

[48365]

[48366] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 5385 (GAM5385), which modulates expression of respective target genes thereof, the function and utility of which tar-

get genes is known in the art.

[48367] GAM5385 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM5385 was detected is described hereinabove with reference to Figs. 8-15.

[48368] GAM5385 gene, herein designated GAM GENE, and GAM5385 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[48369] GAM5385 gene encodes a GAM5385 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM5385 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM5385 precursor RNA is designated SEQ ID:22, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:22 is located at position 35621433 relative to chromosome 3.

[48370] GAM5385 precursor RNA folds onto itself, forming GAM5385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence

of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[48371] GAM5385 precursor RNA folds onto itself, forming GAM5385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[48372] Nucleotide sequence of GAM5385 precursor RNA, designated SEQ-ID: 22, and a schematic representation of a predicted secondary folding of GAM5385 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[48373] An enzyme complex designated DICER COMPLEX, `dices` the GAM5385 folded precursor RNA into GAM5385 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: A) nucleotide sequence of GAM5385 RNA is designated SEQ ID:218, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[48374] GAM5385 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM5385 target RNA, herein designated GAM TARGET RNA. GAM5385 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[48375] GAM5385 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM5385 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM5385 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated

that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM5385 RNA may have a different number of target binding sites in untranslated regions of a GAM5385 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[48376] The complementary binding of GAM5385 RNA, herein designated GAM RNA, to target binding sites on GAM5385 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM5385 target RNA into GAM5385 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[48377] It is appreciated that GAM5385 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM5385 target genes. The mRNA of each one of this plurality of GAM5385 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM5385 RNA, herein designated GAM RNA, and which when bound by

GAM5385 RNA causes inhibition of translation of respective one or more GAM5385 target proteins.

[48378] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM5385 gene, herein designated GAM GENE, on one or more GAM5385 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[48379] It is appreciated that specific functions and accordingly utilities of GAM5385 correlate with, and may be deduced from, the identity of the target genes which GAM5385 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[48380]

[48381]

[48382] Actin binding lim protein 1 (ABLIM1, Accession NP_006710.2) is a GAM5385 target gene, herein designated TARGET GENE. ABLIM1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABLIM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABLIM1 BINDING SITE, designated SEQ ID:16103, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48383] A function of GAM5385 is therefore inhibition of Actin binding lim protein 1 (ABLIM1, Accession NP_006710.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABLIM1.

[48384] Actin binding lim protein 1 (ABLIM1, Accession NP_006711.2) is another GAM5385 target gene, herein designated TARGET GENE. ABLIM1 BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by ABLIM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABLIM1 BINDING SITE, designated SEQ ID:16103, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48385] Another function of GAM5385 is therefore inhibition of Actin binding lim protein 1 (ABLIM1, Accession NP_006711.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABLIM1.

[48386] Actin binding lim protein 1 (ABLIM1, Accession NP_002304.2) is another GAM5385 target gene, herein designated TARGET GENE. ABLIM1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ABLIM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABLIM1 BINDING SITE, designated SEQ ID:16103, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48387] Another function of GAM5385 is therefore inhibition of Actin binding lim protein 1 (ABLIM1, Accession NP_002304.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABLIM1.

[48388] Acetyl-coenzyme a acyltransferase 2 (mitochondrial 3-oxoacyl-coenzyme a thiolase) (ACAA2, Accession NP_006102.1) is another GAM5385 target gene, herein designated TARGET GENE. ACAA2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ACAA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ACAA2 BINDING SITE, designated SEQ ID:10451, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48389] Another function of GAM5385 is therefore inhibition of Acetyl-coenzyme a acyltransferase 2 (mitochondrial 3-oxoacyl-coenzyme a thiolase) (ACAA2, Accession NP_006102.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACAA2.

[48390] AD-020 (Accession NP_064526.1) is another GAM5385 target gene, herein designated TARGET GENE. AD-020 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AD-020, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AD-020 BINDING SITE, designated SEQ ID:16382, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48391] Another function of GAM5385 is therefore inhibition of AD-020 (Accession NP_064526.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AD-020.

[48392] Arachidonate 15-lipoxygenase, second type (ALOX15B, Accession NP_001132.1) is another GAM5385 target gene, herein designated TARGET GENE. ALOX15B BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALOX15B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALOX15B

BINDING SITE, designated SEQ ID:5527, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48393] Another function of GAM5385 is therefore inhibition of Arachidonate 15-lipoxygenase, second type (ALOX15B, Accession NP_001132.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALOX15B.

[48394] Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_542117.1) is another GAM5385 target gene, herein designated TARGET GENE. AP1GBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1GBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1GBP1 BINDING SITE, designated SEQ ID:14123, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48395] Another function of GAM5385 is therefore inhibition of Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_542117.1) . Accordingly, utilities of GAM5385 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1GBP1.

[48396] Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_009178.2) is another GAM5385 target gene, herein designated TARGET GENE. AP1GBP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1GBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1GBP1 BINDING SITE, designated SEQ ID:14123, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48397] Another function of GAM5385 is therefore inhibition of Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_009178.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1GBP1.

[48398] Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_542118.1) is another GAM5385 target gene, herein designated TARGET GENE. AP1GBP1 BINDING SITE is a target binding site found in the 3` untranslated re-

gion of multiple transcripts of mRNA encoded by AP1GBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1GBP1 BINDING SITE, designated SEQ ID:14123, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48399] Another function of GAM5385 is therefore inhibition of Ap1 gamma subunit binding protein 1 (AP1GBP1, Accession NP_542118.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1GBP1.

[48400] Aprataxin (APTX, Accession NP_060162.1) is another GAM5385 target gene, herein designated TARGET GENE. APTX BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by APTX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated SEQ ID:9973, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ

ID:218.

[48401] Another function of GAM5385 is therefore inhibition of Aprataxin (APTX, Accession NP_060162.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APTX.

[48402] Aprataxin (APTX, Accession NP_778241.1) is another GAM5385 target gene, herein designated TARGET GENE. APTX BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by APTX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated SEQ ID:9973, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48403] Another function of GAM5385 is therefore inhibition of Aprataxin (APTX, Accession NP_778241.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APTX.

[48404] Ras homolog gene family, member e (ARHE, Accession

NP_005159.1) is another GAM5385 target gene, herein designated TARGET GENE. ARHE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHE BINDING SITE, designated SEQ ID:5435, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48405] Another function of GAM5385 is therefore inhibition of Ras homolog gene family, member e (ARHE, Accession NP_005159.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHE.

[48406] Rho guanine nucleotide exchange factor (gef) 4 (ARHGEF4, Accession NP_056135.2) is another GAM5385 target gene, herein designated TARGET GENE. ARHGEF4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ARHGEF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of ARHGEF4 BINDING SITE, designated SEQ ID:15522, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48407] Another function of GAM5385 is therefore inhibition of Rho guanine nucleotide exchange factor (gef) 4 (ARHGEF4, Accession NP_056135.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF4.

[48408] Rho guanine nucleotide exchange factor (gef) 4 (ARHGEF4, Accession NP_127462.1) is another GAM5385 target gene, herein designated TARGET GENE. ARHGEF4 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ARHGEF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGEF4 BINDING SITE, designated SEQ ID:15522, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48409] Another function of GAM5385 is therefore inhibition of Rho guanine nucleotide exchange factor (gef) 4 (ARHGEF4,

Accession NP_127462.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF4.

[48410] ARL8 (Accession NP_848930.1) is another GAM5385 target gene, herein designated TARGET GENE. ARL8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ARL8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARL8 BINDING SITE, designated SEQ ID:13890, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48411] Another function of GAM5385 is therefore inhibition of ARL8 (Accession NP_848930.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARL8.

[48412] ARL8 (Accession XP_167671.1) is another GAM5385 target gene, herein designated TARGET GENE. ARL8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ARL8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of ARL8 BINDING SITE, designated SEQ ID:13890, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48413] Another function of GAM5385 is therefore inhibition of ARL8 (Accession XP_167671.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARL8.

[48414] Attractin (ATRN, Accession NP_647537.1) is another GAM5385 target gene, herein designated TARGET GENE. ATRN BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by ATRN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATRN BINDING SITE, designated SEQ ID:14810, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48415] Another function of GAM5385 is therefore inhibition of Attractin (ATRN, Accession NP_647537.1), a gene which is involved in the initial immune cell clustering during inflammatory response. Accordingly, utilities of GAM5385

include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATRN.

[48416] The function of ATRN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Barren homolog (drosophila) (BRRN1, Accession NP_056156.2) is another GAM5385 target gene, herein designated TARGET GENE. BRRN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BRRN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BRRN1 BINDING SITE, designated SEQ ID:8848, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48417] Another function of GAM5385 is therefore inhibition of Barren homolog (drosophila) (BRRN1, Accession NP_056156.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRRN1.

[48418] Chromosome 20 open reading frame 158 (C20orf158, Accession NP_689515.1) is another GAM5385 target gene,

herein designated TARGET GENE. C20orf158 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf158, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf158 BINDING SITE, designated SEQ ID:1219, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48419] Another function of GAM5385 is therefore inhibition of Chromosome 20 open reading frame 158 (C20orf158, Accession NP_689515.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf158.

[48420] Chromosome 20 open reading frame 174 (C20orf174, Accession XP_066058.2) is another GAM5385 target gene, herein designated TARGET GENE. C20orf174 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C20orf174, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf174 BINDING SITE, designated SEQ ID:13482, to the nucleotide

sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48421] Another function of GAM5385 is therefore inhibition of Chromosome 20 open reading frame 174 (C20orf174, Accession XP_066058.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf174.

[48422] Chromosome 21 open reading frame 93 (C21orf93, Accession NP_660162.1) is another GAM5385 target gene, herein designated TARGET GENE. C21orf93 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C21orf93, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C21orf93 BINDING SITE, designated SEQ ID:4794, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48423] Another function of GAM5385 is therefore inhibition of Chromosome 21 open reading frame 93 (C21orf93, Accession NP_660162.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf93.

[48424] Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) is another GAM5385 target gene, herein designated TARGET GENE. CEACAM8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CEACAM8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CEACAM8 BINDING SITE, designated SEQ ID:3579, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48425] Another function of GAM5385 is therefore inhibition of Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEACAM8.

[48426] CG012 (Accession XP_096710.1) is another GAM5385 target gene, herein designated TARGET GENE. CG012 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CG012, corresponding to a target binding site such as BINDING SITE I, BINDING

SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CG012 BINDING SITE, designated SEQ ID:19634, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48427] Another function of GAM5385 is therefore inhibition of CG012 (Accession XP_096710.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CG012.

[48428] Cytokine inducible sh2-containing protein (CISH, Accession NP_659508.1) is another GAM5385 target gene, herein designated TARGET GENE. CISH BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CISH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CISH BINDING SITE, designated SEQ ID:2516, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48429] Another function of GAM5385 is therefore inhibition of Cytokine inducible sh2-containing protein (CISH, Accession NP_659508.1), a gene which intervenes in the nega-

tive regulation of cytokines. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CISH.

[48430] The function of CISH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Cytokine inducible sh2-containing protein (CISH, Accession NP_037456.4) is another GAM5385 target gene, herein designated TARGET GENE. CISH BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CISH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CISH BINDING SITE, designated SEQ ID:2516, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48431] Another function of GAM5385 is therefore inhibition of Cytokine inducible sh2-containing protein (CISH, Accession NP_037456.4), a gene which intervenes in the negative regulation of cytokines. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CISH.

[48432] The function of CISH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.CLONE24945 (Accession NP_056498.1) is another GAM5385 target gene, herein designated TARGET GENE. CLONE24945 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLONE24945, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLONE24945 BINDING SITE, designated SEQ ID:19577, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48433] Another function of GAM5385 is therefore inhibition of CLONE24945 (Accession NP_056498.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLONE24945.

[48434] Colony stimulating factor 1 (macrophage) (CSF1, Accession NP_757350.1) is another GAM5385 target gene, herein designated TARGET GENE. CSF1 BINDING SITE is a target binding site found in the 3` untranslated region of

multiple transcripts of mRNA encoded by CSF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSF1 BINDING SITE, designated SEQ ID:13158, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48435] Another function of GAM5385 is therefore inhibition of Colony stimulating factor 1 (macrophage) (CSF1, Accession NP_757350.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSF1.

[48436] Colony stimulating factor 1 (macrophage) (CSF1, Accession NP_000748.3) is another GAM5385 target gene, herein designated TARGET GENE. CSF1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CSF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CSF1 BINDING SITE, designated SEQ ID:13158, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48437] Another function of GAM5385 is therefore inhibition of Colony stimulating factor 1 (macrophage) (CSF1, Accession NP_000748.3) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSF1.

[48438] D-aspartate oxidase (DDO, Accession NP_004023.1) is another GAM5385 target gene, herein designated TARGET GENE. DDO BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DDO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDO BINDING SITE, designated SEQ ID:6520, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48439] Another function of GAM5385 is therefore inhibition of D-aspartate oxidase (DDO, Accession NP_004023.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDO.

[48440] D-aspartate oxidase (DDO, Accession NP_003640.1) is another GAM5385 target gene, herein designated TARGET

GENE. DDO BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DDO, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DDO BINDING SITE, designated SEQ ID:6520, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48441] Another function of GAM5385 is therefore inhibition of D-aspartate oxidase (DDO, Accession NP_003640.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDO.

[48442] Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1) is another GAM5385 target gene, herein designated TARGET GENE. DISC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DISC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DISC1 BINDING SITE, designated SEQ ID:8442, to the nucleotide sequence of GAM5385

RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48443] Another function of GAM5385 is therefore inhibition of Disrupted in schizophrenia 1 (DISC1, Accession NP_061132.1), a gene which has globular N- terminal domain(s) and a helical C- terminal domain. and therefore may be associated with Schizophrenia . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of Schizophrenia ., and of other diseases and clinical conditions associated with DISC1.

[48444] The function of DISC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM116.1.DKFZP564D166 (Accession NP_056438.1) is another GAM5385 target gene, herein designated TARGET GENE. DKFZP564D166 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by DKFZP564D166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564D166 BINDING SITE, designated SEQ ID:775, to the nucleotide sequence of GAM5385 RNA, herein designated

GAM RNA, also designated SEQ ID:218.

[48445] Another function of GAM5385 is therefore inhibition of DKFZP564D166 (Accession NP_056438.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D166.

[48446] DKFZP586A0522 (Accession NP_054752.1) is another GAM5385 target gene, herein designated TARGET GENE. DKFZP586A0522 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586A0522, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586A0522 BINDING SITE, designated SEQ ID:12685, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48447] Another function of GAM5385 is therefore inhibition of DKFZP586A0522 (Accession NP_054752.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586A0522.

[48448] Dnaj (hsp40) homolog, subfamily c, member 5 (DNAJC5,

Accession XP_028966.2) is another GAM5385 target gene, herein designated TARGET GENE. DNAJC5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DNAJC5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DNAJC5 BINDING SITE, designated SEQ ID:5877, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48449] Another function of GAM5385 is therefore inhibition of Dnaj (hsp40) homolog, subfamily c, member 5 (DNAJC5, Accession XP_028966.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAJC5.

[48450] DOT1L (Accession NP_115871.1) is another GAM5385 target gene, herein designated TARGET GENE. DOT1L BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DOT1L, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DOT1L BINDING SITE, designated SEQ ID:13923, to the nucleotide

sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48451] Another function of GAM5385 is therefore inhibition of DOT1L (Accession NP_115871.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DOT1L.

[48452] Dual specificity phosphatase 16 (DUSP16, Accession XP_039106.1) is another GAM5385 target gene, herein designated TARGET GENE. DUSP16 BINDING SITE1 and DUSP16 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DUSP16, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DUSP16 BINDING SITE1 and DUSP16 BINDING SITE2, designated SEQ ID:19356 and SEQ ID:10606 respectively, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48453] Another function of GAM5385 is therefore inhibition of Dual specificity phosphatase 16 (DUSP16, Accession XP_039106.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP16.

[48454] Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 2 (DYRK2, Accession NP_003574.1) is another GAM5385 target gene, herein designated TARGET GENE. DYRK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DYRK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DYRK2 BINDING SITE, designated SEQ ID:19011, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48455] Another function of GAM5385 is therefore inhibition of Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 2 (DYRK2, Accession NP_003574.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DYRK2.

[48456] Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 2 (DYRK2, Accession NP_006473.1) is another GAM5385 target gene, herein designated TARGET GENE. DYRK2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA

encoded by DYRK2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DYRK2 BINDING SITE, designated SEQ ID:19011, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48457] Another function of GAM5385 is therefore inhibition of Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 2 (DYRK2, Accession NP_006473.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DYRK2.

[48458] Egf-like-domain, multiple 4 (EGFL4, Accession XP_290821.1) is another GAM5385 target gene, herein designated TARGET GENE. EGFL4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EGFL4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EGFL4 BINDING SITE, designated SEQ ID:14183, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ

ID:218.

[48459] Another function of GAM5385 is therefore inhibition of Egf-like-domain, multiple 4 (EGFL4, Accession XP_290821.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGFL4.

[48460] Erythrocyte membrane protein band 4.9 (dematin) (EPB49, Accession NP_001969.1) is another GAM5385 target gene, herein designated TARGET GENE. EPB49 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by EPB49, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EPB49 BINDING SITE, designated SEQ ID:11878, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48461] Another function of GAM5385 is therefore inhibition of Erythrocyte membrane protein band 4.9 (dematin) (EPB49, Accession NP_001969.1), a gene which is an actin-bundling protein. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPB49.

[48462] The function of EPB49 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.ERG-1 (Accession NP_071317.2) is another GAM5385 target gene, herein designated TARGET GENE. ERG-1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ERG-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ERG-1 BINDING SITE, designated SEQ ID:13141, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48463] Another function of GAM5385 is therefore inhibition of ERG-1 (Accession NP_071317.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERG-1.

[48464] Fibulin 1 (FBLN1, Accession NP_006478.1) is another GAM5385 target gene, herein designated TARGET GENE. FBLN1 BINDING SITE1 and FBLN1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FBLN1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE

II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBLN1 BINDING SITE1 and FBLN1 BINDING SITE2, designated SEQ ID:12051 and SEQ ID:16278 respectively, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48465] Another function of GAM5385 is therefore inhibition of Fibulin 1 (FBLN1, Accession NP_006478.1), a gene which secreted glycoprotein; has EGF- like repeats, similar to anaphylatoxins C3a, C4a, and C5a. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBLN1.

[48466] The function of FBLN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM179.1.Fc fragment of igg, high affinity ia, receptor for (cd64) (FCGR1A, Accession NP_000557.1) is another GAM5385 target gene, herein designated TARGET GENE. FCGR1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FCGR1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide se-

quences of FCGR1A BINDING SITE, designated SEQ ID:11092, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48467] Another function of GAM5385 is therefore inhibition of Fc fragment of igg, high affinity ia, receptor for (cd64) (FCGR1A, Accession NP_000557.1), a gene which binds to the fc region of immunoglobulins gamma. high affinity receptor. and therefore may be associated with Igg receptor i, phagocytic, familial deficiency of. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of Igg receptor i, phagocytic, familial deficiency of, and of other diseases and clinical conditions associated with FCGR1A.

[48468] The function of FCGR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM206.1.Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075599.1) is another GAM5385 target gene, herein designated TARGET GENE. FGFR1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by FGFR1, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE, designated SEQ ID:4651, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48469] Another function of GAM5385 is therefore inhibition of Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075599.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1.

[48470] Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075596.1) is another GAM5385 target gene, herein designated TARGET GENE. FGFR1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by FGFR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE, designated SEQ ID:4651, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48471] Another function of GAM5385 is therefore inhibition of Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075596.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1.

[48472] Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075593.1) is another GAM5385 target gene, herein designated TARGET GENE. FGFR1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by FGFR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE, designated SEQ ID:4651, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48473] Another function of GAM5385 is therefore inhibition of Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075593.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with FGFR1.

[48474] Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075595.1) is another GAM5385 target gene, herein designated TARGET GENE. FGFR1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by FGFR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE, designated SEQ ID:4651, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48475] Another function of GAM5385 is therefore inhibition of Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075595.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1.

[48476] Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_000595.1) is another GAM5385 target gene, herein designated TARGET GENE. FGFR1 BINDING SITE is a target

binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by FGFR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE, designated SEQ ID:4651, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48477] Another function of GAM5385 is therefore inhibition of Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_000595.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1.

[48478] Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_056934.2) is another GAM5385 target gene, herein designated TARGET GENE. FGFR1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by FGFR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR1

BINDING SITE, designated SEQ ID:4651, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48479] Another function of GAM5385 is therefore inhibition of Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_056934.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1.

[48480] Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075594.1) is another GAM5385 target gene, herein designated TARGET GENE. FGFR1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by FGFR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE, designated SEQ ID:4651, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48481] Another function of GAM5385 is therefore inhibition of Fibroblast growth factor receptor 1 (fms-related tyrosine

kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075594.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1.

[48482] Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075598.1) is another GAM5385 target gene, herein designated TARGET GENE. FGFR1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by FGFR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE, designated SEQ ID:4651, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48483] Another function of GAM5385 is therefore inhibition of Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075598.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1.

[48484] Fibroblast growth factor receptor 1 (fms-related tyrosine

kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075597.1) is another GAM5385 target gene, herein designated TARGET GENE. FGFR1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by FGFR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE, designated SEQ ID:4651, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48485] Another function of GAM5385 is therefore inhibition of Fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome) (FGFR1, Accession NP_075597.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1.

[48486] FLJ10420 (Accession NP_060560.1) is another GAM5385 target gene, herein designated TARGET GENE. FLJ10420 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10420, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ10420 BINDING SITE, designated SEQ ID:14824, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48487] Another function of GAM5385 is therefore inhibition of FLJ10420 (Accession NP_060560.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10420.

[48488] FLJ10706 (Accession NP_060656.1) is another GAM5385 target gene, herein designated TARGET GENE. FLJ10706 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10706, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10706 BINDING SITE, designated SEQ ID:11748, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48489] Another function of GAM5385 is therefore inhibition of FLJ10706 (Accession NP_060656.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ10706.

[48490] FLJ10916 (Accession NP_060741.1) is another GAM5385 target gene, herein designated TARGET GENE. FLJ10916 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10916, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10916 BINDING SITE, designated SEQ ID:13403, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48491] Another function of GAM5385 is therefore inhibition of FLJ10916 (Accession NP_060741.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10916.

[48492] FLJ11800 (Accession NP_079250.1) is another GAM5385 target gene, herein designated TARGET GENE. FLJ11800 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11800, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ11800 BINDING SITE, designated SEQ ID:1416, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48493] Another function of GAM5385 is therefore inhibition of FLJ11800 (Accession NP_079250.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11800.

[48494] FLJ20184 (Accession NP_060170.1) is another GAM5385 target gene, herein designated TARGET GENE. FLJ20184 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20184, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20184 BINDING SITE, designated SEQ ID:17813, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48495] Another function of GAM5385 is therefore inhibition of FLJ20184 (Accession NP_060170.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20184.

[48496] FLJ20464 (Accession NP_060304.1) is another GAM5385 target gene, herein designated TARGET GENE. FLJ20464 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20464, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20464 BINDING SITE, designated SEQ ID:17685, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48497] Another function of GAM5385 is therefore inhibition of FLJ20464 (Accession NP_060304.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20464.

[48498] FLJ22494 (Accession NP_079091.1) is another GAM5385 target gene, herein designated TARGET GENE. FLJ22494 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22494, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22494 BINDING SITE, designated SEQ ID:4622, to the

nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48499] Another function of GAM5385 is therefore inhibition of FLJ22494 (Accession NP_079091.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22494.

[48500] FLJ32112 (Accession NP_694580.1) is another GAM5385 target gene, herein designated TARGET GENE. FLJ32112 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32112, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32112 BINDING SITE, designated SEQ ID:10311, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48501] Another function of GAM5385 is therefore inhibition of FLJ32112 (Accession NP_694580.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32112.

[48502] FLJ32115 (Accession NP_689534.1) is another GAM5385

target gene, herein designated TARGET GENE. FLJ32115 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32115, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32115 BINDING SITE, designated SEQ ID:6946, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48503] Another function of GAM5385 is therefore inhibition of FLJ32115 (Accession NP_689534.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32115.

[48504] Ftsj homolog 2 (e. coli) (FTSJ2, Accession NP_803191.1) is another GAM5385 target gene, herein designated TARGET GENE. FTSJ2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FTSJ2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FTSJ2 BINDING SITE, designated SEQ ID:3879, to the nucleotide sequence of

GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48505] Another function of GAM5385 is therefore inhibition of Ftsj homolog 2 (e. coli) (FTSJ2, Accession NP_803191.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FTSJ2.

[48506] G2 (Accession XP_039515.8) is another GAM5385 target gene, herein designated TARGET GENE. G2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G2 BINDING SITE, designated SEQ ID:15665, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48507] Another function of GAM5385 is therefore inhibition of G2 (Accession XP_039515.8) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G2.

[48508] Glutamic pyruvate transaminase (alanine aminotransferase) 2 (GPT2, Accession NP_597700.1) is another

GAM5385 target gene, herein designated TARGET GENE. GPT2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GPT2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPT2 BINDING SITE, designated SEQ ID:12001, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48509] Another function of GAM5385 is therefore inhibition of Glutamic pyruvate transaminase (alanine aminotransferase) 2 (GPT2, Accession NP_597700.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPT2.

[48510] Glyoxylate reductase/hydroxypyruvate reductase (GRHPR, Accession NP_036335.1) is another GAM5385 target gene, herein designated TARGET GENE. GRHPR BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GRHPR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRHPR BINDING

SITE, designated SEQ ID:3593, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48511] Another function of GAM5385 is therefore inhibition of Glyoxylate reductase/hydroxypyruvate reductase (GRHPR, Accession NP_036335.1), a gene which has widespread tissue expression and has a role in metabolism. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRHPR.

[48512] The function of GRHPR has been established by previous studies. Cramer et al. (1999) and Rumsby and Cregeen (1999) independently identified a glyoxylate reductase/ hydroxypyruvate reductase (GRHPR; EC 1.1.1.79) cDNA clone from a human liver EST library. The GRHPR gene encodes a predicted 328- amino acid protein with a mass of 35,563 Da. By transient transfection of the cDNA clone into COS cells, Cramer et al. (1999) verified that GRHPR encodes an enzyme with hydroxypyruvate reductase, glyoxylate reductase, and D- glycerate dehydrogenase enzymatic activities. Database analysis of human ESTs revealed widespread tissue expression, indicating that the enzyme may have a role in metabolism. Cramer et al. (1999) de-

termined that the human GRHPR gene spans approximately 9 kb and is composed of 9 exons and 8 introns. In 2 pairs of sibs from 2 unrelated families with type II hyperoxaluria (OMIM Ref. No. 260000), Cramer et al. (1999) identified a 1- bp deletion in the GRHPR gene (103delG; 604296.0001) by SSCP analysis. All 4 patients were homozygous for the same mutation. Webster et al. (2000) identified 5 other mutations in patients with type II hyperoxaluria. Ten of 11 patients that they had genotyped were homozygous for 1 of the 6 known mutations. In the case of two- thirds of the patients, the parents were related. Genotyping also showed the possible presence of a founder effect for the 2 most common mutations: 103delG and arg99 to ter (604296.0002).

[48513]

[48514] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[48515] Cramer, S. D.; Ferree, P. M.; Lin, K.; Milliner, D. S.; Holmes, R. P. : The gene encoding hydroxypyruvate reductase (GRHPR) is mutated in patients with primary hyperoxaluria type II. Hum. Molec. Genet. 8: 2063- 2069, 1999. ; and

[48516] Webster, K. E.; Ferree, P. M.; Holmes, R. P.; Cramer, S. D. :

Identification of missense, nonsense, and deletion mutations in the GRHPR gene in patients with primary hyperoxaluria type.

[48517] Further studies establishing the function and utilities of GRHPR are found in John Hopkins OMIM database record ID 604296, and in cited publications listed in Table 5, which are hereby incorporated by reference.Glutamate receptor, ionotropic, delta 1 (GRID1, Accession XP_043613.8) is another GAM5385 target gene, herein designated TARGET GENE. GRID1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GRID1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GRID1 BINDING SITE, designated SEQ ID:9369, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48518] Another function of GAM5385 is therefore inhibition of Glutamate receptor, ionotropic, delta 1 (GRID1, Accession XP_043613.8) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRID1.

[48519] H-plk (Accession NP_056936.1) is another GAM5385 target gene, herein designated TARGET GENE. H-plk BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by H-plk, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H-plk BINDING SITE, designated SEQ ID:8719, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48520] Another function of GAM5385 is therefore inhibition of H-plk (Accession NP_056936.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H-plk.

[48521] HGC6.2 (Accession NP_055171.1) is another GAM5385 target gene, herein designated TARGET GENE. HGC6.2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HGC6.2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HGC6.2 BINDING SITE, designated SEQ ID:11193, to the nucleotide sequence of GAM5385 RNA, herein designated

GAM RNA, also designated SEQ ID:218.

[48522] Another function of GAM5385 is therefore inhibition of HGC6.2 (Accession NP_055171.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HGC6.2.

[48523] Hla-g histocompatibility antigen, class i, g (HLA-G, Accession NP_002118.1) is another GAM5385 target gene, herein designated TARGET GENE. HLA-G BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HLA-G, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HLA-G BINDING SITE, designated SEQ ID:17163, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48524] Another function of GAM5385 is therefore inhibition of Hla-g histocompatibility antigen, class i, g (HLA-G, Accession NP_002118.1), a gene which involved in the presentation of foreign antigens to the immune system. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with HLA-G.

[48525] The function of HLA-G and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM504.1.Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) is another GAM5385 target gene, herein designated TARGET GENE. IRF4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IRF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRF4 BINDING SITE, designated SEQ ID:2090, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48526] Another function of GAM5385 is therefore inhibition of Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRF4.

[48527] Integrin, alpha l (antigen cd11a (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL, Accession NP_002200.1) is another GAM5385 target gene,

herein designated TARGET GENE. ITGAL BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ITGAL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ITGAL BINDING SITE, designated SEQ ID:16142, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48528] Another function of GAM5385 is therefore inhibition of Integrin, alpha l (antigen cd11a (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL, Accession NP_002200.1), a gene which s a receptor for icam1, icam2, icam3 and icam4. it is involved in a variety of immune phenomena including leukocyte- endothelial cell interaction, cytotoxic t- cell mediated killing, and antibody dependent killing by granulocytes and monocytes. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAL.

[48529] The function of ITGAL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM148.1.KIAA0317 (Accession NP_055636.1) is another GAM5385 target gene, herein designated TARGET GENE. KIAA0317 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0317, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0317 BINDING SITE, designated SEQ ID:14991, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48530] Another function of GAM5385 is therefore inhibition of KIAA0317 (Accession NP_055636.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0317.

[48531] KIAA0352 (Accession NP_055645.1) is another GAM5385 target gene, herein designated TARGET GENE. KIAA0352 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0352, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA0352 BINDING SITE, designated SEQ ID:18577, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48532] Another function of GAM5385 is therefore inhibition of KIAA0352 (Accession NP_055645.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0352.

[48533] KIAA0514 (Accession NP_055511.1) is another GAM5385 target gene, herein designated TARGET GENE. KIAA0514 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0514, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0514 BINDING SITE, designated SEQ ID:1534, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48534] Another function of GAM5385 is therefore inhibition of KIAA0514 (Accession NP_055511.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0514.

[48535] KIAA0721 (Accession NP_067680.2) is another GAM5385 target gene, herein designated TARGET GENE. KIAA0721 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0721, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0721 BINDING SITE, designated SEQ ID:4456, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48536] Another function of GAM5385 is therefore inhibition of KIAA0721 (Accession NP_067680.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0721.

[48537] KIAA0876 (Accession XP_290852.1) is another GAM5385 target gene, herein designated TARGET GENE. KIAA0876 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0876, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0876 BINDING SITE, designated SEQ ID:10335, to the

nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48538] Another function of GAM5385 is therefore inhibition of KIAA0876 (Accession XP_290852.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0876.

[48539] KIAA0972 (Accession NP_055745.1) is another GAM5385 target gene, herein designated TARGET GENE. KIAA0972 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0972 BINDING SITE, designated SEQ ID:10280, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48540] Another function of GAM5385 is therefore inhibition of KIAA0972 (Accession NP_055745.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0972.

[48541] KIAA1754 (Accession NP_203755.1) is another GAM5385

target gene, herein designated TARGET GENE. KIAA1754 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1754, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1754 BINDING SITE, designated SEQ ID:14851, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48542] Another function of GAM5385 is therefore inhibition of KIAA1754 (Accession NP_203755.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1754.

[48543] KIAA1904 (Accession XP_056282.1) is another GAM5385 target gene, herein designated TARGET GENE. KIAA1904 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1904, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1904 BINDING SITE, designated SEQ ID:19375, to the nucleotide sequence of GAM5385 RNA, herein designated

GAM RNA, also designated SEQ ID:218.

[48544] Another function of GAM5385 is therefore inhibition of KIAA1904 (Accession XP_056282.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1904.

[48545] KIDINS220 (Accession XP_291015.1) is another GAM5385 target gene, herein designated TARGET GENE. KIDINS220 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIDINS220, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIDINS220 BINDING SITE, designated SEQ ID:2942, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48546] Another function of GAM5385 is therefore inhibition of KIDINS220 (Accession XP_291015.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIDINS220.

[48547] Lectin, galactoside-binding, soluble, 3 (galectin 3) (LGALS3, Accession NP_002297.1) is another GAM5385

target gene, herein designated TARGET GENE. LGALS3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LGALS3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LGALS3 BINDING SITE, designated SEQ ID:506, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48548] Another function of GAM5385 is therefore inhibition of Lectin, galactoside-binding, soluble, 3 (galectin 3) (LGALS3, Accession NP_002297.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGALS3.

[48549] Lim domain only 4 (LMO4, Accession NP_006760.1) is another GAM5385 target gene, herein designated TARGET GENE. LMO4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LMO4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LMO4 BINDING SITE, designated SEQ ID:3198,

to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48550] Another function of GAM5385 is therefore inhibition of Lim domain only 4 (LMO4, Accession NP_006760.1), a gene which promotes myogenic differentiation. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LMO4.

[48551] The function of LMO4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM467.2.LOC113612 (Accession XP_054492.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC113612 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC113612, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC113612 BINDING SITE, designated SEQ ID:821, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48552] Another function of GAM5385 is therefore inhibition of

LOC113612 (Accession XP_054492.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113612.

[48553] LOC126917 (Accession XP_059091.2) is another GAM5385 target gene, herein designated TARGET GENE. LOC126917 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC126917, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126917 BINDING SITE, designated SEQ ID:2569, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48554] Another function of GAM5385 is therefore inhibition of LOC126917 (Accession XP_059091.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126917.

[48555] LOC127262 (Accession XP_072073.5) is another GAM5385 target gene, herein designated TARGET GENE. LOC127262 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC127262, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC127262 BINDING SITE, designated SEQ ID:14394, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48556] Another function of GAM5385 is therefore inhibition of LOC127262 (Accession XP_072073.5) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127262.

[48557] LOC128239 (Accession XP_059223.4) is another GAM5385 target gene, herein designated TARGET GENE. LOC128239 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC128239, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC128239 BINDING SITE, designated SEQ ID:1443, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:218.

[48558] Another function of GAM5385 is therefore inhibition of LOC128239 (Accession XP_059223.4) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128239.

[48559] LOC130633 (Accession XP_059463.2) is another GAM5385 target gene, herein designated TARGET GENE. LOC130633 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC130633, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130633 BINDING SITE, designated SEQ ID:17789, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48560] Another function of GAM5385 is therefore inhibition of LOC130633 (Accession XP_059463.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130633.

[48561] LOC135521 (Accession XP_059776.1) is another

GAM5385 target gene, herein designated TARGET GENE. LOC135521 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135521, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135521 BINDING SITE, designated SEQ ID:18796, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48562] Another function of GAM5385 is therefore inhibition of LOC135521 (Accession XP_059776.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135521.

[48563] LOC143381 (Accession XP_084501.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC143381 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC143381, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143381 BINDING SITE, desig-

nated SEQ ID:9647, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48564] Another function of GAM5385 is therefore inhibition of LOC143381 (Accession XP_084501.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143381.

[48565] LOC144467 (Accession NP_612482.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC144467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144467 BINDING SITE, designated SEQ ID:16762, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48566] Another function of GAM5385 is therefore inhibition of LOC144467 (Accession NP_612482.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC144467.

[48567] LOC144678 (Accession XP_096656.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC144678 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144678, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144678 BINDING SITE, designated SEQ ID:18404, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48568] Another function of GAM5385 is therefore inhibition of LOC144678 (Accession XP_096656.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144678.

[48569] LOC145980 (Accession XP_096914.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC145980 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145980, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145980 BINDING SITE, designated SEQ ID:16415, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48570] Another function of GAM5385 is therefore inhibition of LOC145980 (Accession XP_096914.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145980.

[48571] LOC147808 (Accession XP_097313.2) is another GAM5385 target gene, herein designated TARGET GENE. LOC147808 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147808, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147808 BINDING SITE, designated SEQ ID:8092, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48572] Another function of GAM5385 is therefore inhibition of LOC147808 (Accession XP_097313.2) . Accordingly, utili-

ties of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147808.

[48573] LOC148418 (Accession XP_086188.6) is another GAM5385 target gene, herein designated TARGET GENE. LOC148418 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148418, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148418 BINDING SITE, designated SEQ ID:14739, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48574] Another function of GAM5385 is therefore inhibition of LOC148418 (Accession XP_086188.6) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148418.

[48575] LOC148823 (Accession NP_660321.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC148823 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC148823, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148823 BINDING SITE, designated SEQ ID:7024, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48576] Another function of GAM5385 is therefore inhibition of LOC148823 (Accession NP_660321.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148823.

[48577] LOC150527 (Accession XP_086942.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC150527 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150527, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150527 BINDING SITE, designated SEQ ID:2809, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48578] Another function of GAM5385 is therefore inhibition of LOC150527 (Accession XP_086942.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150527.

[48579] LOC152790 (Accession XP_098264.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC152790 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152790, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152790 BINDING SITE, designated SEQ ID:6839, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48580] Another function of GAM5385 is therefore inhibition of LOC152790 (Accession XP_098264.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152790.

[48581] LOC153146 (Accession XP_098319.1) is another GAM5385 target gene, herein designated TARGET GENE.

LOC153146 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC153146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153146 BINDING SITE, designated SEQ ID:7502, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48582] Another function of GAM5385 is therefore inhibition of LOC153146 (Accession XP_098319.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153146.

[48583] LOC158381 (Accession XP_048461.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC158381 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158381, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158381 BINDING SITE, designated SEQ ID:5669, to the nucleotide sequence of

GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48584] Another function of GAM5385 is therefore inhibition of LOC158381 (Accession XP_048461.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158381.

[48585] LOC200169 (Accession XP_211599.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC200169 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC200169, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200169 BINDING SITE, designated SEQ ID:5297, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48586] Another function of GAM5385 is therefore inhibition of LOC200169 (Accession XP_211599.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200169.

[48587] LOC202551 (Accession XP_011448.4) is another GAM5385 target gene, herein designated TARGET GENE. LOC202551 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC202551, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202551 BINDING SITE, designated SEQ ID:16316, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48588] Another function of GAM5385 is therefore inhibition of LOC202551 (Accession XP_011448.4) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202551.

[48589] LOC203249 (Accession XP_116805.2) is another GAM5385 target gene, herein designated TARGET GENE. LOC203249 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC203249, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC203249 BINDING SITE, designated SEQ ID:6033, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48590] Another function of GAM5385 is therefore inhibition of LOC203249 (Accession XP_116805.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203249.

[48591] LOC219690 (Accession XP_167572.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC219690 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC219690, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219690 BINDING SITE, designated SEQ ID:14755, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48592] Another function of GAM5385 is therefore inhibition of LOC219690 (Accession XP_167572.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC219690.

[48593] LOC255870 (Accession XP_170628.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC255870 BINDING SITE1 and LOC255870 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC255870, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC255870 BINDING SITE1 and LOC255870 BINDING SITE2, designated SEQ ID:17784 and SEQ ID:8949 respectively, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48594] Another function of GAM5385 is therefore inhibition of LOC255870 (Accession XP_170628.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255870.

[48595] LOC283167 (Accession XP_210921.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC283167 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC283167, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283167 BINDING SITE, designated SEQ ID:6144, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48596] Another function of GAM5385 is therefore inhibition of LOC283167 (Accession XP_210921.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283167.

[48597] LOC283293 (Accession XP_210962.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC283293 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283293 BINDING SITE, designated SEQ ID:4599, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48598] Another function of GAM5385 is therefore inhibition of LOC283293 (Accession XP_210962.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283293.

[48599] LOC283465 (Accession XP_208686.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC283465 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283465, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283465 BINDING SITE, designated SEQ ID:1830, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48600] Another function of GAM5385 is therefore inhibition of LOC283465 (Accession XP_208686.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283465.

[48601] LOC283484 (Accession XP_211053.1) is another GAM5385 target gene, herein designated TARGET GENE.

LOC283484 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283484, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283484 BINDING SITE, designated SEQ ID:3455, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48602] Another function of GAM5385 is therefore inhibition of LOC283484 (Accession XP_211053.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283484.

[48603] LOC283661 (Accession XP_208102.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC283661 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283661, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283661 BINDING SITE, designated SEQ ID:1336, to the nucleotide sequence of

GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48604] Another function of GAM5385 is therefore inhibition of LOC283661 (Accession XP_208102.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283661.

[48605] LOC284048 (Accession XP_208152.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC284048 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284048, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284048 BINDING SITE, designated SEQ ID:1416, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48606] Another function of GAM5385 is therefore inhibition of LOC284048 (Accession XP_208152.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284048.

[48607] LOC284101 (Accession XP_209019.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC284101 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284101 BINDING SITE, designated SEQ ID:6084, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48608] Another function of GAM5385 is therefore inhibition of LOC284101 (Accession XP_209019.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284101.

[48609] LOC284158 (Accession XP_209041.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC284158 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284158, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284158 BINDING SITE, designated SEQ ID:17928, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48610] Another function of GAM5385 is therefore inhibition of LOC284158 (Accession XP_209041.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284158.

[48611] LOC284263 (Accession XP_211400.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC284263 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284263, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284263 BINDING SITE, designated SEQ ID:10396, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48612] Another function of GAM5385 is therefore inhibition of LOC284263 (Accession XP_211400.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284263.

[48613] LOC284555 (Accession XP_211518.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC284555 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284555, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284555 BINDING SITE, designated SEQ ID:5552, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48614] Another function of GAM5385 is therefore inhibition of LOC284555 (Accession XP_211518.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284555.

[48615] LOC284737 (Accession XP_211612.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC284737 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284737, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284737 BINDING SITE, designated SEQ ID:6441, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48616] Another function of GAM5385 is therefore inhibition of LOC284737 (Accession XP_211612.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284737.

[48617] LOC284759 (Accession XP_209363.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC284759 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284759, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284759 BINDING SITE, designated SEQ ID:10735, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48618] Another function of GAM5385 is therefore inhibition of

LOC284759 (Accession XP_209363.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284759.

[48619] LOC284898 (Accession XP_211685.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC284898 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284898, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284898 BINDING SITE, designated SEQ ID:13073, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48620] Another function of GAM5385 is therefore inhibition of LOC284898 (Accession XP_211685.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284898.

[48621] LOC338825 (Accession XP_294723.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC338825 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC338825, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC338825 BINDING SITE, designated SEQ ID:12400, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48622] Another function of GAM5385 is therefore inhibition of LOC338825 (Accession XP_294723.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC338825.

[48623] LOC339216 (Accession XP_290762.2) is another GAM5385 target gene, herein designated TARGET GENE. LOC339216 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339216, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339216 BINDING SITE, designated SEQ ID:6084, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:218.

[48624] Another function of GAM5385 is therefore inhibition of LOC339216 (Accession XP_290762.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339216.

[48625] LOC339282 (Accession XP_294900.2) is another GAM5385 target gene, herein designated TARGET GENE. LOC339282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC339282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC339282 BINDING SITE, designated SEQ ID:6084, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48626] Another function of GAM5385 is therefore inhibition of LOC339282 (Accession XP_294900.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC339282.

[48627] LOC340178 (Accession XP_295181.1) is another

GAM5385 target gene, herein designated TARGET GENE. LOC340178 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC340178, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC340178 BINDING SITE, designated SEQ ID:3108, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48628] Another function of GAM5385 is therefore inhibition of LOC340178 (Accession XP_295181.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC340178.

[48629] LOC341036 (Accession XP_295967.2) is another GAM5385 target gene, herein designated TARGET GENE. LOC341036 BINDING SITE1 and LOC341036 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC341036, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC341036

BINDING SITE1 and LOC341036 BINDING SITE2, designated SEQ ID:2544 and SEQ ID:4152 respectively, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48630] Another function of GAM5385 is therefore inhibition of LOC341036 (Accession XP_295967.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC341036.

[48631] LOC341640 (Accession XP_292193.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC341640 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC341640, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC341640 BINDING SITE, designated SEQ ID:8348, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48632] Another function of GAM5385 is therefore inhibition of LOC341640 (Accession XP_292193.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC341640.

[48633] LOC343265 (Accession XP_291488.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC343265 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC343265, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC343265 BINDING SITE, designated SEQ ID:5095, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48634] Another function of GAM5385 is therefore inhibition of LOC343265 (Accession XP_291488.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC343265.

[48635] LOC348529 (Accession XP_302813.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC348529 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC348529, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348529 BINDING SITE, designated SEQ ID:18900, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48636] Another function of GAM5385 is therefore inhibition of LOC348529 (Accession XP_302813.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348529.

[48637] LOC348734 (Accession XP_211718.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC348734 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC348734, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC348734 BINDING SITE, designated SEQ ID:2809, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48638] Another function of GAM5385 is therefore inhibition of

LOC348734 (Accession XP_211718.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC348734.

[48639] LOC351012 (Accession XP_304617.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC351012 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC351012, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC351012 BINDING SITE, designated SEQ ID:18415, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48640] Another function of GAM5385 is therefore inhibition of LOC351012 (Accession XP_304617.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC351012.

[48641] LOC352051 (Accession XP_305365.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC352051 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC352051, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC352051 BINDING SITE, designated SEQ ID:1884, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48642] Another function of GAM5385 is therefore inhibition of LOC352051 (Accession XP_305365.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC352051.

[48643] LOC55908 (Accession NP_061157.2) is another GAM5385 target gene, herein designated TARGET GENE. LOC55908 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC55908, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC55908 BINDING SITE, designated SEQ ID:6986, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48644] Another function of GAM5385 is therefore inhibition of LOC55908 (Accession NP_061157.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC55908.

[48645] LOC90719 (Accession XP_033704.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC90719 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC90719, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC90719 BINDING SITE, designated SEQ ID:17254, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48646] Another function of GAM5385 is therefore inhibition of LOC90719 (Accession XP_033704.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90719.

[48647] LOC91947 (Accession XP_041721.2) is another GAM5385 target gene, herein designated TARGET GENE. LOC91947 BINDING SITE1 and LOC91947 BINDING SITE2 are target

binding sites found in untranslated regions of mRNA encoded by LOC91947, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC91947 BINDING SITE1 and LOC91947 BINDING SITE2, designated SEQ ID:7137 and SEQ ID:13311 respectively, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48648] Another function of GAM5385 is therefore inhibition of LOC91947 (Accession XP_041721.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91947.

[48649] LOC96597 (Accession XP_039922.1) is another GAM5385 target gene, herein designated TARGET GENE. LOC96597 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC96597, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC96597 BINDING SITE, designated SEQ ID:9062, to the nucleotide sequence of GAM5385 RNA, herein designated

GAM RNA, also designated SEQ ID:218.

[48650] Another function of GAM5385 is therefore inhibition of LOC96597 (Accession XP_039922.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC96597.

[48651] Loss of heterozygosity, 11, chromosomal region 2, gene a (LOH11CR2A, Accession NP_055437.1) is another GAM5385 target gene, herein designated TARGET GENE. LOH11CR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOH11CR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOH11CR2A BINDING SITE, designated SEQ ID:14358, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48652] Another function of GAM5385 is therefore inhibition of Loss of heterozygosity, 11, chromosomal region 2, gene a (LOH11CR2A, Accession NP_055437.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOH11CR2A.

[48653] Mads box transcription enhancer factor 2, polypeptide b (myocyte enhancer factor 2b) (MEF2B, Accession NP_005910.1) is another GAM5385 target gene, herein designated TARGET GENE. MEF2B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MEF2B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MEF2B BINDING SITE, designated SEQ ID:13472, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48654] Another function of GAM5385 is therefore inhibition of Mads box transcription enhancer factor 2, polypeptide b (myocyte enhancer factor 2b) (MEF2B, Accession NP_005910.1), a gene which binds a consensus sequence that regulates transcription. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEF2B.

[48655] The function of MEF2B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to GAM31.1.MGC11061 (Accession NP_115688.1) is another GAM5385 target gene, herein designated TARGET GENE. MGC11061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by MGC11061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC11061 BINDING SITE, designated SEQ ID:10669, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48656] Another function of GAM5385 is therefore inhibition of MGC11061 (Accession NP_115688.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11061.

[48657] MGC18216 (Accession NP_689665.1) is another GAM5385 target gene, herein designated TARGET GENE. MGC18216 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC18216, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

MGC18216 BINDING SITE, designated SEQ ID:8207, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48658] Another function of GAM5385 is therefore inhibition of MGC18216 (Accession NP_689665.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC18216.

[48659] MGC34713 (Accession NP_775936.1) is another GAM5385 target gene, herein designated TARGET GENE. MGC34713 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by MGC34713, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of MGC34713 BINDING SITE, designated SEQ ID:10134, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48660] Another function of GAM5385 is therefore inhibition of MGC34713 (Accession NP_775936.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC34713.

[48661] Nuclear receptor subfamily 2, group f, member 2 (NR2F2, Accession NP_066285.1) is another GAM5385 target gene, herein designated TARGET GENE. NR2F2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NR2F2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NR2F2 BINDING SITE, designated SEQ ID:11718, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48662] Another function of GAM5385 is therefore inhibition of Nuclear receptor subfamily 2, group f, member 2 (NR2F2, Accession NP_066285.1), a gene which is the regulation of the apolipoprotein ai gene transcription. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR2F2.

[48663] The function of NR2F2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM386.1.NY-REN-25 (Accession XP_027116.6) is another GAM5385 target gene, herein designated TARGET

GENE. NY-REN-25 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NY-REN-25, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NY-REN-25 BINDING SITE, designated SEQ ID:974, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48664] Another function of GAM5385 is therefore inhibition of NY-REN-25 (Accession XP_027116.6) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NY-REN-25.

[48665] NY-REN-41 (Accession NP_542385.1) is another GAM5385 target gene, herein designated TARGET GENE. NY-REN-41 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by NY-REN-41, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of NY-REN-41 BINDING SITE, designated SEQ ID:4623, to the nucleotide sequence of

GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48666] Another function of GAM5385 is therefore inhibition of NY-REN-41 (Accession NP_542385.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NY-REN-41.

[48667] Oxysterol binding protein-like 10 (OSBPL10, Accession NP_060254.2) is another GAM5385 target gene, herein designated TARGET GENE. OSBPL10 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by OSBPL10, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of OSBPL10 BINDING SITE, designated SEQ ID:2040, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48668] Another function of GAM5385 is therefore inhibition of Oxysterol binding protein-like 10 (OSBPL10, Accession NP_060254.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL10.

[48669] Paired box gene 7 (PAX7, Accession NP_002575.1) is another GAM5385 target gene, herein designated TARGET GENE. PAX7 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PAX7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PAX7 BINDING SITE, designated SEQ ID:16405, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48670] Another function of GAM5385 is therefore inhibition of Paired box gene 7 (PAX7, Accession NP_002575.1), a gene which involves in myogenesis and therefore is associated with Rhabdomyosarcoma- 2. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of Rhabdomyosarcoma- 2, and of other diseases and clinical conditions associated with PAX7.

[48671] The function of PAX7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Paired box gene 7 (PAX7, Accession NP_039236.1) is another GAM5385 target gene, herein

designated TARGET GENE. PAX7 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by PAX7, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PAX7 BINDING SITE, designated SEQ ID:16405, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48672] Another function of GAM5385 is therefore inhibition of Paired box gene 7 (PAX7, Accession NP_039236.1), a gene which involves in myogenesis and therefore is associated with Rhabdomyosarcoma- 2. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of Rhabdomyosarcoma- 2, and of other diseases and clinical conditions associated with PAX7.

[48673] The function of PAX7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM94.1.Phosphoglycerate dehydrogenase (PHGDH, Accession NP_006614.2) is another GAM5385 target gene, herein designated TARGET GENE. PHGDH BINDING SITE is a target binding site found in the 3` untranslated region

of mRNA encoded by PHGDH, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PHGDH BINDING SITE, designated SEQ ID:14461, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48674] Another function of GAM5385 is therefore inhibition of Phosphoglycerate dehydrogenase (PHGDH, Accession NP_006614.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHGDH.

[48675] Pleckstrin homology domain containing, family a (phosphoinositide binding specific) member 4 (PLEKHA4, Accession NP_065955.1) is another GAM5385 target gene, herein designated TARGET GENE. PLEKHA4 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by PLEKHA4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PLEKHA4 BINDING SITE, designated SEQ ID:6785, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA,

also designated SEQ ID:218.

[48676] Another function of GAM5385 is therefore inhibition of Pleckstrin homology domain containing, family a (phosphoinositide binding specific) member 4 (PLEKHA4, Accession NP_065955.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLEKHA4.

[48677] Pro-melanin-concentrating hormone-like 1 (PMCHL1, Accession NP_114093.1) is another GAM5385 target gene, herein designated TARGET GENE. PMCHL1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMCHL1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMCHL1 BINDING SITE, designated SEQ ID:10293, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48678] Another function of GAM5385 is therefore inhibition of Pro-melanin-concentrating hormone-like 1 (PMCHL1, Accession NP_114093.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMCHL1.

[48679] Pro-melanin-concentrating hormone-like 2 (PMCHL2, Accession NP_114094.1) is another GAM5385 target gene, herein designated TARGET GENE. PMCHL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PMCHL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of PMCHL2 BINDING SITE, designated SEQ ID:3755, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48680] Another function of GAM5385 is therefore inhibition of Pro-melanin-concentrating hormone-like 2 (PMCHL2, Accession NP_114094.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMCHL2.

[48681] Protein tyrosine phosphatase, non-receptor type 9 (PTPN9, Accession NP_002824.1) is another GAM5385 target gene, herein designated TARGET GENE. PTPN9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by PTPN9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of PTPN9 BINDING SITE, designated SEQ ID:13095, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48682] Another function of GAM5385 is therefore inhibition of Protein tyrosine phosphatase, non-receptor type 9 (PTPN9, Accession NP_002824.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN9.

[48683] Ras, dexamethasone-induced 1 (RASD1, Accession NP_057168.1) is another GAM5385 target gene, herein designated TARGET GENE. RASD1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RASD1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RASD1 BINDING SITE, designated SEQ ID:9061, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48684] Another function of GAM5385 is therefore inhibition of Ras, dexamethasone-induced 1 (RASD1, Accession NP_057168.1), a gene which is a novel physiologic NO ef-

fector. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASD1.

[48685] The function of RASD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM842.2.Regulator of g-protein signalling 2, 24kda (RGS2, Accession NP_002914.1) is another GAM5385 target gene, herein designated TARGET GENE. RGS2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RGS2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RGS2 BINDING SITE, designated SEQ ID:19470, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48686] Another function of GAM5385 is therefore inhibition of Regulator of g-protein signalling 2, 24kda (RGS2, Accession NP_002914.1), a gene which inhibits signal transduction by increasing the gtpase activity of g protein thereby driving them into their inactive gdp- bound form. and therefore may be associated with Rieger syndrome. Ac-

cordingly, utilities of GAM5385 include diagnosis, prevention and treatment of Rieger syndrome, and of other diseases and clinical conditions associated with RGS2.

[48687] The function of RGS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM374.2.Regulator of g-protein signalling 6 (RGS6, Accession NP_004287.3) is another GAM5385 target gene, herein designated TARGET GENE. RGS6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RGS6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RGS6 BINDING SITE, designated SEQ ID:19481, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48688] Another function of GAM5385 is therefore inhibition of Regulator of g-protein signalling 6 (RGS6, Accession NP_004287.3) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS6.

[48689] RIS (Accession NP_057647.1) is another GAM5385 target

gene, herein designated TARGET GENE. RIS BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by RIS, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of RIS BINDING SITE, designated SEQ ID:6292, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48690] Another function of GAM5385 is therefore inhibition of RIS (Accession NP_057647.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIS.

[48691] S100A15 (Accession NP_789793.1) is another GAM5385 target gene, herein designated TARGET GENE. S100A15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by S100A15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of S100A15 BINDING SITE, designated SEQ ID:5854, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48692] Another function of GAM5385 is therefore inhibition of S100A15 (Accession NP_789793.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with S100A15.

[48693] Secretory carrier membrane protein 3 (SCAMP3, Accession NP_443069.1) is another GAM5385 target gene, herein designated TARGET GENE. SCAMP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SCAMP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAMP3 BINDING SITE, designated SEQ ID:12492, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48694] Another function of GAM5385 is therefore inhibition of Secretory carrier membrane protein 3 (SCAMP3, Accession NP_443069.1), a gene which functions in post- golgi recycling pathways and acts as a recycling carrier to the cell surface. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP3.

[48695] The function of SCAMP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM610.1.Secretory carrier membrane protein 3 (SCAMP3, Accession NP_005689.2) is another GAM5385 target gene, herein designated TARGET GENE. SCAMP3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by SCAMP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SCAMP3 BINDING SITE, designated SEQ ID:12492, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48696] Another function of GAM5385 is therefore inhibition of Secretory carrier membrane protein 3 (SCAMP3, Accession NP_005689.2), a gene which functions in post- golgi recycling pathways and acts as a recycling carrier to the cell surface. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP3.

[48697] The function of SCAMP3 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM610.1.SEC61A1 (Accession NP_037468.1) is another GAM5385 target gene, herein designated TARGET GENE. SEC61A1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEC61A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEC61A1 BINDING SITE, designated SEQ ID:9945, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48698] Another function of GAM5385 is therefore inhibition of SEC61A1 (Accession NP_037468.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC61A1.

[48699] Selenoprotein x, 1 (SEPX1, Accession NP_057416.1) is another GAM5385 target gene, herein designated TARGET GENE. SEPX1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SEPX1, corresponding to a target binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SEPX1 BINDING SITE, designated SEQ ID:5607, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48700] Another function of GAM5385 is therefore inhibition of Selenoprotein x, 1 (SEPX1, Accession NP_057416.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEPX1.

[48701] Serine (or cysteine) proteinase inhibitor, clade i (neuroserpin), member 2 (SERPINI2, Accession NP_006208.1) is another GAM5385 target gene, herein designated TARGET GENE. SERPINI2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SERPINI2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SERPINI2 BINDING SITE, designated SEQ ID:7346, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48702] Another function of GAM5385 is therefore inhibition of

Serine (or cysteine) proteinase inhibitor, clade i (neuroserpin), member 2 (SERPINI2, Accession NP_006208.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINI2.

[48703] Solute carrier family 21 (organic anion transporter), member 14 (SLC21A14, Accession NP_059131.1) is another GAM5385 target gene, herein designated TARGET GENE. SLC21A14 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by SLC21A14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC21A14 BINDING SITE, designated SEQ ID:6067, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48704] Another function of GAM5385 is therefore inhibition of Solute carrier family 21 (organic anion transporter), member 14 (SLC21A14, Accession NP_059131.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC21A14.

[48705] SLC37A3 (Accession NP_115671.1) is another GAM5385 target gene, herein designated TARGET GENE. SLC37A3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by SLC37A3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of SLC37A3 BINDING SITE, designated SEQ ID:18317, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48706] Another function of GAM5385 is therefore inhibition of SLC37A3 (Accession NP_115671.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC37A3.

[48707] Tbc1 domain family, member 4 (TBC1D4, Accession NP_055647.1) is another GAM5385 target gene, herein designated TARGET GENE. TBC1D4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TBC1D4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TBC1D4 BINDING

SITE, designated SEQ ID:20148, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48708] Another function of GAM5385 is therefore inhibition of Tbc1 domain family, member 4 (TBC1D4, Accession NP_055647.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBC1D4.

[48709] TLP19 (Accession NP_056997.1) is another GAM5385 target gene, herein designated TARGET GENE. TLP19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TLP19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TLP19 BINDING SITE, designated SEQ ID:12082, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48710] Another function of GAM5385 is therefore inhibition of TLP19 (Accession NP_056997.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLP19.

[48711] TRIM43 (Accession NP_620155.1) is another GAM5385

target gene, herein designated TARGET GENE. TRIM43 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by TRIM43, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TRIM43 BINDING SITE, designated SEQ ID:17789, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48712] Another function of GAM5385 is therefore inhibition of TRIM43 (Accession NP_620155.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM43.

[48713] Tubby homolog (mouse) (TUB, Accession NP_003311.2) is another GAM5385 target gene, herein designated TARGET GENE. TUB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TUB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUB BINDING SITE, designated SEQ ID:20119, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:218.

[48714] Another function of GAM5385 is therefore inhibition of Tubby homolog (mouse) (TUB, Accession NP_003311.2) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUB.

[48715] Tubby homolog (mouse) (TUB, Accession NP_813977.1) is another GAM5385 target gene, herein designated TARGET GENE. TUB BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by TUB, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of TUB BINDING SITE, designated SEQ ID:20119, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48716] Another function of GAM5385 is therefore inhibition of Tubby homolog (mouse) (TUB, Accession NP_813977.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUB.

[48717] Ubiquitin-like 3 (UBL3, Accession NP_009037.1) is an-

other GAM5385 target gene, herein designated TARGET GENE. UBL3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by UBL3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UBL3 BINDING SITE, designated SEQ ID:17405, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48718] Another function of GAM5385 is therefore inhibition of Ubiquitin-like 3 (UBL3, Accession NP_009037.1), a gene which appears to have a diverse range of cellular functions. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBL3.

[48719] The function of UBL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM240.1.UPF2 (Accession NP_542166.1) is another GAM5385 target gene, herein designated TARGET GENE. UPF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UPF2, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UPF2 BINDING SITE, designated SEQ ID:17322, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48720] Another function of GAM5385 is therefore inhibition of UPF2 (Accession NP_542166.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UPF2.

[48721] UPF2 (Accession NP_056357.1) is another GAM5385 target gene, herein designated TARGET GENE. UPF2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by UPF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of UPF2 BINDING SITE, designated SEQ ID:17322, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48722] Another function of GAM5385 is therefore inhibition of UPF2 (Accession NP_056357.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with UPF2.

[48723] Ubiquitin specific protease 15 (USP15, Accession NP_006304.1) is another GAM5385 target gene, herein designated TARGET GENE. USP15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by USP15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of USP15 BINDING SITE, designated SEQ ID:7999, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48724] Another function of GAM5385 is therefore inhibition of Ubiquitin specific protease 15 (USP15, Accession NP_006304.1) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP15.

[48725] XT3 (Accession NP_071800.1) is another GAM5385 target gene, herein designated TARGET GENE. XT3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by XT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of XT3 BINDING SITE, designated SEQ ID:9855, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48726] Another function of GAM5385 is therefore inhibition of XT3 (Accession NP_071800.1), a gene which is a Kidney-specific orphan transporter. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XT3.

[48727] The function of XT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.XT3 (Accession NP_064593.1) is another GAM5385 target gene, herein designated TARGET GENE. XT3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by XT3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of XT3 BINDING SITE, designated SEQ ID:9855, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48728] Another function of GAM5385 is therefore inhibition of

XT3 (Accession NP_064593.1), a gene which is a Kidney-specific orphan transporter. Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XT3.

[48729] The function of XT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.1.Zinc finger protein 272 (ZNF272, Accession XP_030227.3) is another GAM5385 target gene, herein designated TARGET GENE. ZNF272 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ZNF272, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF272 BINDING SITE, designated SEQ ID:19140, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48730] Another function of GAM5385 is therefore inhibition of Zinc finger protein 272 (ZNF272, Accession XP_030227.3) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF272.

[48731] ZNF463 (Accession NP_061025.3) is another GAM5385 target gene, herein designated TARGET GENE. ZNF463 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ZNF463, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ZNF463 BINDING SITE, designated SEQ ID:1764, to the nucleotide sequence of GAM5385 RNA, herein designated GAM RNA, also designated SEQ ID:218.

[48732] Another function of GAM5385 is therefore inhibition of ZNF463 (Accession NP_061025.3) . Accordingly, utilities of GAM5385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF463.

[48733]

[48734] Fig. 8 further provides a conceptual description of a novel bioinformatically detected of the present invention, referred to here as Genomic Address Messenger 7052 (GAM7052), which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[48735] GAM7052 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM7052 was detected is described hereinabove with reference to Figs. 8-15.

[48736] GAM7052 gene, herein designated GAM GENE, and GAM7052 target gene, herein designated TARGET GENE, are human genes contained in the human genome.

[48737] GAM7052 gene encodes a GAM7052 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM7052 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM7052 precursor RNA is designated SEQ ID:10, and is provided hereinbelow with reference to the sequence listing part.

[48738] GAM7052 precursor RNA folds onto itself, forming GAM7052 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[48739] GAM7052 precursor RNA folds onto itself, forming GAM7052 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial reverse-complementary sequence of the nucleotide sequence of the second half thereof.

[48740] Nucleotide sequence of GAM7052 precursor RNA, designated SEQ-ID: 10, and a schematic representation of a predicted secondary folding of GAM7052 folded precursor RNA are further described with reference to Table 2, hereby incorporated by reference.

[48741] An enzyme complex designated DICER COMPLEX, `dices` the GAM7052 folded precursor RNA into GAM7052 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (GAM Prediction Accuracy Group: C) nucleotide sequence of GAM7052 RNA is desig-

nated SEQ ID:296, and is provided hereinbelow with references to the sequence listing part and Table 3, hereby incorporated by reference.

[48742] GAM7052 target gene, herein designated TARGET GENE, encodes a corresponding messenger RNA, GAM7052 target RNA, herein designated GAM TARGET RNA. GAM7052 target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[48743] GAM7052 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM7052 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM7052 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM7052 RNA may have a different number of target

binding sites in untranslated regions of a GAM7052 target RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3`UTR region, this is meant as an example only these target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[48744] The complementary binding of GAM7052 RNA, herein designated GAM RNA, to target binding sites on GAM7052 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM7052 target RNA into GAM7052 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[48745] It is appreciated that GAM7052 target gene, herein designated TARGET GENE, in fact represents a plurality of GAM7052 target genes. The mRNA of each one of this plurality of GAM7052 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM7052 RNA, herein designated GAM RNA, and which when bound by GAM7052 RNA causes inhibition of translation of respective one or more GAM7052 target proteins.

[48746] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM7052 gene, herein designated GAM GENE, on one or more GAM7052 target genes, herein collectively designated TARGET GENE, is common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[48747] It is appreciated that specific functions and accordingly utilities of GAM7052 correlate with, and may be deduced from, the identity of the target genes which GAM7052 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[48748]

[48749]

[48750] (Accession NP_054819.1) is a GAM7052 target gene, herein designated TARGET GENE. BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BINDING SITE, designated SEQ ID:17475, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48751] A function of GAM7052 is therefore inhibition of (Accession NP_054819.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with .

[48752] Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2) is another GAM7052 target gene, herein designated TARGET GENE. A1BG BINDING SITE1 through A1BG BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by A1BG, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A1BG BINDING SITE1 through A1BG BINDING SITE3, designated SEQ

ID:4738, SEQ ID:19222 and SEQ ID:1831 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48753] Another function of GAM7052 is therefore inhibition of Alpha-1-b glycoprotein (A1BG, Accession NP_570602.2), a gene which a plasma protein of unknown function. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A1BG.

[48754] The function of A1BG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.A2BP1 (Accession NP_665898.1) is another GAM7052 target gene, herein designated TARGET GENE. A2BP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by A2BP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A2BP1 BINDING SITE, designated SEQ ID:11694, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48755] Another function of GAM7052 is therefore inhibition of A2BP1 (Accession NP_665898.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A2BP1.

[48756] A2BP1 (Accession NP_665900.1) is another GAM7052 target gene, herein designated TARGET GENE. A2BP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by A2BP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A2BP1 BINDING SITE, designated SEQ ID:11694, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48757] Another function of GAM7052 is therefore inhibition of A2BP1 (Accession NP_665900.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A2BP1.

[48758] A2BP1 (Accession NP_665899.1) is another GAM7052 target gene, herein designated TARGET GENE. A2BP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by

A2BP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A2BP1 BINDING SITE, designated SEQ ID:11694, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48759] Another function of GAM7052 is therefore inhibition of A2BP1 (Accession NP_665899.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A2BP1.

[48760] A2BP1 (Accession NP_061193.2) is another GAM7052 target gene, herein designated TARGET GENE. A2BP1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by A2BP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of A2BP1 BINDING SITE, designated SEQ ID:11694, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48761] Another function of GAM7052 is therefore inhibition of

A2BP1 (Accession NP_061193.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A2BP1.

[48762] Atp-binding cassette, sub-family b (mdr/tap), member 5 (ABCB5, Accession XP_291215.1) is another GAM7052 target gene, herein designated TARGET GENE. ABCB5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ABCB5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABCB5 BINDING SITE, designated SEQ ID:15685, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48763] Another function of GAM7052 is therefore inhibition of Atp-binding cassette, sub-family b (mdr/tap), member 5 (ABCB5, Accession XP_291215.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCB5.

[48764] Ankyrin repeat and btb (poz) domain containing 1 (ABTB1, Accession NP_115937.1) is another GAM7052 target gene, herein designated TARGET GENE. ABTB1 BINDING SITE is a target binding site found in the 5` untranslated region of

multiple transcripts of mRNA encoded by ABTB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ABTB1 BINDING SITE, designated SEQ ID:17325, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48765] Another function of GAM7052 is therefore inhibition of Ankyrin repeat and btb (poz) domain containing 1 (ABTB1, Accession NP_115937.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABTB1.

[48766] A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4 (ADAMTS4, Accession NP_005090.1) is another GAM7052 target gene, herein designated TARGET GENE. ADAMTS4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ADAMTS4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADAMTS4 BINDING SITE, designated SEQ ID:6395, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA,

also designated SEQ ID:296.

[48767] Another function of GAM7052 is therefore inhibition of A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4 (ADAMTS4, Accession NP_005090.1), a gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAMTS4.

[48768] The function of ADAMTS4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Adenylate cyclase 6 (ADCY6, Accession NP_056085.1) is another GAM7052 target gene, herein designated TARGET GENE. ADCY6 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by ADCY6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ADCY6 BINDING SITE, designated SEQ ID:20175, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48769] Another function of GAM7052 is therefore inhibition of Adenylate cyclase 6 (ADCY6, Accession NP_056085.1), a gene which this a membrane- bound, ca(2+)- inhibitable adenylyl cyclase (by similarity). Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY6.

[48770] The function of ADCY6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM67.2.Atp/gtp binding protein 1 (AGTPBP1, Accession NP_056054.1) is another GAM7052 target gene, herein designated TARGET GENE. AGTPBP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AGTPBP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AGTPBP1 BINDING SITE, designated SEQ ID:16343, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48771] Another function of GAM7052 is therefore inhibition of Atp/gtp binding protein 1 (AGTPBP1, Accession NP_056054.1), a gene which a zinc carboxypeptidase .

Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGTPBP1.

[48772] The function of AGTPBP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM480.1.Aldo-keto reductase family 1, member a1 (aldehyde reductase) (AKR1A1, Accession NP_006057.1) is another GAM7052 target gene, herein designated TARGET GENE. AKR1A1 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by AKR1A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AKR1A1 BINDING SITE, designated SEQ ID:18726, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48773] Another function of GAM7052 is therefore inhibition of Aldo-keto reductase family 1, member a1 (aldehyde reductase) (AKR1A1, Accession NP_006057.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with AKR1A1.

[48774] Aldehyde dehydrogenase 1 family, member b1 (ALDH1B1, Accession NP_000683.3) is another GAM7052 target gene, herein designated TARGET GENE. ALDH1B1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALDH1B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALDH1B1 BINDING SITE, designated SEQ ID:17862, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48775] Another function of GAM7052 is therefore inhibition of Aldehyde dehydrogenase 1 family, member b1 (ALDH1B1, Accession NP_000683.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH1B1.

[48776] Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1) is another GAM7052 target gene, herein designated TARGET GENE. ALOX15 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ALOX15, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ALOX15 BINDING SITE, designated SEQ ID:11095, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48777] Another function of GAM7052 is therefore inhibition of Arachidonate 15-lipoxygenase (ALOX15, Accession NP_001131.1), a gene which converts arachidonic acid to 15s- hydroperoxyeicosatetraenoic acid. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALOX15.

[48778] The function of ALOX15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.AP1S3 (Accession XP_291023.1) is another GAM7052 target gene, herein designated TARGET GENE. AP1S3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AP1S3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP1S3 BINDING SITE, designated

SEQ ID:809, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48779] Another function of GAM7052 is therefore inhibition of AP1S3 (Accession XP_291023.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1S3.

[48780] Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) is another GAM7052 target gene, herein designated TARGET GENE. AP3S2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by AP3S2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AP3S2 BINDING SITE, designated SEQ ID:6157, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48781] Another function of GAM7052 is therefore inhibition of Adaptor-related protein complex 3, sigma 2 subunit (AP3S2, Accession NP_005820.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3S2.

[48782] Amyloid beta precursor protein (cytoplasmic tail) binding

protein 2 (APPBP2, Accession NP_006371.2) is another GAM7052 target gene, herein designated TARGET GENE. APPBP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APPBP2 BINDING SITE, designated SEQ ID:14578, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48783] Another function of GAM7052 is therefore inhibition of Amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2, Accession NP_006371.2), a gene which interacts with the basolateral sorting signal of amyloid precursor protein. and therefore may be associated with Alzheimer's disease. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of Alzheimer's disease, and of other diseases and clinical conditions associated with APPBP2.

[48784] The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.Aprataxin (APTX, Accession NP_060162.1) is

another GAM7052 target gene, herein designated TARGET GENE. APTX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APTX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated SEQ ID:2203, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48785] Another function of GAM7052 is therefore inhibition of Aprataxin (APTX, Accession NP_060162.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APTX.

[48786] Aprataxin (APTX, Accession NP_778239.1) is another GAM7052 target gene, herein designated TARGET GENE. APTX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APTX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated

SEQ ID:2203, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48787] Another function of GAM7052 is therefore inhibition of Aprataxin (APTX, Accession NP_778239.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APTX.

[48788] Aprataxin (APTX, Accession NP_778243.1) is another GAM7052 target gene, herein designated TARGET GENE. APTX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APTX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated SEQ ID:2203, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48789] Another function of GAM7052 is therefore inhibition of Aprataxin (APTX, Accession NP_778243.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with APTX.

[48790] Aprataxin (APTX, Accession NP_778242.1) is another GAM7052 target gene, herein designated TARGET GENE. APTX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APTX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated SEQ ID:2203, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48791] Another function of GAM7052 is therefore inhibition of Aprataxin (APTX, Accession NP_778242.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APTX.

[48792] Aprataxin (APTX, Accession NP_778241.1) is another GAM7052 target gene, herein designated TARGET GENE. APTX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by APTX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated SEQ ID:2203, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48793] Another function of GAM7052 is therefore inhibition of Aprataxin (APTX, Accession NP_778241.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APTX.

[48794] Aquaporin 6, kidney specific (AQP6, Accession NP_001643.1) is another GAM7052 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:11163, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48795] Another function of GAM7052 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession

NP_001643.1), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[48796] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1) is another GAM7052 target gene, herein designated TARGET GENE. AQP6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AQP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:11163, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48797] Another function of GAM7052 is therefore inhibition of Aquaporin 6, kidney specific (AQP6, Accession NP_445738.1), a gene which participates in distinct physi-

ologic function such as glomerular filtration, tubular endocytosis, and acid- base metabolism. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6.

[48798] The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM51.1.Archain 1 (ARCN1, Accession NP_001646.2) is another GAM7052 target gene, herein designated TARGET GENE. ARCN1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARCN1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARCN1 BINDING SITE, designated SEQ ID:14158, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48799] Another function of GAM7052 is therefore inhibition of Archain 1 (ARCN1, Accession NP_001646.2), a gene which plays a fundamental role in eukaryotic cell biology. Accordingly, utilities of GAM7052 include diagnosis, preven-

tion and treatment of diseases and clinical conditions associated with ARCN1.

[48800] The function of ARCN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Ras homolog gene family, member f (in filopodia) (ARHF, Accession NP_061907.1) is another GAM7052 target gene, herein designated TARGET GENE. ARHF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARHF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHF BINDING SITE, designated SEQ ID:13834, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48801] Another function of GAM7052 is therefore inhibition of Ras homolog gene family, member f (in filopodia) (ARHF, Accession NP_061907.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHF.

[48802] Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) is another GAM7052 target gene, herein

designated TARGET GENE. ARHGAP1 BINDING SITE1 and ARHGAP1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ARHGAP1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARHGAP1 BINDING SITE1 and ARHGAP1 BINDING SITE2, designated SEQ ID:13952 and SEQ ID:15853 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48803] Another function of GAM7052 is therefore inhibition of Rho gtpase activating protein 1 (ARHGAP1, Accession NP_004299.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP1.

[48804] ARPP-19 (Accession NP_006619.1) is another GAM7052 target gene, herein designated TARGET GENE. ARPP-19 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ARPP-19, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ARPP-19 BINDING SITE, designated SEQ ID:4389, to the

nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48805] Another function of GAM7052 is therefore inhibition of ARPP-19 (Accession NP_006619.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARPP-19.

[48806] Ankyrin repeat and socs box-containing 16 (ASB16, Accession NP_543139.4) is another GAM7052 target gene, herein designated TARGET GENE. ASB16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASB16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB16 BINDING SITE, designated SEQ ID:10273, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48807] Another function of GAM7052 is therefore inhibition of Ankyrin repeat and socs box-containing 16 (ASB16, Accession NP_543139.4) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB16.

[48808] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) is another GAM7052 target gene, herein designated TARGET GENE. ASB6 BINDING SITE1 and ASB6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by ASB6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE1 and ASB6 BINDING SITE2, designated SEQ ID:9847 and SEQ ID:13406 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48809] Another function of GAM7052 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_821066.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[48810] Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) is another GAM7052 target gene, herein designated TARGET GENE. ASB6 BINDING SITE1 and ASB6 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA en-

coded by ASB6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASB6 BINDING SITE1 and ASB6 BINDING SITE2, designated SEQ ID:9847 and SEQ ID:13406 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48811] Another function of GAM7052 is therefore inhibition of Ankyrin repeat and socs box-containing 6 (ASB6, Accession NP_060343.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB6.

[48812] ASE-1 (Accession NP_036231.1) is another GAM7052 target gene, herein designated TARGET GENE. ASE-1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ASE-1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ASE-1 BINDING SITE, designated SEQ ID:6396, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48813] Another function of GAM7052 is therefore inhibition of ASE-1 (Accession NP_036231.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASE-1.

[48814] Atpase, (na+)/k+ transporting, beta 4 polypeptide (ATP1B4, Accession NP_036201.1) is another GAM7052 target gene, herein designated TARGET GENE. ATP1B4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP1B4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP1B4 BINDING SITE, designated SEQ ID:11229, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48815] Another function of GAM7052 is therefore inhibition of Atpase, (na+)/k+ transporting, beta 4 polypeptide (ATP1B4, Accession NP_036201.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B4.

[48816] Atpase, h+ transporting, lysosomal 38kda, v0 subunit d isoform 2 (ATP6V0D2, Accession NP_689778.1) is another

GAM7052 target gene, herein designated TARGET GENE. ATP6V0D2 BINDING SITE1 and ATP6V0D2 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by ATP6V0D2, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP6V0D2 BINDING SITE1 and ATP6V0D2 BINDING SITE2, designated SEQ ID:6393 and SEQ ID:14828 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48817] Another function of GAM7052 is therefore inhibition of Atpase, h+ transporting, lysosomal 38kda, v0 subunit d isoform 2 (ATP6V0D2, Accession NP_689778.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V0D2.

[48818] ATP6V1A (Accession NP_001681.2) is another GAM7052 target gene, herein designated TARGET GENE. ATP6V1A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP6V1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of ATP6V1A BINDING SITE, designated SEQ ID:16885, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48819] Another function of GAM7052 is therefore inhibition of ATP6V1A (Accession NP_001681.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V1A.

[48820] Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) is another GAM7052 target gene, herein designated TARGET GENE. ATP7A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:3639, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48821] Another function of GAM7052 is therefore inhibition of Atpase, cu++ transporting, alpha polypeptide (menkes syndrome) (ATP7A, Accession NP_000043.1) . Accord-

ingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A.

[48822] Atpase, class i, type 8b, member 2 (ATP8B2, Accession XP_290875.1) is another GAM7052 target gene, herein designated TARGET GENE. ATP8B2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ATP8B2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ATP8B2 BINDING SITE, designated SEQ ID:11229, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48823] Another function of GAM7052 is therefore inhibition of Atpase, class i, type 8b, member 2 (ATP8B2, Accession XP_290875.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8B2.

[48824] Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) is another GAM7052 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multi-

ple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:9692, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48825] Another function of GAM7052 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_068713.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[48826] Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) is another GAM7052 target gene, herein designated TARGET GENE. AXL BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by AXL, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE, designated SEQ ID:9692, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48827] Another function of GAM7052 is therefore inhibition of Axl receptor tyrosine kinase (AXL, Accession NP_001690.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL.

[48828] Udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5, Accession NP_149360.1) is another GAM7052 target gene, herein designated TARGET GENE. B3GALT5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by B3GALT5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B3GALT5 BINDING SITE, designated SEQ ID:7881, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48829] Another function of GAM7052 is therefore inhibition of Udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5, Accession NP_149360.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GALT5.

[48830] Udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5, Accession NP_149363.1) is another GAM7052 target gene, herein designated TARGET GENE. B3GALT5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by B3GALT5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B3GALT5 BINDING SITE, designated SEQ ID:7881, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48831] Another function of GAM7052 is therefore inhibition of Udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5, Accession NP_149363.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GALT5.

[48832] Udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5, Accession NP_149361.1) is another GAM7052 target gene, herein designated TARGET GENE. B3GALT5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts

of mRNA encoded by B3GALT5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B3GALT5 BINDING SITE, designated SEQ ID:7881, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48833] Another function of GAM7052 is therefore inhibition of Udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5, Accession NP_149361.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GALT5.

[48834] Udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5, Accession NP_149362.1) is another GAM7052 target gene, herein designated TARGET GENE. B3GALT5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by B3GALT5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B3GALT5 BINDING SITE, designated SEQ ID:7881, to the nucleotide se-

quence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48835] Another function of GAM7052 is therefore inhibition of Udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5, Accession NP_149362.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GALT5.

[48836] Udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5, Accession NP_006048.1) is another GAM7052 target gene, herein designated TARGET GENE. B3GALT5 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by B3GALT5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of B3GALT5 BINDING SITE, designated SEQ ID:7881, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48837] Another function of GAM7052 is therefore inhibition of Udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5, Accession NP_006048.1) . Ac-

cordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GALT5.

[48838] Bcl2-associated athanogene 5 (BAG5, Accession NP_004864.1) is another GAM7052 target gene, herein designated TARGET GENE. BAG5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BAG5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BAG5 BINDING SITE, designated SEQ ID:19275, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48839] Another function of GAM7052 is therefore inhibition of Bcl2-associated athanogene 5 (BAG5, Accession NP_004864.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAG5.

[48840] BCAP31 (Accession NP_005736.2) is another GAM7052 target gene, herein designated TARGET GENE. BCAP31 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BCAP31, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCAP31 BINDING SITE, designated SEQ ID:13785, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48841] Another function of GAM7052 is therefore inhibition of BCAP31 (Accession NP_005736.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCAP31.

[48842] BCLG (Accession NP_110393.1) is another GAM7052 target gene, herein designated TARGET GENE. BCLG BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BCLG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCLG BINDING SITE, designated SEQ ID:10887, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48843] Another function of GAM7052 is therefore inhibition of BCLG (Accession NP_110393.1) . Accordingly, utilities of

GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCLG.

[48844] BCLG (Accession NP_620048.1) is another GAM7052 target gene, herein designated TARGET GENE. BCLG BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by BCLG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BCLG BINDING SITE, designated SEQ ID:10887, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48845] Another function of GAM7052 is therefore inhibition of BCLG (Accession NP_620048.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCLG.

[48846] BM-002 (Accession NP_057701.1) is another GAM7052 target gene, herein designated TARGET GENE. BM-002 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BM-002, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

BM-002 BINDING SITE, designated SEQ ID:9516, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48847] Another function of GAM7052 is therefore inhibition of BM-002 (Accession NP_057701.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BM-002.

[48848] Breast cancer 1, early onset (BRCA1, Accession NP_009237.1) is another GAM7052 target gene, herein designated TARGET GENE. BRCA1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by BRCA1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BRCA1 BINDING SITE, designated SEQ ID:19804, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48849] Another function of GAM7052 is therefore inhibition of Breast cancer 1, early onset (BRCA1, Accession NP_009237.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with BRCA1.

[48850] BRIP1 (Accession NP_114432.1) is another GAM7052 target gene, herein designated TARGET GENE. BRIP1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BRIP1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BRIP1 BINDING SITE, designated SEQ ID:16280, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48851] Another function of GAM7052 is therefore inhibition of BRIP1 (Accession NP_114432.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRIP1.

[48852] BXDC1 (Accession XP_166303.1) is another GAM7052 target gene, herein designated TARGET GENE. BXDC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by BXDC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of BXDC1 BINDING SITE, designated SEQ ID:10897, to the nucleotide

sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48853] Another function of GAM7052 is therefore inhibition of BXDC1 (Accession XP_166303.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BXDC1.

[48854] C19orf9 (Accession XP_290171.1) is another GAM7052 target gene, herein designated TARGET GENE. C19orf9 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C19orf9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C19orf9 BINDING SITE, designated SEQ ID:7215, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48855] Another function of GAM7052 is therefore inhibition of C19orf9 (Accession XP_290171.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C19orf9.

[48856] C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) is another GAM7052

target gene, herein designated TARGET GENE. C1QTNF6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C1QTNF6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C1QTNF6 BINDING SITE, designated SEQ ID:13966, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48857] Another function of GAM7052 is therefore inhibition of C1q and tumor necrosis factor related protein 6 (C1QTNF6, Accession NP_114116.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QTNF6.

[48858] Chromosome 20 open reading frame 161 (C20orf161, Accession NP_690857.1) is another GAM7052 target gene, herein designated TARGET GENE. C20orf161 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C20orf161, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of C20orf161 BINDING SITE, designated SEQ ID:16361, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48859] Another function of GAM7052 is therefore inhibition of Chromosome 20 open reading frame 161 (C20orf161, Accession NP_690857.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf161.

[48860] Chromosome 20 open reading frame 161 (C20orf161, Accession NP_219489.1) is another GAM7052 target gene, herein designated TARGET GENE. C20orf161 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by C20orf161, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C20orf161 BINDING SITE, designated SEQ ID:16361, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48861] Another function of GAM7052 is therefore inhibition of Chromosome 20 open reading frame 161 (C20orf161, Ac-

cession NP_219489.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf161.

[48862] C4orf9 (Accession XP_035572.1) is another GAM7052 target gene, herein designated TARGET GENE. C4orf9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C4orf9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C4orf9 BINDING SITE, designated SEQ ID:4343, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48863] Another function of GAM7052 is therefore inhibition of C4orf9 (Accession XP_035572.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C4orf9.

[48864] C6orf141 (Accession NP_699175.1) is another GAM7052 target gene, herein designated TARGET GENE. C6orf141 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf141, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of C6orf141 BINDING SITE, designated SEQ ID:17672, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48865] Another function of GAM7052 is therefore inhibition of C6orf141 (Accession NP_699175.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf141.

[48866] C6orf57 (Accession NP_660310.1) is another GAM7052 target gene, herein designated TARGET GENE. C6orf57 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C6orf57, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C6orf57 BINDING SITE, designated SEQ ID:5864, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48867] Another function of GAM7052 is therefore inhibition of C6orf57 (Accession NP_660310.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

C6orf57.

[48868] Chromosome 8 open reading frame 12 (C8orf12, Accession NP_473358.1) is another GAM7052 target gene, herein designated TARGET GENE. C8orf12 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by C8orf12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C8orf12 BINDING SITE, designated SEQ ID:8627, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48869] Another function of GAM7052 is therefore inhibition of Chromosome 8 open reading frame 12 (C8orf12, Accession NP_473358.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf12.

[48870] Chromosome 9 open reading frame 9 (C9orf9, Accession NP_061829.2) is another GAM7052 target gene, herein designated TARGET GENE. C9orf9 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by C9orf9, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III

of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of C9orf9 BINDING SITE, designated SEQ ID:16870, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48871] Another function of GAM7052 is therefore inhibition of Chromosome 9 open reading frame 9 (C9orf9, Accession NP_061829.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf9.

[48872] Calcium channel, voltage-dependent, gamma subunit 6 (CACNG6, Accession NP_665814.1) is another GAM7052 target gene, herein designated TARGET GENE. CACNG6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CACNG6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CACNG6 BINDING SITE, designated SEQ ID:10214, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48873] Another function of GAM7052 is therefore inhibition of

Calcium channel, voltage-dependent, gamma subunit 6 (CACNG6, Accession NP_665814.1), a gene which plays a role in excitation- contraction coupling. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNG6.

[48874] The function of CACNG6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Calcium channel, voltage-dependent, gamma subunit 6 (CACNG6, Accession NP_665813.1) is another GAM7052 target gene, herein designated TARGET GENE. CACNG6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CACNG6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CACNG6 BINDING SITE, designated SEQ ID:10214, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48875] Another function of GAM7052 is therefore inhibition of Calcium channel, voltage-dependent, gamma subunit 6

(CACNG6, Accession NP_665813.1), a gene which plays a role in excitation- contraction coupling. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNG6.

[48876] The function of CACNG6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Calcium channel, voltage-dependent, gamma subunit 6 (CACNG6, Accession NP_114103.2) is another GAM7052 target gene, herein designated TARGET GENE. CACNG6 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CACNG6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CACNG6 BINDING SITE, designated SEQ ID:10214, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48877] Another function of GAM7052 is therefore inhibition of Calcium channel, voltage-dependent, gamma subunit 6 (CACNG6, Accession NP_114103.2), a gene which plays a

role in excitation- contraction coupling. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNG6.

[48878] The function of CACNG6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.Calcium modulating ligand (CAMLG, Accession NP_001736.1) is another GAM7052 target gene, herein designated TARGET GENE. CAMLG BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAMLG, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAMLG BINDING SITE, designated SEQ ID:2107, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48879] Another function of GAM7052 is therefore inhibition of Calcium modulating ligand (CAMLG, Accession NP_001736.1), a gene which is likely involved in the mobilization of calcium as a result of the tcr/cd3 complex interaction. Accordingly, utilities of GAM7052 include diag-

nosis, prevention and treatment of diseases and clinical conditions associated with CAMLG.

[48880] The function of CAMLG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.CAPRI (Accession NP_008920.3) is another GAM7052 target gene, herein designated TARGET GENE. CAPRI BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CAPRI, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CAPRI BINDING SITE, designated SEQ ID:7042, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48881] Another function of GAM7052 is therefore inhibition of CAPRI (Accession NP_008920.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPRI.

[48882] Caspase recruitment domain family, member 6 (CARD6, Accession NP_115976.2) is another GAM7052 target gene, herein designated TARGET GENE. CARD6 BINDING SITE is a target binding site found in the 3` untranslated region of

mRNA encoded by CARD6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CARD6 BINDING SITE, designated SEQ ID:2824, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48883] Another function of GAM7052 is therefore inhibition of Caspase recruitment domain family, member 6 (CARD6, Accession NP_115976.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD6.

[48884] Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_005084.1) is another GAM7052 target gene, herein designated TARGET GENE. CBFA2T2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CBFA2T2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CBFA2T2 BINDING SITE, designated SEQ ID:1249, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA,

also designated SEQ ID:296.

[48885] Another function of GAM7052 is therefore inhibition of Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_005084.1), a gene which is a putative transcription factor. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T2.

[48886] The function of CBFA2T2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_787060.1) is another GAM7052 target gene, herein designated TARGET GENE. CBFA2T2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CBFA2T2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CBFA2T2 BINDING SITE, designated SEQ ID:1249, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48887] Another function of GAM7052 is therefore inhibition of Core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2, Accession NP_787060.1), a gene which is a putative transcription factor. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T2.

[48888] The function of CBFA2T2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM55.1.Chemokine (c-c motif) ligand 16 (CCL16, Accession NP_004581.1) is another GAM7052 target gene, herein designated TARGET GENE. CCL16 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCL16, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL16 BINDING SITE, designated SEQ ID:12626, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48889] Another function of GAM7052 is therefore inhibition of Chemokine (c-c motif) ligand 16 (CCL16, Accession

NP_004581.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL16.

[48890] Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) is another GAM7052 target gene, herein designated TARGET GENE. CCL22 BINDING SITE1 and CCL22 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CCL22, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL22 BINDING SITE1 and CCL22 BINDING SITE2, designated SEQ ID:6967 and SEQ ID:13638 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48891] Another function of GAM7052 is therefore inhibition of Chemokine (c-c motif) ligand 22 (CCL22, Accession NP_002981.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL22.

[48892] Chemokine (c-c motif) ligand 28 (CCL28, Accession NP_062820.1) is another GAM7052 target gene, herein designated TARGET GENE. CCL28 BINDING SITE is a target

binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CCL28, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCL28 BINDING SITE, designated SEQ ID:5390, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48893] Another function of GAM7052 is therefore inhibition of Chemokine (c-c motif) ligand 28 (CCL28, Accession NP_062820.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCL28.

[48894] Cyclin f (CCNF, Accession NP_001752.1) is another GAM7052 target gene, herein designated TARGET GENE. CCNF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CCNF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCNF BINDING SITE, designated SEQ ID:8016, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48895] Another function of GAM7052 is therefore inhibition of Cyclin f (CCNF, Accession NP_001752.1), a gene which likely to be involved in the control of the cell cycle during s phase and g2. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNF.

[48896] The function of CCNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.CCNL2 (Accession NP_112199.1) is another GAM7052 target gene, herein designated TARGET GENE. CCNL2 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CCNL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CCNL2 BINDING SITE, designated SEQ ID:8702, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48897] Another function of GAM7052 is therefore inhibition of CCNL2 (Accession NP_112199.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNL2.

[48898] Cd24 antigen (small cell lung carcinoma cluster 4 antigen) (CD24, Accession NP_037362.1) is another GAM7052 target gene, herein designated TARGET GENE. CD24 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CD24, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CD24 BINDING SITE, designated SEQ ID:12740, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48899] Another function of GAM7052 is therefore inhibition of Cd24 antigen (small cell lung carcinoma cluster 4 antigen) (CD24, Accession NP_037362.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD24.

[48900] Cdc14 cell division cycle 14 homolog b (s. cerevisiae) (CDC14B, Accession NP_201589.1) is another GAM7052 target gene, herein designated TARGET GENE. CDC14B BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDC14B, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC14B BINDING SITE, designated SEQ ID:8433, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48901] Another function of GAM7052 is therefore inhibition of Cdc14 cell division cycle 14 homolog b (s. cerevisiae) (CDC14B, Accession NP_201589.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC14B.

[48902] Cell division cycle 2-like 2 (CDC2L2, Accession NP_296370.1) is another GAM7052 target gene, herein designated TARGET GENE. CDC2L2 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by CDC2L2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC2L2 BINDING SITE, designated SEQ ID:14683, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48903] Another function of GAM7052 is therefore inhibition of

Cell division cycle 2-like 2 (CDC2L2, Accession NP_296370.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC2L2.

[48904] Cdc6 cell division cycle 6 homolog (s. cerevisiae) (CDC6, Accession NP_001245.1) is another GAM7052 target gene, herein designated TARGET GENE. CDC6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDC6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDC6 BINDING SITE, designated SEQ ID:2823, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48905] Another function of GAM7052 is therefore inhibition of Cdc6 cell division cycle 6 homolog (s. cerevisiae) (CDC6, Accession NP_001245.1), a gene which is a component of the origin recognition complex (orc) that binds origins of replication. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC6.

[48906] The function of CDC6 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) is another GAM7052 target gene, herein designated TARGET GENE. CDH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CDH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH1 BINDING SITE, designated SEQ ID:15641, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48907] Another function of GAM7052 is therefore inhibition of Cadherin 1, type 1, e-cadherin (epithelial) (CDH1, Accession NP_004351.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH1.

[48908] Cadherin 11, type 2, ob-cadherin (osteoblast) (CDH11, Accession NP_387513.1) is another GAM7052 target gene, herein designated TARGET GENE. CDH11 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by CDH11, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CDH11 BINDING SITE, designated SEQ ID:7516, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48909] Another function of GAM7052 is therefore inhibition of Cadherin 11, type 2, ob-cadherin (osteoblast) (CDH11, Accession NP_387513.1), a gene which plays an role in development and maintenance of tissues. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH11.

[48910] The function of CDH11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM206.1.Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) is another GAM7052 target gene, herein designated TARGET GENE. CEACAM8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CEACAM8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CEACAM8 BINDING SITE, designated SEQ ID:9995, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48911] Another function of GAM7052 is therefore inhibition of Carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8, Accession NP_001807.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEACAM8.

[48912] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) is another GAM7052 target gene, herein designated TARGET GENE. CECR1 BINDING SITE1 and CECR1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CECR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE1 and CECR1 BINDING SITE2, designated SEQ ID:5536 and SEQ ID:5536 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA,

also designated SEQ ID:296.

[48913] Another function of GAM7052 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1.

[48914] Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) is another GAM7052 target gene, herein designated TARGET GENE. CECR1 BINDING SITE1 and CECR1 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by CECR1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE1 and CECR1 BINDING SITE2, designated SEQ ID:16723 and SEQ ID:16723 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48915] Another function of GAM7052 is therefore inhibition of Cat eye syndrome chromosome region, candidate 1 (CECR1, Accession NP_059120.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with CECR1.

[48916] CGI-14 (Accession NP_057028.2) is another GAM7052 target gene, herein designated TARGET GENE. CGI-14 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CGI-14, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-14 BINDING SITE, designated SEQ ID:17011, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48917] Another function of GAM7052 is therefore inhibition of CGI-14 (Accession NP_057028.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-14.

[48918] CGI-18 (Accession NP_057031.1) is another GAM7052 target gene, herein designated TARGET GENE. CGI-18 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CGI-18, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CGI-18 BINDING SITE, designated SEQ ID:16885, to the

nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48919] Another function of GAM7052 is therefore inhibition of CGI-18 (Accession NP_057031.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGI-18.

[48920] Chromatin accessibility complex 1 (CHRAC1, Accession NP_059140.1) is another GAM7052 target gene, herein designated TARGET GENE. CHRAC1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHRAC1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHRAC1 BINDING SITE, designated SEQ ID:8325, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48921] Another function of GAM7052 is therefore inhibition of Chromatin accessibility complex 1 (CHRAC1, Accession NP_059140.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRAC1.

[48922] Cholinergic receptor, nicotinic, beta polypeptide 4

(CHRNB4, Accession NP_000741.1) is another GAM7052 target gene, herein designated TARGET GENE. CHRNB4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHRNB4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHRNB4 BINDING SITE, designated SEQ ID:13754, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48923] Another function of GAM7052 is therefore inhibition of Cholinergic receptor, nicotinic, beta polypeptide 4 (CHRNB4, Accession NP_000741.1), a gene which mediates fast signal transmission at synapses. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRNB4.

[48924] The function of CHRNB4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM76.1.Carbohydrate (chondroitin) synthase 1 (CHSY1, Accession NP_055733.2) is another GAM7052 target gene, herein designated TARGET GENE. CHSY1

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CHSY1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CHSY1 BINDING SITE, designated SEQ ID:9811, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48925] Another function of GAM7052 is therefore inhibition of Carbohydrate (chondroitin) synthase 1 (CHSY1, Accession NP_055733.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHSY1.

[48926] Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2) is another GAM7052 target gene, herein designated TARGET GENE. CIAS1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by CIAS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIAS1 BINDING SITE, designated SEQ ID:12643, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ

ID:296.

[48927] Another function of GAM7052 is therefore inhibition of Cold autoinflammatory syndrome 1 (CIAS1, Accession NP_004886.2), a gene which may mediate protein- protein interactions; contains a leucine rich repeat and therefore may be associated with Familial cold autoinflammatory syndrome, muckle- wells syndrome. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of Familial cold autoinflammatory syndrome, muckle- wells syndrome, and of other diseases and clinical conditions associated with CIAS1.

[48928] The function of CIAS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM90.1.CIP29 (Accession NP_115740.3) is another GAM7052 target gene, herein designated TARGET GENE. CIP29 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CIP29, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CIP29 BINDING SITE, designated SEQ ID:11229, to the nucleotide sequence of GAM7052 RNA, herein designated

GAM RNA, also designated SEQ ID:296.

[48929] Another function of GAM7052 is therefore inhibition of CIP29 (Accession NP_115740.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIP29.

[48930] C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2) is another GAM7052 target gene, herein designated TARGET GENE. CLECSF12 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLECSF12, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLECSF12 BINDING SITE, designated SEQ ID:10135, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48931] Another function of GAM7052 is therefore inhibition of C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 12 (CLECSF12, Accession NP_072092.2), a gene which is a pattern- recognition receptor . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical

conditions associated with CLECSF12.

[48932] The function of CLECSF12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) (CLN8, Accession NP_061764.2) is another GAM7052 target gene, herein designated TARGET GENE. CLN8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CLN8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CLN8 BINDING SITE, designated SEQ ID:3696, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48933] Another function of GAM7052 is therefore inhibition of Ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) (CLN8, Accession NP_061764.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLN8.

[48934] cPLA2delta (Accession NP_828848.1) is another GAM7052 target gene, herein designated TARGET GENE. cPLA2delta BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by cPLA2delta, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of cPLA2delta BINDING SITE, designated SEQ ID:10898, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48935] Another function of GAM7052 is therefore inhibition of cPLA2delta (Accession NP_828848.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with cPLA2delta.

[48936] cPLA2delta (Accession XP_208820.2) is another GAM7052

target gene, herein designated TARGET GENE. cPLA2delta BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by cPLA2delta, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of cPLA2delta BINDING SITE, designated SEQ ID:10898, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48937] Another function of GAM7052 is therefore inhibition of cPLA2delta (Accession XP_208820.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with cPLA2delta.

[48938] Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) is another GAM7052 target gene, herein designated TARGET GENE. CPSF2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CPSF2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CPSF2

BINDING SITE, designated SEQ ID:16291, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48939] Another function of GAM7052 is therefore inhibition of Cleavage and polyadenylation specific factor 2, 100kda (CPSF2, Accession XP_029311.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPSF2.

[48940] Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) is another GAM7052 target gene, herein designated TARGET GENE. CRLF3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRLF3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRLF3 BINDING SITE, designated SEQ ID:10228, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48941] Another function of GAM7052 is therefore inhibition of Cytokine receptor-like factor 3 (CRLF3, Accession NP_057070.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with CRLF3.

[48942] Cofactor required for sp1 transcriptional activation, subunit 6, 77kda (CRSP6, Accession NP_004259.3) is another GAM7052 target gene, herein designated TARGET GENE. CRSP6 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CRSP6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CRSP6 BINDING SITE, designated SEQ ID:5118, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48943] Another function of GAM7052 is therefore inhibition of Cofactor required for sp1 transcriptional activation, subunit 6, 77kda (CRSP6, Accession NP_004259.3), a gene which is required for Sp1 mediated transcriptional activation with TAF(II)s. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRSP6.

[48944] The function of CRSP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.CTEN (Accession NP_116254.3) is another

GAM7052 target gene, herein designated TARGET GENE. CTEN BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CTEN, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CTEN BINDING SITE, designated SEQ ID:4888, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48945] Another function of GAM7052 is therefore inhibition of CTEN (Accession NP_116254.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTEN.

[48946] CYCS (Accession NP_061820.1) is another GAM7052 target gene, herein designated TARGET GENE. CYCS BINDING SITE1 and CYCS BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CYCS, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYCS BINDING SITE1 and CYCS BINDING SITE2, designated SEQ ID:18745 and SEQ ID:6532 respectively, to the nucleotide sequence of GAM7052 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:296.

[48947] Another function of GAM7052 is therefore inhibition of CYCS (Accession NP_061820.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYCS.

[48948] Cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2, Accession NP_001331.1) is another GAM7052 target gene, herein designated TARGET GENE. CYLC2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYLC2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYLC2 BINDING SITE, designated SEQ ID:13498, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48949] Another function of GAM7052 is therefore inhibition of Cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2, Accession NP_001331.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYLC2.

[48950] CYP24A1 (Accession NP_000773.1) is another GAM7052 target gene, herein designated TARGET GENE. CYP24A1

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by CYP24A1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP24A1 BINDING SITE, designated SEQ ID:5450, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48951] Another function of GAM7052 is therefore inhibition of CYP24A1 (Accession NP_000773.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP24A1.

[48952] Cytochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1) is another GAM7052 target gene, herein designated TARGET GENE. CYP2B6 BINDING SITE1 and CYP2B6 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CYP2B6, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of CYP2B6 BINDING SITE1 and CYP2B6 BINDING

SITE2, designated SEQ ID:14638 and SEQ ID:14013 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48953] Another function of GAM7052 is therefore inhibition of Cytochrome p450, subfamily iib (phenobarbital-inducible), polypeptide 6 (CYP2B6, Accession NP_000758.1), a gene which oxidizes a variety of structurally unrelated compounds, including steroids, fatty acids, and xenobiotics. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP2B6.

[48954] The function of CYP2B6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1) is another GAM7052 target gene, herein designated TARGET GENE. CYP8B1 BINDING SITE1 and CYP8B1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by CYP8B1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

CYP8B1 BINDING SITE1 and CYP8B1 BINDING SITE2, designated SEQ ID:5688 and SEQ ID:14961 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48955] Another function of GAM7052 is therefore inhibition of Cytochrome p450, subfamily viiib (sterol 12-alpha-hydroxylase), polypeptide 1 (CYP8B1, Accession NP_004382.1), a gene which functions in bile acid biosynthesis. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP8B1.

[48956] The function of CYP8B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM47.1.Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) is another GAM7052 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ

ID:5712, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48957] Another function of GAM7052 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835365.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[48958] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) is another GAM7052 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:5712, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48959] Another function of GAM7052 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_000546.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[48960] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) is another GAM7052 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:5712, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48961] Another function of GAM7052 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835366.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[48962] Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835364.1) is another GAM7052 target gene, herein designated TARGET GENE. DCX BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DCX, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of DCX BINDING SITE, designated SEQ ID:5712, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48963] Another function of GAM7052 is therefore inhibition of Doublecortex; lissencephaly, x-linked (doublecortin) (DCX, Accession NP_835364.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCX.

[48964] Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1) is another GAM7052 target gene, herein designated TARGET GENE. DFFB BINDING SITE1 and DFFB BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by DFFB, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DFFB BINDING SITE1 and DFFB BINDING SITE2, designated SEQ ID:12740 and SEQ ID:16722 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48965] Another function of GAM7052 is therefore inhibition of

Dna fragmentation factor, 40kda, beta polypeptide (caspase-activated dnase) (DFFB, Accession NP_004393.1), a gene which induces DNA fragmentation and chromatin condensation during apoptosis. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DFFB.

[48966] The function of DFFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.DKFZp434C0923 (Accession NP_060068.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZp434C0923 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp434C0923, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp434C0923 BINDING SITE, designated SEQ ID:8218, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48967] Another function of GAM7052 is therefore inhibition of DKFZp434C0923 (Accession NP_060068.1) . Accordingly,

utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434C0923.

[48968] DKFZP434D146 (Accession NP_056410.2) is another GAM7052 target gene, herein designated TARGET GENE. DKFZP434D146 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP434D146, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434D146 BINDING SITE, designated SEQ ID:2840, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48969] Another function of GAM7052 is therefore inhibition of DKFZP434D146 (Accession NP_056410.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434D146.

[48970] DKFZP434F0318 (Accession NP_110444.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZP434F0318 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

DKFZP434F0318, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP434F0318 BINDING SITE, designated SEQ ID:5215, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48971] Another function of GAM7052 is therefore inhibition of DKFZP434F0318 (Accession NP_110444.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F0318.

[48972] DKFZp547A023 (Accession NP_061174.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZp547A023 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp547A023, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp547A023 BINDING SITE, designated SEQ ID:15974, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48973] Another function of GAM7052 is therefore inhibition of DKFZp547A023 (Accession NP_061174.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547A023.

[48974] DKFZP564G092 (Accession NP_056416.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZP564G092 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZP564G092, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564G092 BINDING SITE, designated SEQ ID:11229, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48975] Another function of GAM7052 is therefore inhibition of DKFZP564G092 (Accession NP_056416.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564G092.

[48976] DKFZP564O0523 (Accession NP_115496.1) is another GAM7052 target gene, herein designated TARGET GENE.

DKFZP564O0523 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O0523, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP564O0523 BINDING SITE, designated SEQ ID:19558, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48977] Another function of GAM7052 is therefore inhibition of DKFZP564O0523 (Accession NP_115496.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564O0523.

[48978] DKFZP566I1024 (Accession NP_056226.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZP566I1024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP566I1024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP566I1024 BINDING SITE, designated SEQ ID:9433, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48979] Another function of GAM7052 is therefore inhibition of DKFZP566I1024 (Accession NP_056226.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566I1024.

[48980] DKFZP586D0919 (Accession NP_056248.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZP586D0919 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586D0919, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZP586D0919 BINDING SITE, designated SEQ ID:9678, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48981] Another function of GAM7052 is therefore inhibition of DKFZP586D0919 (Accession NP_056248.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586D0919.

[48982] DKFZp586I1420 (Accession NP_689960.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZp586I1420 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp586I1420, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp586I1420 BINDING SITE, designated SEQ ID:3745, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48983] Another function of GAM7052 is therefore inhibition of DKFZp586I1420 (Accession NP_689960.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp586I1420.

[48984] DKFZP586M1120 (Accession NP_112584.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZP586M1120 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZP586M1120, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of DKFZP586M1120 BINDING SITE, designated SEQ ID:3746, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48985] Another function of GAM7052 is therefore inhibition of DKFZP586M1120 (Accession NP_112584.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586M1120.

[48986] DKFZp667B1218 (Accession NP_808881.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZp667B1218 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp667B1218, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp667B1218 BINDING SITE, designated SEQ ID:7365, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48987] Another function of GAM7052 is therefore inhibition of DKFZp667B1218 (Accession NP_808881.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZp667B1218.

[48988] DKFZp761B107 (Accession NP_775734.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZp761B107 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761B107, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B107 BINDING SITE, designated SEQ ID:14917, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48989] Another function of GAM7052 is therefore inhibition of DKFZp761B107 (Accession NP_775734.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B107.

[48990] DKFZp761B128 (Accession NP_689650.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZp761B128 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by DKFZp761B128, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761B128 BINDING SITE, designated SEQ ID:3467, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48991] Another function of GAM7052 is therefore inhibition of DKFZp761B128 (Accession NP_689650.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761B128.

[48992] DKFZp761H039 (Accession NP_061181.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZp761H039 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761H039, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761H039 BINDING SITE, designated SEQ ID:3638, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48993] Another function of GAM7052 is therefore inhibition of

DKFZp761H039 (Accession NP_061181.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761H039.

[48994] DKFZp761P1121 (Accession NP_690870.1) is another GAM7052 target gene, herein designated TARGET GENE. DKFZp761P1121 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DKFZp761P1121, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp761P1121 BINDING SITE, designated SEQ ID:6533, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48995] Another function of GAM7052 is therefore inhibition of DKFZp761P1121 (Accession NP_690870.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761P1121.

[48996] DKFZp762L0311 (Accession NP_061189.2) is another GAM7052 target gene, herein designated TARGET GENE. DKFZp762L0311 BINDING SITE is a target binding site

found in the 3` untranslated region of mRNA encoded by DKFZp762L0311, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DKFZp762L0311 BINDING SITE, designated SEQ ID:13279, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48997] Another function of GAM7052 is therefore inhibition of DKFZp762L0311 (Accession NP_061189.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762L0311.

[48998] DLAD (Accession NP_490649.1) is another GAM7052 target gene, herein designated TARGET GENE. DLAD BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by DLAD, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DLAD BINDING SITE, designated SEQ ID:10031, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[48999] Another function of GAM7052 is therefore inhibition of DLAD (Accession NP_490649.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLAD.

[49000] Dihydrolipoamide s-succinyltransferase (e2 component of 2-oxo-glutarate complex) (DLST, Accession NP_001924.2) is another GAM7052 target gene, herein designated TARGET GENE. DLST BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DLST BINDING SITE, designated SEQ ID:9118, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49001] Another function of GAM7052 is therefore inhibition of Dihydrolipoamide s-succinyltransferase (e2 component of 2-oxo-glutarate complex) (DLST, Accession NP_001924.2), a gene which catalyzes the oxidative decarboxylation of alpha- keto acids. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLST.

[49002] The function of DLST and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM507.1.Desmocollin 3 (DSC3, Accession NP_077741.1) is another GAM7052 target gene, herein designated TARGET GENE. DSC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE, designated SEQ ID:9847, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49003] Another function of GAM7052 is therefore inhibition of Desmocollin 3 (DSC3, Accession NP_077741.1), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC3.

[49004] The function of DSC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Desmocollin 3 (DSC3, Accession

NP_001932.1) is another GAM7052 target gene, herein designated TARGET GENE. DSC3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by DSC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE, designated SEQ ID:9847, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49005] Another function of GAM7052 is therefore inhibition of Desmocollin 3 (DSC3, Accession NP_001932.1), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC3.

[49006] The function of DSC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NP_567824.1) is another GAM7052 target gene, herein designated TARGET GENE. DYRK1A BINDING SITE is a target binding site found

in the 5` untranslated region of multiple transcripts of mRNA encoded by DYRK1A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of DYRK1A BINDING SITE, designated SEQ ID:17441, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49007] Another function of GAM7052 is therefore inhibition of Dual-specificity tyrosine-(y)-phosphorylation regulated kinase 1a (DYRK1A, Accession NP_567824.1), a gene which regulates cell proliferation and may be involved in brain development . and therefore may be associated with Down syndrome. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of Down syndrome, and of other diseases and clinical conditions associated with DYRK1A.

[49008] The function of DYRK1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.EDEM (Accession NP_055489.1) is another GAM7052 target gene, herein designated TARGET GENE. EDEM BINDING SITE is a target binding site found in the 3`

untranslated region of mRNA encoded by EDEM, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EDEM BINDING SITE, designated SEQ ID:12749, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49009] Another function of GAM7052 is therefore inhibition of EDEM (Accession NP_055489.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDEM.

[49010] EEF2K (Accession NP_037434.1) is another GAM7052 target gene, herein designated TARGET GENE. EEF2K BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EEF2K, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EEF2K BINDING SITE, designated SEQ ID:13359, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49011] Another function of GAM7052 is therefore inhibition of EEF2K (Accession NP_037434.1), a gene which phospho-

rylates serine or threonine on the eukaryotic elongation factor- 2 and therefore may be associated with Systemic lupus erythematosus and cancer. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of Systemic lupus erythematosus and cancer, and of other diseases and clinical conditions associated with EEF2K.

[49012] The function of EEF2K and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Early growth response 1 (EGR1, Accession NP_001955.1) is another GAM7052 target gene, herein designated TARGET GENE. EGR1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EGR1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EGR1 BINDING SITE, designated SEQ ID:10941, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49013] Another function of GAM7052 is therefore inhibition of Early growth response 1 (EGR1, Accession NP_001955.1) . Accordingly, utilities of GAM7052 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with EGR1.

[49014] Eh-domain containing 2 (EHD2, Accession NP_055416.2) is another GAM7052 target gene, herein designated TARGET GENE. EHD2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by EHD2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of EHD2 BINDING SITE, designated SEQ ID:10698, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49015] Another function of GAM7052 is therefore inhibition of Eh-domain containing 2 (EHD2, Accession NP_055416.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHD2.

[49016] ELP3 (Accession NP_060561.3) is another GAM7052 target gene, herein designated TARGET GENE. ELP3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ELP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the comple-

mentarity of the nucleotide sequences of ELP3 BINDING SITE, designated SEQ ID:8011, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49017] Another function of GAM7052 is therefore inhibition of ELP3 (Accession NP_060561.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELP3.

[49018] Endothelial cell-specific molecule 1 (ESM1, Accession NP_008967.1) is another GAM7052 target gene, herein designated TARGET GENE. ESM1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by ESM1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ESM1 BINDING SITE, designated SEQ ID:1018, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49019] Another function of GAM7052 is therefore inhibition of Endothelial cell-specific molecule 1 (ESM1, Accession NP_008967.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with ESM1.

[49020] ET(B)R-LP-2 (Accession NP_004758.2) is another GAM7052 target gene, herein designated TARGET GENE. ET(B)R-LP-2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by ET(B)R-LP-2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of ET(B)R-LP-2 BINDING SITE, designated SEQ ID:9691, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49021] Another function of GAM7052 is therefore inhibition of ET(B)R-LP-2 (Accession NP_004758.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ET(B)R-LP-2.

[49022] F11R (Accession NP_653086.1) is another GAM7052 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:9554, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49023] Another function of GAM7052 is therefore inhibition of F11R (Accession NP_653086.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[49024] F11R (Accession NP_653085.1) is another GAM7052 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:9554, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49025] Another function of GAM7052 is therefore inhibition of F11R (Accession NP_653085.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[49026] F11R (Accession NP_653087.1) is another GAM7052 tar-

get gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:9554, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49027] Another function of GAM7052 is therefore inhibition of F11R (Accession NP_653087.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[49028] F11R (Accession NP_058642.1) is another GAM7052 target gene, herein designated TARGET GENE. F11R BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by F11R, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F11R BINDING SITE, designated SEQ ID:9554, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49029] Another function of GAM7052 is therefore inhibition of F11R (Accession NP_058642.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F11R.

[49030] Coagulation factor ii (thrombin) receptor-like 2 (F2RL2, Accession NP_004092.1) is another GAM7052 target gene, herein designated TARGET GENE. F2RL2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F2RL2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F2RL2 BINDING SITE, designated SEQ ID:6476, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49031] Another function of GAM7052 is therefore inhibition of Coagulation factor ii (thrombin) receptor-like 2 (F2RL2, Accession NP_004092.1), a gene which receptor for activated thrombin coupled to g proteins that stimulate phosphoinositide hydrolysis. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2RL2.

[49032] The function of F2RL2 and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1) is another GAM7052 target gene, herein designated TARGET GENE. F3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by F3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of F3 BINDING SITE, designated SEQ ID:14740, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49033] Another function of GAM7052 is therefore inhibition of Coagulation factor iii (thromboplastin, tissue factor) (F3, Accession NP_001984.1), a gene which functions in normal hemostasis. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F3.

[49034] The function of F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM136.1.Fatty acid binding protein 2, intestinal

(FABP2, Accession NP_000125.1) is another GAM7052 target gene, herein designated TARGET GENE. FABP2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FABP2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FABP2 BINDING SITE, designated SEQ ID:17010, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49035] Another function of GAM7052 is therefore inhibition of Fatty acid binding protein 2, intestinal (FABP2, Accession NP_000125.1), a gene which may have a role in dietary fat uptake or processing. and therefore may be associated with Cardiovascular disease and type 2 diabetes. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of Cardiovascular disease and type 2 diabetes., and of other diseases and clinical conditions associated with FABP2.

[49036] The function of FABP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Fanconi anemia, complementation group e

(FANCE, Accession NP_068741.1) is another GAM7052 target gene, herein designated TARGET GENE. FANCE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCE BINDING SITE, designated SEQ ID:1495, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49037] Another function of GAM7052 is therefore inhibition of Fanconi anemia, complementation group e (FANCE, Accession NP_068741.1), a gene which is a possible regulator of lymphocyte and platelet function. and therefore is associated with Fanconi anemia, complementation group e. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of Fanconi anemia, complementation group e., and of other diseases and clinical conditions associated with FANCE.

[49038] The function of FANCE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Fanconi anemia, complementation group f

(FANCF, Accession NP_073562.1) is another GAM7052 target gene, herein designated TARGET GENE. FANCF BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FANCF, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FANCF BINDING SITE, designated SEQ ID:13765, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49039] Another function of GAM7052 is therefore inhibition of Fanconi anemia, complementation group f (FANCF, Accession NP_073562.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCF.

[49040] F-box only protein 32 (FBXO32, Accession NP_478136.1) is another GAM7052 target gene, herein designated TARGET GENE. FBXO32 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXO32, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXO32 BINDING

SITE, designated SEQ ID:4134, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49041] Another function of GAM7052 is therefore inhibition of F-box only protein 32 (FBXO32, Accession NP_478136.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO32.

[49042] F-box only protein 32 (FBXO32, Accession NP_680482.1) is another GAM7052 target gene, herein designated TARGET GENE. FBXO32 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXO32, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXO32 BINDING SITE, designated SEQ ID:4134, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49043] Another function of GAM7052 is therefore inhibition of F-box only protein 32 (FBXO32, Accession NP_680482.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with FBXO32.

[49044] FBXW8 (Accession NP_699179.2) is another GAM7052 target gene, herein designated TARGET GENE. FBXW8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXW8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FBXW8 BINDING SITE, designated SEQ ID:8434, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49045] Another function of GAM7052 is therefore inhibition of FBXW8 (Accession NP_699179.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW8.

[49046] FBXW8 (Accession NP_036306.1) is another GAM7052 target gene, herein designated TARGET GENE. FBXW8 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FBXW8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of FBXW8 BINDING SITE, designated SEQ ID:8434, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49047] Another function of GAM7052 is therefore inhibition of FBXW8 (Accession NP_036306.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXW8.

[49048] Fc fragment of igg, low affinity iia, receptor for (cd32) (FCGR2A, Accession NP_067674.1) is another GAM7052 target gene, herein designated TARGET GENE. FCGR2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FCGR2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCGR2A BINDING SITE, designated SEQ ID:6966, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49049] Another function of GAM7052 is therefore inhibition of Fc fragment of igg, low affinity iia, receptor for (cd32) (FCGR2A, Accession NP_067674.1), a gene which binds IgG immune complexes; member of the immunoglobulin

superfamily. and therefore may be associated with Lupus nephritis. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of Lupus nephritis., and of other diseases and clinical conditions associated with FCGR2A.

[49050] The function of FCGR2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.FCRH1 (Accession NP_443170.1) is another GAM7052 target gene, herein designated TARGET GENE. FCRH1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FCRH1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FCRH1 BINDING SITE, designated SEQ ID:6123, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49051] Another function of GAM7052 is therefore inhibition of FCRH1 (Accession NP_443170.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCRH1.

[49052] Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1)

is another GAM7052 target gene, herein designated TARGET GENE. FER1L4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FER1L4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FER1L4 BINDING SITE, designated SEQ ID:20036, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49053] Another function of GAM7052 is therefore inhibition of Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1). Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER1L4.

[49054] Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) is another GAM7052 target gene, herein designated TARGET GENE. FER1L4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FER1L4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FER1L4 BINDING SITE, designated

SEQ ID:20036, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49055] Another function of GAM7052 is therefore inhibition of Fer-1-like 4 (c. elegans) (FER1L4, Accession XP_300246.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER1L4.

[49056] Fasciculation and elongation protein zeta 1 (zygin i) (FEZ1, Accession NP_072043.1) is another GAM7052 target gene, herein designated TARGET GENE. FEZ1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FEZ1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FEZ1 BINDING SITE, designated SEQ ID:4759, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49057] Another function of GAM7052 is therefore inhibition of Fasciculation and elongation protein zeta 1 (zygin i) (FEZ1, Accession NP_072043.1), a gene which Zygin 1; may have a role in axonal outgrowth; has similarity to C. elegans

UNC- 76. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEZ1.

[49058] The function of FEZ1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Fibroblast growth factor 5 (FGF5, Accession NP_149134.1) is another GAM7052 target gene, herein designated TARGET GENE. FGF5 BINDING SITE1 and FGF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FGF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE1 and FGF5 BINDING SITE2, designated SEQ ID:14043 and SEQ ID:17245 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49059] Another function of GAM7052 is therefore inhibition of Fibroblast growth factor 5 (FGF5, Accession NP_149134.1), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with FGF5.

[49060] The function of FGF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.1.Fibroblast growth factor 5 (FGF5, Accession NP_004455.1) is another GAM7052 target gene, herein designated TARGET GENE. FGF5 BINDING SITE1 and FGF5 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by FGF5, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FGF5 BINDING SITE1 and FGF5 BINDING SITE2, designated SEQ ID:17245 and SEQ ID:14043 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49061] Another function of GAM7052 is therefore inhibition of Fibroblast growth factor 5 (FGF5, Accession NP_004455.1), a gene which induces transformation and may regulate neuronal differentiation. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF5.

[49062] The function of FGF5 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM106.1.FLJ10232 (Accession NP_060503.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ10232 BINDING SITE1 and FLJ10232 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ10232, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10232 BINDING SITE1 and FLJ10232 BINDING SITE2, designated SEQ ID:6964 and SEQ ID:15854 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49063] Another function of GAM7052 is therefore inhibition of FLJ10232 (Accession NP_060503.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10232.

[49064] FLJ10346 (Accession NP_060535.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ10346 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10346, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10346 BINDING SITE, designated SEQ ID:14573, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49065] Another function of GAM7052 is therefore inhibition of FLJ10346 (Accession NP_060535.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10346.

[49066] FLJ10560 (Accession NP_060608.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ10560 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10560, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10560 BINDING SITE, designated SEQ ID:9847, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49067] Another function of GAM7052 is therefore inhibition of FLJ10560 (Accession NP_060608.1) . Accordingly, utilities

of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10560.

[49068] FLJ10613 (Accession NP_061940.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ10613 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10613, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10613 BINDING SITE, designated SEQ ID:3913, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49069] Another function of GAM7052 is therefore inhibition of FLJ10613 (Accession NP_061940.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10613.

[49070] FLJ10620 (Accession NP_060627.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ10620 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10620, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10620 BINDING SITE, designated SEQ ID:8748, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49071] Another function of GAM7052 is therefore inhibition of FLJ10620 (Accession NP_060627.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10620.

[49072] FLJ10640 (Accession NP_061896.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ10640 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ10640, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10640 BINDING SITE, designated SEQ ID:9332, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49073] Another function of GAM7052 is therefore inhibition of FLJ10640 (Accession NP_061896.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ10640.

[49074] FLJ10847 (Accession NP_060712.2) is another GAM7052 target gene, herein designated TARGET GENE. FLJ10847 BINDING SITE1 and FLJ10847 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ10847, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10847 BINDING SITE1 and FLJ10847 BINDING SITE2, designated SEQ ID:19185 and SEQ ID:16146 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49075] Another function of GAM7052 is therefore inhibition of FLJ10847 (Accession NP_060712.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10847.

[49076] FLJ10901 (Accession NP_060735.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ10901 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10901, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10901 BINDING SITE, designated SEQ ID:1578, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49077] Another function of GAM7052 is therefore inhibition of FLJ10901 (Accession NP_060735.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10901.

[49078] FLJ10922 (Accession NP_060743.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ10922 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ10922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ10922 BINDING SITE, designated SEQ ID:857, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49079] Another function of GAM7052 is therefore inhibition of FLJ10922 (Accession NP_060743.1) . Accordingly, utilities

of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10922.

[49080] FLJ11467 (Accession NP_079239.2) is another GAM7052 target gene, herein designated TARGET GENE. FLJ11467 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11467, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11467 BINDING SITE, designated SEQ ID:18821, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49081] Another function of GAM7052 is therefore inhibition of FLJ11467 (Accession NP_079239.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11467.

[49082] FLJ11827 (Accession NP_079369.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ11827 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ11827, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ11827 BINDING SITE, designated SEQ ID:11535, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49083] Another function of GAM7052 is therefore inhibition of FLJ11827 (Accession NP_079369.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11827.

[49084] FLJ12363 (Accession NP_115543.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ12363 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12363, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12363 BINDING SITE, designated SEQ ID:8012, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49085] Another function of GAM7052 is therefore inhibition of FLJ12363 (Accession NP_115543.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12363.

[49086] FLJ12572 (Accession NP_075056.2) is another GAM7052 target gene, herein designated TARGET GENE. FLJ12572 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12572, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12572 BINDING SITE, designated SEQ ID:1348, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49087] Another function of GAM7052 is therefore inhibition of FLJ12572 (Accession NP_075056.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12572.

[49088] FLJ12649 (Accession XP_291344.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ12649 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12649, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ12649 BINDING SITE, designated SEQ ID:10699, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49089] Another function of GAM7052 is therefore inhibition of FLJ12649 (Accession XP_291344.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12649.

[49090] FLJ12747 (Accession XP_290972.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ12747 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12747, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12747 BINDING SITE, designated SEQ ID:2107, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49091] Another function of GAM7052 is therefore inhibition of FLJ12747 (Accession XP_290972.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ12747.

[49092] FLJ12787 (Accession NP_115551.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ12787 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12787, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12787 BINDING SITE, designated SEQ ID:9691, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49093] Another function of GAM7052 is therefore inhibition of FLJ12787 (Accession NP_115551.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12787.

[49094] FLJ12903 (Accession NP_073590.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ12903 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12903, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ12903 BINDING SITE, designated SEQ ID:17852, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49095] Another function of GAM7052 is therefore inhibition of FLJ12903 (Accession NP_073590.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12903.

[49096] FLJ12973 (Accession NP_079184.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ12973 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ12973, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ12973 BINDING SITE, designated SEQ ID:13360, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49097] Another function of GAM7052 is therefore inhibition of FLJ12973 (Accession NP_079184.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12973.

[49098] FLJ13072 (Accession XP_117117.2) is another GAM7052 target gene, herein designated TARGET GENE. FLJ13072 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13072, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13072 BINDING SITE, designated SEQ ID:16722, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49099] Another function of GAM7052 is therefore inhibition of FLJ13072 (Accession XP_117117.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13072.

[49100] FLJ13171 (Accession NP_076412.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ13171 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ13171, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13171 BINDING SITE, designated SEQ ID:10344, to the

nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49101] Another function of GAM7052 is therefore inhibition of FLJ13171 (Accession NP_076412.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13171.

[49102] FLJ13188 (Accession NP_071346.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ13188 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13188, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13188 BINDING SITE, designated SEQ ID:11689, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49103] Another function of GAM7052 is therefore inhibition of FLJ13188 (Accession NP_071346.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13188.

[49104] FLJ13204 (Accession NP_079037.2) is another GAM7052

target gene, herein designated TARGET GENE. FLJ13204 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ13204, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ13204 BINDING SITE, designated SEQ ID:7003, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49105] Another function of GAM7052 is therefore inhibition of FLJ13204 (Accession NP_079037.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13204.

[49106] FLJ14442 (Accession NP_116174.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ14442 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14442, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14442 BINDING SITE, designated SEQ ID:9691, to the nucleotide sequence of GAM7052 RNA, herein designated

GAM RNA, also designated SEQ ID:296.

[49107] Another function of GAM7052 is therefore inhibition of FLJ14442 (Accession NP_116174.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14442.

[49108] FLJ14803 (Accession NP_116231.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ14803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ14803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ14803 BINDING SITE, designated SEQ ID:7216, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49109] Another function of GAM7052 is therefore inhibition of FLJ14803 (Accession NP_116231.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14803.

[49110] FLJ20045 (Accession NP_060108.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ20045

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20045, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20045 BINDING SITE, designated SEQ ID:5969, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49111] Another function of GAM7052 is therefore inhibition of FLJ20045 (Accession NP_060108.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20045.

[49112] FLJ20079 (Accession NP_060126.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ20079 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20079, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20079 BINDING SITE, designated SEQ ID:17687, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49113] Another function of GAM7052 is therefore inhibition of FLJ20079 (Accession NP_060126.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20079.

[49114] FLJ20136 (Accession NP_060154.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ20136 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20136, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20136 BINDING SITE, designated SEQ ID:9023, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49115] Another function of GAM7052 is therefore inhibition of FLJ20136 (Accession NP_060154.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20136.

[49116] FLJ20245 (Accession NP_060193.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ20245 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ20245, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20245 BINDING SITE, designated SEQ ID:12481, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49117] Another function of GAM7052 is therefore inhibition of FLJ20245 (Accession NP_060193.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20245.

[49118] FLJ20276 (Accession NP_060208.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ20276 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20276, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20276 BINDING SITE, designated SEQ ID:14443, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49119] Another function of GAM7052 is therefore inhibition of

FLJ20276 (Accession NP_060208.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20276.

[49120] FLJ20507 (Accession NP_060319.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ20507 BINDING SITE1 and FLJ20507 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ20507, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20507 BINDING SITE1 and FLJ20507 BINDING SITE2, designated SEQ ID:16723 and SEQ ID:3913 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49121] Another function of GAM7052 is therefore inhibition of FLJ20507 (Accession NP_060319.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20507.

[49122] FLJ20511 (Accession NP_060323.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ20511

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ20511, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ20511 BINDING SITE, designated SEQ ID:9847, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49123] Another function of GAM7052 is therefore inhibition of FLJ20511 (Accession NP_060323.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20511.

[49124] FLJ21865 (Accession NP_073596.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ21865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ21865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ21865 BINDING SITE, designated SEQ ID:3914, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49125] Another function of GAM7052 is therefore inhibition of FLJ21865 (Accession NP_073596.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21865.

[49126] FLJ22531 (Accession NP_078926.2) is another GAM7052 target gene, herein designated TARGET GENE. FLJ22531 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ22531, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22531 BINDING SITE, designated SEQ ID:7027, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49127] Another function of GAM7052 is therefore inhibition of FLJ22531 (Accession NP_078926.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22531.

[49128] FLJ22593 (Accession NP_078979.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ22593 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by FLJ22593, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22593 BINDING SITE, designated SEQ ID:8875, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49129] Another function of GAM7052 is therefore inhibition of FLJ22593 (Accession NP_078979.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22593.

[49130] FLJ22679 (Accession NP_115603.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ22679 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ22679, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22679 BINDING SITE, designated SEQ ID:19747, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49131] Another function of GAM7052 is therefore inhibition of FLJ22679 (Accession NP_115603.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22679.

[49132] FLJ22679 (Accession NP_060168.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ22679 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by FLJ22679, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22679 BINDING SITE, designated SEQ ID:19747, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49133] Another function of GAM7052 is therefore inhibition of FLJ22679 (Accession NP_060168.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22679.

[49134] FLJ22794 (Accession NP_071357.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ22794

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22794, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22794 BINDING SITE, designated SEQ ID:9450, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49135] Another function of GAM7052 is therefore inhibition of FLJ22794 (Accession NP_071357.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22794.

[49136] FLJ22965 (Accession NP_071384.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ22965 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ22965, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ22965 BINDING SITE, designated SEQ ID:2108, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49137] Another function of GAM7052 is therefore inhibition of FLJ22965 (Accession NP_071384.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22965.

[49138] FLJ23024 (Accession NP_079212.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ23024 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23024, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23024 BINDING SITE, designated SEQ ID:14741, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49139] Another function of GAM7052 is therefore inhibition of FLJ23024 (Accession NP_079212.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23024.

[49140] FLJ23151 (Accession NP_079048.2) is another GAM7052 target gene, herein designated TARGET GENE. FLJ23151 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by FLJ23151, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23151 BINDING SITE, designated SEQ ID:6505, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49141] Another function of GAM7052 is therefore inhibition of FLJ23151 (Accession NP_079048.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23151.

[49142] FLJ23392 (Accession NP_079060.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ23392 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23392, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23392 BINDING SITE, designated SEQ ID:18508, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49143] Another function of GAM7052 is therefore inhibition of

FLJ23392 (Accession NP_079060.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23392.

[49144] FLJ23416 (Accession NP_115614.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ23416 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23416, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23416 BINDING SITE, designated SEQ ID:1770, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49145] Another function of GAM7052 is therefore inhibition of FLJ23416 (Accession NP_115614.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23416.

[49146] FLJ23556 (Accession NP_079156.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ23556 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23556, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23556 BINDING SITE, designated SEQ ID:19274, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49147] Another function of GAM7052 is therefore inhibition of FLJ23556 (Accession NP_079156.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23556.

[49148] FLJ23563 (Accession XP_041701.4) is another GAM7052 target gene, herein designated TARGET GENE. FLJ23563 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ23563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ23563 BINDING SITE, designated SEQ ID:3638, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49149] Another function of GAM7052 is therefore inhibition of FLJ23563 (Accession XP_041701.4) . Accordingly, utilities

of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23563.

[49150] FLJ25033 (Accession NP_689779.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ25033 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25033, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25033 BINDING SITE, designated SEQ ID:1524, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49151] Another function of GAM7052 is therefore inhibition of FLJ25033 (Accession NP_689779.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25033.

[49152] FLJ25067 (Accession NP_689717.2) is another GAM7052 target gene, herein designated TARGET GENE. FLJ25067 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25067, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25067 BINDING SITE, designated SEQ ID:16676, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49153] Another function of GAM7052 is therefore inhibition of FLJ25067 (Accession NP_689717.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25067.

[49154] FLJ25429 (Accession NP_689589.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ25429 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25429, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25429 BINDING SITE, designated SEQ ID:12652, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49155] Another function of GAM7052 is therefore inhibition of FLJ25429 (Accession NP_689589.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ25429.

[49156] FLJ25795 (Accession NP_689633.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ25795 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ25795, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ25795 BINDING SITE, designated SEQ ID:11825, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49157] Another function of GAM7052 is therefore inhibition of FLJ25795 (Accession NP_689633.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25795.

[49158] FLJ30507 (Accession NP_694555.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ30507 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ30507, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of FLJ30507 BINDING SITE, designated SEQ ID:6534, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49159] Another function of GAM7052 is therefore inhibition of FLJ30507 (Accession NP_694555.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30507.

[49160] FLJ30532 (Accession NP_653325.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ30532 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ30532, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ30532 BINDING SITE, designated SEQ ID:4754, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49161] Another function of GAM7052 is therefore inhibition of FLJ30532 (Accession NP_653325.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ30532.

[49162] FLJ31139 (Accession NP_775928.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ31139 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31139, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31139 BINDING SITE, designated SEQ ID:16723, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49163] Another function of GAM7052 is therefore inhibition of FLJ31139 (Accession NP_775928.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31139.

[49164] FLJ31338 (Accession NP_689682.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ31338 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31338, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ31338 BINDING SITE, designated SEQ ID:13983, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49165] Another function of GAM7052 is therefore inhibition of FLJ31338 (Accession NP_689682.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31338.

[49166] FLJ31393 (Accession NP_694569.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ31393 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ31393, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31393 BINDING SITE, designated SEQ ID:4686, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49167] Another function of GAM7052 is therefore inhibition of FLJ31393 (Accession NP_694569.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31393.

[49168] FLJ31958 (Accession NP_694575.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ31958 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ31958, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ31958 BINDING SITE, designated SEQ ID:18462, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49169] Another function of GAM7052 is therefore inhibition of FLJ31958 (Accession NP_694575.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31958.

[49170] FLJ32096 (Accession NP_776156.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ32096 BINDING SITE1 and FLJ32096 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ32096, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32096 BINDING SITE1 and

FLJ32096 BINDING SITE2, designated SEQ ID:12527 and SEQ ID:1832 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49171] Another function of GAM7052 is therefore inhibition of FLJ32096 (Accession NP_776156.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32096.

[49172] FLJ32130 (Accession NP_689671.2) is another GAM7052 target gene, herein designated TARGET GENE. FLJ32130 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32130, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32130 BINDING SITE, designated SEQ ID:14068, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49173] Another function of GAM7052 is therefore inhibition of FLJ32130 (Accession NP_689671.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ32130.

[49174] FLJ32803 (Accession NP_694584.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ32803 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32803, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ32803 BINDING SITE, designated SEQ ID:702, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49175] Another function of GAM7052 is therefore inhibition of FLJ32803 (Accession NP_694584.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32803.

[49176] FLJ32865 (Accession NP_653214.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ32865 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ32865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

FLJ32865 BINDING SITE, designated SEQ ID:16885, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49177] Another function of GAM7052 is therefore inhibition of FLJ32865 (Accession NP_653214.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865.

[49178] FLJ33655 (Accession NP_775912.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ33655 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33655, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33655 BINDING SITE, designated SEQ ID:19276, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49179] Another function of GAM7052 is therefore inhibition of FLJ33655 (Accession NP_775912.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33655.

[49180] FLJ33814 (Accession NP_775781.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ33814 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ33814, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ33814 BINDING SITE, designated SEQ ID:13609, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49181] Another function of GAM7052 is therefore inhibition of FLJ33814 (Accession NP_775781.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33814.

[49182] FLJ34817 (Accession NP_689516.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ34817 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ34817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34817 BINDING SITE, designated SEQ ID:5119, to the

nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49183] Another function of GAM7052 is therefore inhibition of FLJ34817 (Accession NP_689516.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34817.

[49184] FLJ34922 (Accession NP_689483.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ34922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ34922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34922 BINDING SITE, designated SEQ ID:11941, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49185] Another function of GAM7052 is therefore inhibition of FLJ34922 (Accession NP_689483.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34922.

[49186] FLJ34969 (Accession XP_114353.1) is another GAM7052

target gene, herein designated TARGET GENE. FLJ34969 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ34969, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ34969 BINDING SITE, designated SEQ ID:6275, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49187] Another function of GAM7052 is therefore inhibition of FLJ34969 (Accession XP_114353.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ34969.

[49188] FLJ35105 (Accession NP_689890.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ35105 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ35105, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ35105 BINDING SITE, designated SEQ ID:6938, to the nucleotide sequence of GAM7052 RNA, herein designated

GAM RNA, also designated SEQ ID:296.

[49189] Another function of GAM7052 is therefore inhibition of FLJ35105 (Accession NP_689890.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ35105.

[49190] FLJ36445 (Accession NP_694965.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ36445 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ36445, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ36445 BINDING SITE, designated SEQ ID:9024, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49191] Another function of GAM7052 is therefore inhibition of FLJ36445 (Accession NP_694965.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ36445.

[49192] FLJ37078 (Accession NP_694588.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ37078

BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by FLJ37078, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37078 BINDING SITE, designated SEQ ID:15855, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49193] Another function of GAM7052 is therefore inhibition of FLJ37078 (Accession NP_694588.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37078.

[49194] FLJ37433 (Accession NP_848612.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ37433 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37433, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37433 BINDING SITE, designated SEQ ID:4384, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49195] Another function of GAM7052 is therefore inhibition of FLJ37433 (Accession NP_848612.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37433.

[49196] FLJ37543 (Accession NP_775938.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ37543 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ37543, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ37543 BINDING SITE, designated SEQ ID:17646, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49197] Another function of GAM7052 is therefore inhibition of FLJ37543 (Accession NP_775938.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ37543.

[49198] FLJ38101 (Accession NP_694993.2) is another GAM7052 target gene, herein designated TARGET GENE. FLJ38101 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ38101, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38101 BINDING SITE, designated SEQ ID:1941, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49199] Another function of GAM7052 is therefore inhibition of FLJ38101 (Accession NP_694993.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38101.

[49200] FLJ38149 (Accession XP_091919.5) is another GAM7052 target gene, herein designated TARGET GENE. FLJ38149 BINDING SITE1 and FLJ38149 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ38149, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38149 BINDING SITE1 and FLJ38149 BINDING SITE2, designated SEQ ID:15374 and SEQ ID:14014 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:296.

[49201] Another function of GAM7052 is therefore inhibition of FLJ38149 (Accession XP_091919.5) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38149.

[49202] FLJ38281 (Accession NP_689814.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ38281 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38281, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38281 BINDING SITE, designated SEQ ID:7430, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49203] Another function of GAM7052 is therefore inhibition of FLJ38281 (Accession NP_689814.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38281.

[49204] FLJ38607 (Accession NP_689867.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ38607

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38607, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38607 BINDING SITE, designated SEQ ID:8761, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49205] Another function of GAM7052 is therefore inhibition of FLJ38607 (Accession NP_689867.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38607.

[49206] FLJ38716 (Accession NP_689580.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ38716 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38716, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38716 BINDING SITE, designated SEQ ID:10312, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49207] Another function of GAM7052 is therefore inhibition of FLJ38716 (Accession NP_689580.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38716.

[49208] FLJ38723 (Accession NP_776166.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ38723 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38723, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38723 BINDING SITE, designated SEQ ID:7203, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49209] Another function of GAM7052 is therefore inhibition of FLJ38723 (Accession NP_776166.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38723.

[49210] FLJ38819 (Accession NP_665872.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ38819 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by FLJ38819, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38819 BINDING SITE, designated SEQ ID:5470, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49211] Another function of GAM7052 is therefore inhibition of FLJ38819 (Accession NP_665872.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38819.

[49212] FLJ38991 (Accession NP_776188.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ38991 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ38991, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ38991 BINDING SITE, designated SEQ ID:16971, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49213] Another function of GAM7052 is therefore inhibition of

FLJ38991 (Accession NP_776188.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ38991.

[49214] FLJ39058 (Accession NP_775851.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ39058 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39058, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39058 BINDING SITE, designated SEQ ID:4759, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49215] Another function of GAM7052 is therefore inhibition of FLJ39058 (Accession NP_775851.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39058.

[49216] FLJ39075 (Accession NP_689553.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ39075 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39075, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39075 BINDING SITE, designated SEQ ID:6073, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49217] Another function of GAM7052 is therefore inhibition of FLJ39075 (Accession NP_689553.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39075.

[49218] FLJ39599 (Accession NP_776164.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ39599 BINDING SITE1 and FLJ39599 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ39599, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39599 BINDING SITE1 and FLJ39599 BINDING SITE2, designated SEQ ID:3756 and SEQ ID:2431 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49219] Another function of GAM7052 is therefore inhibition of FLJ39599 (Accession NP_776164.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39599.

[49220] FLJ39639 (Accession XP_290687.1) is another GAM7052 target gene, herein designated TARGET GENE. FLJ39639 BINDING SITE1 and FLJ39639 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FLJ39639, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39639 BINDING SITE1 and FLJ39639 BINDING SITE2, designated SEQ ID:14740 and SEQ ID:8837 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49221] Another function of GAM7052 is therefore inhibition of FLJ39639 (Accession XP_290687.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39639.

[49222] FLJ39821 (Accession NP_775971.1) is another GAM7052

target gene, herein designated TARGET GENE. FLJ39821 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by FLJ39821, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of FLJ39821 BINDING SITE, designated SEQ ID:648, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49223] Another function of GAM7052 is therefore inhibition of FLJ39821 (Accession NP_775971.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ39821.

[49224] Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) is another GAM7052 target gene, herein designated TARGET GENE. FUT1 BINDING SITE1 and FUT1 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by FUT1, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of FUT1 BINDING SITE1 and FUT1 BINDING SITE2, designated SEQ ID:9847 and SEQ ID:16237 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49225] Another function of GAM7052 is therefore inhibition of Fucosyltransferase 1 (galactoside 2-alpha-l-fucosyltransferase, bombay phenotype included) (FUT1, Accession NP_000139.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUT1.

[49226] G2A (Accession NP_037477.1) is another GAM7052 target gene, herein designated TARGET GENE. G2A BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by G2A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of G2A BINDING SITE, designated SEQ ID:4759, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49227] Another function of GAM7052 is therefore inhibition of

G2A (Accession NP_037477.1), a gene which may mediate some of the effects of extracellular atp on insulin secretion. and therefore may be associated with Autoimmune disease. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of Autoimmune disease., and of other diseases and clinical conditions associated with G2A.

[49228] The function of G2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Glial fibrillary acidic protein (GFAP, Accession NP_002046.1) is another GAM7052 target gene, herein designated TARGET GENE. GFAP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GFAP BINDING SITE, designated SEQ ID:18063, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49229] Another function of GAM7052 is therefore inhibition of Glial fibrillary acidic protein (GFAP, Accession

NP_002046.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFAP.

[49230] Growth factor, augmenter of liver regeneration (erv1 homolog, s. cerevisiae) (GFER, Accession NP_005253.2) is another GAM7052 target gene, herein designated TARGET GENE. GFER BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GFER, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GFER BINDING SITE, designated SEQ ID:1984, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49231] Another function of GAM7052 is therefore inhibition of Growth factor, augmenter of liver regeneration (erv1 homolog, s. cerevisiae) (GFER, Accession NP_005253.2), a gene which has a function in liver regeneration and spermatogenesis (by similarity). Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFER.

[49232] The function of GFER and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to GAM385.2.Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) is another GAM7052 target gene, herein designated TARGET GENE. GGA2 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE, designated SEQ ID:15132, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49233] Another function of GAM7052 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_619581.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[49234] Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) is another GAM7052 target gene, herein designated TARGET GENE. GGA2 BINDING SITE is a target binding site found in the

3` untranslated region of multiple transcripts of mRNA encoded by GGA2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE, designated SEQ ID:15132, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49235] Another function of GAM7052 is therefore inhibition of Golgi associated, gamma adaptin ear containing, arf binding protein 2 (GGA2, Accession NP_055859.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2.

[49236] Growth hormone receptor (GHR, Accession NP_000154.1) is another GAM7052 target gene, herein designated TARGET GENE. GHR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GHR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GHR BINDING SITE, designated SEQ ID:2927, to the nucleotide sequence of GAM7052 RNA, herein desig-

nated GAM RNA, also designated SEQ ID:296.

[49237] Another function of GAM7052 is therefore inhibition of Growth hormone receptor (GHR, Accession NP_000154.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GHR.

[49238] GNE (Accession NP_005467.1) is another GAM7052 target gene, herein designated TARGET GENE. GNE BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNE, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNE BINDING SITE, designated SEQ ID:10442, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49239] Another function of GAM7052 is therefore inhibition of GNE (Accession NP_005467.1), a gene which has roles in sialic acid biosynthesis and regulates cell surface sialylation. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNE.

[49240] The function of GNE and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Guanine nucleotide binding protein (g protein), gamma 4 (GNG4, Accession NP_004476.1) is another GAM7052 target gene, herein designated TARGET GENE. GNG4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNG4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNG4 BINDING SITE, designated SEQ ID:16886, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49241] Another function of GAM7052 is therefore inhibition of Guanine nucleotide binding protein (g protein), gamma 4 (GNG4, Accession NP_004476.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNG4.

[49242] GNPNAT1 (Accession XP_085119.1) is another GAM7052 target gene, herein designated TARGET GENE. GNPNAT1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GNPNAT1, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GNPNAT1 BINDING SITE, designated SEQ ID:3158, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49243] Another function of GAM7052 is therefore inhibition of GNPNAT1 (Accession XP_085119.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNPNAT1.

[49244] Golgi autoantigen, golgin subfamily a, 3 (GOLGA3, Accession NP_005886.2) is another GAM7052 target gene, herein designated TARGET GENE. GOLGA3 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by GOLGA3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GOLGA3 BINDING SITE, designated SEQ ID:11625, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49245] Another function of GAM7052 is therefore inhibition of Golgi autoantigen, golgin subfamily a, 3 (GOLGA3, Acces-

sion NP_005886.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLGA3.

[49246] Glycoprotein v (platelet) (GP5, Accession NP_004479.1) is another GAM7052 target gene, herein designated TARGET GENE. GP5 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GP5, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GP5 BINDING SITE, designated SEQ ID:3078, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49247] Another function of GAM7052 is therefore inhibition of Glycoprotein v (platelet) (GP5, Accession NP_004479.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GP5.

[49248] G protein-coupled receptor 56 (GPR56, Accession NP_005673.2) is another GAM7052 target gene, herein designated TARGET GENE. GPR56 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GPR56, corresponding to a target binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GPR56 BINDING SITE, designated SEQ ID:3347, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49249] Another function of GAM7052 is therefore inhibition of G protein-coupled receptor 56 (GPR56, Accession NP_005673.2), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR56.

[49250] The function of GPR56 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM63.1.GR6 (Accession NP_031380.1) is another GAM7052 target gene, herein designated TARGET GENE. GR6 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GR6, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

GR6 BINDING SITE, designated SEQ ID:14557, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49251] Another function of GAM7052 is therefore inhibition of GR6 (Accession NP_031380.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GR6.

[49252] General transcription factor iie, polypeptide 1, alpha 56kda (GTF2E1, Accession NP_005504.1) is another GAM7052 target gene, herein designated TARGET GENE. GTF2E1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by GTF2E1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTF2E1 BINDING SITE, designated SEQ ID:3032, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49253] Another function of GAM7052 is therefore inhibition of General transcription factor iie, polypeptide 1, alpha 56kda (GTF2E1, Accession NP_005504.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with GTF2E1.

[49254] GTPBG3 (Accession NP_116009.1) is another GAM7052 target gene, herein designated TARGET GENE. GTPBG3 BINDING SITE1 and GTPBG3 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by GTPBG3, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GTPBG3 BINDING SITE1 and GTPBG3 BINDING SITE2, designated SEQ ID:1434 and SEQ ID:16887 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49255] Another function of GAM7052 is therefore inhibition of GTPBG3 (Accession NP_116009.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTPBG3.

[49256] GYLTL1B (Accession NP_689525.1) is another GAM7052 target gene, herein designated TARGET GENE. GYLTL1B BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by GYLTL1B, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of GYLTL1B BINDING SITE, designated SEQ ID:14235, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49257] Another function of GAM7052 is therefore inhibition of GYLTL1B (Accession NP_689525.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GYLTL1B.

[49258] H-plk (Accession NP_056936.1) is another GAM7052 target gene, herein designated TARGET GENE. H-plk BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by H-plk, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H-plk BINDING SITE, designated SEQ ID:5790, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49259] Another function of GAM7052 is therefore inhibition of H-plk (Accession NP_056936.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of

diseases and clinical conditions associated with H-plk.

[49260] H2AV (Accession NP_619541.1) is another GAM7052 target gene, herein designated TARGET GENE. H2AV BINDING SITE1 and H2AV BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by H2AV, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H2AV BINDING SITE1 and H2AV BINDING SITE2, designated SEQ ID:9267 and SEQ ID:17174 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49261] Another function of GAM7052 is therefore inhibition of H2AV (Accession NP_619541.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H2AV.

[49262] H63 (Accession NP_816929.1) is another GAM7052 target gene, herein designated TARGET GENE. H63 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H63, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4

illustrates the complementarity of the nucleotide sequences of H63 BINDING SITE, designated SEQ ID:1187, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49263] Another function of GAM7052 is therefore inhibition of H63 (Accession NP_816929.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H63.

[49264] H63 (Accession NP_612432.2) is another GAM7052 target gene, herein designated TARGET GENE. H63 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by H63, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of H63 BINDING SITE, designated SEQ ID:1187, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49265] Another function of GAM7052 is therefore inhibition of H63 (Accession NP_612432.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H63.

[49266] Hepatitis a virus cellular receptor 2 (HAVCR2, Accession

NP_116171.2) is another GAM7052 target gene, herein designated TARGET GENE. HAVCR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HAVCR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HAVCR2 BINDING SITE, designated SEQ ID:5471, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49267] Another function of GAM7052 is therefore inhibition of Hepatitis a virus cellular receptor 2 (HAVCR2, Accession NP_116171.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAVCR2.

[49268] HBP17 (Accession NP_005121.1) is another GAM7052 target gene, herein designated TARGET GENE. HBP17 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HBP17, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HBP17 BINDING SITE, designated SEQ ID:8507, to the nucleotide

sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49269] Another function of GAM7052 is therefore inhibition of HBP17 (Accession NP_005121.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HBP17.

[49270] Hypoxia inducible factor 3, alpha subunit (HIF3A, Accession NP_690009.1) is another GAM7052 target gene, herein designated TARGET GENE. HIF3A BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by HIF3A, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HIF3A BINDING SITE, designated SEQ ID:4583, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49271] Another function of GAM7052 is therefore inhibition of Hypoxia inducible factor 3, alpha subunit (HIF3A, Accession NP_690009.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIF3A.

[49272] Histamine receptor h4 (HRH4, Accession NP_067637.2) is

another GAM7052 target gene, herein designated TARGET GENE. HRH4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HRH4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HRH4 BINDING SITE, designated SEQ ID:10866, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49273] Another function of GAM7052 is therefore inhibition of Histamine receptor h4 (HRH4, Accession NP_067637.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRH4.

[49274] Hydroxysteroid (17-beta) dehydrogenase 1 (HSD17B1, Accession NP_000404.1) is another GAM7052 target gene, herein designated TARGET GENE. HSD17B1 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HSD17B1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSD17B1 BINDING SITE, designated SEQ ID:13157, to the nucleotide

sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49275] Another function of GAM7052 is therefore inhibition of Hydroxysteroid (17-beta) dehydrogenase 1 (HSD17B1, Accession NP_000404.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSD17B1.

[49276] HSMPP8 (Accession XP_167894.1) is another GAM7052 target gene, herein designated TARGET GENE. HSMPP8 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSMPP8, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSMPP8 BINDING SITE, designated SEQ ID:5864, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49277] Another function of GAM7052 is therefore inhibition of HSMPP8 (Accession XP_167894.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSMPP8.

[49278] HSPC065 (Accession NP_054876.2) is another GAM7052

target gene, herein designated TARGET GENE. HSPC065 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HSPC065, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HSPC065 BINDING SITE, designated SEQ ID:686, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49279] Another function of GAM7052 is therefore inhibition of HSPC065 (Accession NP_054876.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC065.

[49280] 5-hydroxytryptamine (serotonin) receptor 1e (HTR1E, Accession NP_000856.1) is another GAM7052 target gene, herein designated TARGET GENE. HTR1E BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by HTR1E, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HTR1E BINDING SITE, designated SEQ ID:19389, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49281] Another function of GAM7052 is therefore inhibition of 5-hydroxytryptamine (serotonin) receptor 1e (HTR1E, Accession NP_000856.1), a gene which belongs to g- protein coupled receptors. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR1E.

[49282] The function of HTR1E and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM161.1.Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1) is another GAM7052 target gene, herein designated TARGET GENE. HUS1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by HUS1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of HUS1 BINDING SITE, designated SEQ ID:16890, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49283] Another function of GAM7052 is therefore inhibition of

Hus1 checkpoint homolog (s. pombe) (HUS1, Accession NP_004498.1), a gene which May form DNA damage- responsive protein complex . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUS1.

[49284] The function of HUS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.Interferon (alpha, beta and omega) receptor 2 (IFNAR2, Accession NP_000865.2) is another GAM7052 target gene, herein designated TARGET GENE. IFNAR2 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IFNAR2, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IFNAR2 BINDING SITE, designated SEQ ID:10469, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49285] Another function of GAM7052 is therefore inhibition of Interferon (alpha, beta and omega) receptor 2 (IFNAR2, Accession NP_000865.2), a gene which is a receptor for interferons alpha and beta. Accordingly, utilities of

GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IFNAR2.

[49286] The function of IFNAR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM30.1.Insulin-like growth factor 1 (somatomedin c) (IGF1, Accession NP_000609.1) is another GAM7052 target gene, herein designated TARGET GENE. IGF1 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IGF1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IGF1 BINDING SITE, designated SEQ ID:8011, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49287] Another function of GAM7052 is therefore inhibition of Insulin-like growth factor 1 (somatomedin c) (IGF1, Accession NP_000609.1), a gene which are structurally and functionally related to insulin but have a much higher growth- promoting activity and therefore may be associated with Growth retardation with sensorineural deafness and mental retardation. Accordingly, utilities of GAM7052

include diagnosis, prevention and treatment of Growth retardation with sensorineural deafness and mental retardation, and of other diseases and clinical conditions associated with IGF1.

[49288] The function of IGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM66.2.Interleukin 12 receptor, beta 1 (IL12RB1, Accession NP_714912.1) is another GAM7052 target gene, herein designated TARGET GENE. IL12RB1 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL12RB1, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL12RB1 BINDING SITE, designated SEQ ID:12219, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49289] Another function of GAM7052 is therefore inhibition of Interleukin 12 receptor, beta 1 (IL12RB1, Accession NP_714912.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL12RB1.

[49290] Interleukin 28 receptor, alpha (IL28RA, Accession NP_775088.1) is another GAM7052 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:1187, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49291] Another function of GAM7052 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_775088.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[49292] Interleukin 28 receptor, alpha (IL28RA, Accession NP_734464.1) is another GAM7052 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates

the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:1187, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49293] Another function of GAM7052 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_734464.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[49294] Interleukin 28 receptor, alpha (IL28RA, Accession NP_775087.1) is another GAM7052 target gene, herein designated TARGET GENE. IL28RA BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by IL28RA, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IL28RA BINDING SITE, designated SEQ ID:1187, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49295] Another function of GAM7052 is therefore inhibition of Interleukin 28 receptor, alpha (IL28RA, Accession NP_775087.1) . Accordingly, utilities of GAM7052 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with IL28RA.

[49296] IMPACT (Accession NP_060909.1) is another GAM7052 target gene, herein designated TARGET GENE. IMPACT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IMPACT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IMPACT BINDING SITE, designated SEQ ID:11567, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49297] Another function of GAM7052 is therefore inhibition of IMPACT (Accession NP_060909.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMPACT.

[49298] Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) is another GAM7052 target gene, herein designated TARGET GENE. INMT BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by INMT, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the

nucleotide sequences of INMT BINDING SITE, designated SEQ ID:16621, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49299] Another function of GAM7052 is therefore inhibition of Indolethylamine n-methyltransferase (INMT, Accession NP_006765.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INMT.

[49300] Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) is another GAM7052 target gene, herein designated TARGET GENE. IRF4 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by IRF4, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of IRF4 BINDING SITE, designated SEQ ID:3531, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49301] Another function of GAM7052 is therefore inhibition of Interferon regulatory factor 4 (IRF4, Accession NP_002451.1) . Accordingly, utilities of GAM7052 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with IRF4.

[49302] Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3, Accession NP_000206.1) is another GAM7052 target gene, herein designated TARGET GENE. JAK3 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JAK3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JAK3 BINDING SITE, designated SEQ ID:7364, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49303] Another function of GAM7052 is therefore inhibition of Janus kinase 3 (a protein tyrosine kinase, leukocyte) (JAK3, Accession NP_000206.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAK3.

[49304] JM11 (Accession NP_296375.1) is another GAM7052 target gene, herein designated TARGET GENE. JM11 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by JM11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of JM11 BINDING SITE, designated SEQ ID:19302, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49305] Another function of GAM7052 is therefore inhibition of JM11 (Accession NP_296375.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JM11.

[49306] Potassium inwardly-rectifying channel, subfamily j, member 11 (KCNJ11, Accession NP_000516.2) is another GAM7052 target gene, herein designated TARGET GENE. KCNJ11 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KCNJ11, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KCNJ11 BINDING SITE, designated SEQ ID:4460, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49307] Another function of GAM7052 is therefore inhibition of Potassium inwardly-rectifying channel, subfamily j, member 11 (KCNJ11, Accession NP_000516.2), a gene which is

controlled by g proteins. inward rectifier k+ channels are characterized by a greater tendancy to allow potassium to flow into the cell rather than out of it. and therefore is associated with Persistent hyperinsulinemic hypoglycemia of infancy. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of Persistent hyperinsulinemic hypoglycemia of infancy, and of other diseases and clinical conditions associated with KCNJ11.

[49308] The function of KCNJ11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM189.1.KIAA0087 (Accession NP_055584.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0087 BINDING SITE1 and KIAA0087 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0087, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0087 BINDING SITE1 and KIAA0087 BINDING SITE2, designated SEQ ID:16774 and SEQ ID:18062 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49309] Another function of GAM7052 is therefore inhibition of KIAA0087 (Accession NP_055584.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0087.

[49310] KIAA0117 (Accession XP_290939.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0117 BINDING SITE, designated SEQ ID:11163, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49311] Another function of GAM7052 is therefore inhibition of KIAA0117 (Accession XP_290939.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0117.

[49312] KIAA0186 (Accession NP_066545.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0186 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA0186, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0186 BINDING SITE, designated SEQ ID:4041, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49313] Another function of GAM7052 is therefore inhibition of KIAA0186 (Accession NP_066545.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0186.

[49314] KIAA0406 (Accession NP_055472.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0406 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0406, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0406 BINDING SITE, designated SEQ ID:17968, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49315] Another function of GAM7052 is therefore inhibition of

KIAA0406 (Accession NP_055472.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0406.

[49316] KIAA0459 (Accession XP_027862.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0459 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:7366, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49317] Another function of GAM7052 is therefore inhibition of KIAA0459 (Accession XP_027862.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459.

[49318] KIAA0472 (Accession XP_290898.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0472 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0472, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0472 BINDING SITE, designated SEQ ID:12393, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49319] Another function of GAM7052 is therefore inhibition of KIAA0472 (Accession XP_290898.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0472.

[49320] KIAA0475 (Accession NP_055679.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0475 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:7779, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49321] Another function of GAM7052 is therefore inhibition of KIAA0475 (Accession NP_055679.1) . Accordingly, utilities

of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475.

[49322] KIAA0495 (Accession XP_031397.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0495 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0495, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0495 BINDING SITE, designated SEQ ID:4636, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49323] Another function of GAM7052 is therefore inhibition of KIAA0495 (Accession XP_031397.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0495.

[49324] KIAA0513 (Accession NP_055547.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0513 BINDING SITE1 and KIAA0513 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0513, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE1 and KIAA0513 BINDING SITE2, designated SEQ ID:19867 and SEQ ID:5592 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49325] Another function of GAM7052 is therefore inhibition of KIAA0513 (Accession NP_055547.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513.

[49326] KIAA0555 (Accession NP_055605.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0555 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0555, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0555 BINDING SITE, designated SEQ ID:8953, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49327] Another function of GAM7052 is therefore inhibition of

KIAA0555 (Accession NP_055605.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0555.

[49328] KIAA0557 (Accession XP_085507.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0557 BINDING SITE1 and KIAA0557 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA0557, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0557 BINDING SITE1 and KIAA0557 BINDING SITE2, designated SEQ ID:14583 and SEQ ID:9434 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49329] Another function of GAM7052 is therefore inhibition of KIAA0557 (Accession XP_085507.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0557.

[49330] KIAA0562 (Accession NP_055519.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0562

BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0562 BINDING SITE, designated SEQ ID:5466, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49331] Another function of GAM7052 is therefore inhibition of KIAA0562 (Accession NP_055519.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0562.

[49332] KIAA0563 (Accession NP_055649.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0563 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0563, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0563 BINDING SITE, designated SEQ ID:697, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49333] Another function of GAM7052 is therefore inhibition of KIAA0563 (Accession NP_055649.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0563.

[49334] KIAA0605 (Accession NP_055509.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0605 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0605, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0605 BINDING SITE, designated SEQ ID:5865, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49335] Another function of GAM7052 is therefore inhibition of KIAA0605 (Accession NP_055509.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0605.

[49336] KIAA0643 (Accession NP_079069.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0643 BINDING SITE is a target binding site found in the 5` un-

translated region of mRNA encoded by KIAA0643, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0643 BINDING SITE, designated SEQ ID:6764, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49337] Another function of GAM7052 is therefore inhibition of KIAA0643 (Accession NP_079069.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0643.

[49338] KIAA0663 (Accession NP_055642.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0663 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA0663, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0663 BINDING SITE, designated SEQ ID:19611, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49339] Another function of GAM7052 is therefore inhibition of

KIAA0663 (Accession NP_055642.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0663.

[49340] KIAA0831 (Accession NP_055739.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0831 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0831, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0831 BINDING SITE, designated SEQ ID:10893, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49341] Another function of GAM7052 is therefore inhibition of KIAA0831 (Accession NP_055739.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0831.

[49342] KIAA0841 (Accession XP_049237.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0841 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0841, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0841 BINDING SITE, designated SEQ ID:5866, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49343] Another function of GAM7052 is therefore inhibition of KIAA0841 (Accession XP_049237.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0841.

[49344] KIAA0861 (Accession NP_055893.2) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0861 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0861, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0861 BINDING SITE, designated SEQ ID:9847, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49345] Another function of GAM7052 is therefore inhibition of KIAA0861 (Accession NP_055893.2) . Accordingly, utilities

of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0861.

[49346] KIAA0931 (Accession XP_041191.2) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0931 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0931, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0931 BINDING SITE, designated SEQ ID:8012, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49347] Another function of GAM7052 is therefore inhibition of KIAA0931 (Accession XP_041191.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0931.

[49348] KIAA0962 (Accession XP_290942.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0962 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0962, corresponding to a target binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0962 BINDING SITE, designated SEQ ID:2109, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49349] Another function of GAM7052 is therefore inhibition of KIAA0962 (Accession XP_290942.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0962.

[49350] KIAA0972 (Accession NP_055745.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0972 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0972, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0972 BINDING SITE, designated SEQ ID:16232, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49351] Another function of GAM7052 is therefore inhibition of KIAA0972 (Accession NP_055745.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA0972.

[49352] KIAA0981 (Accession XP_028867.2) is another GAM7052 target gene, herein designated TARGET GENE. KIAA0981 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA0981, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA0981 BINDING SITE, designated SEQ ID:7266, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49353] Another function of GAM7052 is therefore inhibition of KIAA0981 (Accession XP_028867.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0981.

[49354] KIAA1002 (Accession XP_290584.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1002 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1002, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA1002 BINDING SITE, designated SEQ ID:11806, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49355] Another function of GAM7052 is therefore inhibition of KIAA1002 (Accession XP_290584.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1002.

[49356] KIAA1041 (Accession NP_055762.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1041 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1041, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1041 BINDING SITE, designated SEQ ID:18227, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49357] Another function of GAM7052 is therefore inhibition of KIAA1041 (Accession NP_055762.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1041.

[49358] KIAA1054 (Accession XP_043493.5) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1054 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1054, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1054 BINDING SITE, designated SEQ ID:3041, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49359] Another function of GAM7052 is therefore inhibition of KIAA1054 (Accession XP_043493.5) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1054.

[49360] KIAA1061 (Accession XP_048786.4) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1061 BINDING SITE, designated SEQ ID:13719, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49361] Another function of GAM7052 is therefore inhibition of KIAA1061 (Accession XP_048786.4) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1061.

[49362] KIAA1128 (Accession NP_061872.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1128 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1128, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1128 BINDING SITE, designated SEQ ID:5120, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49363] Another function of GAM7052 is therefore inhibition of KIAA1128 (Accession NP_061872.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1128.

[49364] KIAA1185 (Accession NP_065761.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1185 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1185, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1185 BINDING SITE, designated SEQ ID:2092, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49365] Another function of GAM7052 is therefore inhibition of KIAA1185 (Accession NP_065761.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1185.

[49366] KIAA1193 (Accession XP_041843.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1193 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1193, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1193 BINDING SITE, designated SEQ ID:12481, to the

nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49367] Another function of GAM7052 is therefore inhibition of KIAA1193 (Accession XP_041843.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1193.

[49368] KIAA1198 (Accession NP_065765.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by KIAA1198, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE1 through KIAA1198 BINDING SITE3, designated SEQ ID:18274, SEQ ID:1359 and SEQ ID:12377 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49369] Another function of GAM7052 is therefore inhibition of KIAA1198 (Accession NP_065765.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1198.

[49370] KIAA1200 (Accession XP_031054.4) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1200 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1200, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1200 BINDING SITE, designated SEQ ID:10959, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49371] Another function of GAM7052 is therefore inhibition of KIAA1200 (Accession XP_031054.4) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1200.

[49372] KIAA1209 (Accession XP_027307.2) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1209 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1209, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1209 BINDING SITE, designated SEQ ID:15011, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49373] Another function of GAM7052 is therefore inhibition of KIAA1209 (Accession XP_027307.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1209.

[49374] KIAA1257 (Accession XP_031577.2) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1257 BINDING SITE1 and KIAA1257 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1257, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1257 BINDING SITE1 and KIAA1257 BINDING SITE2, designated SEQ ID:7935 and SEQ ID:12291 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49375] Another function of GAM7052 is therefore inhibition of KIAA1257 (Accession XP_031577.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KIAA1257.

[49376] KIAA1268 (Accession XP_291055.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1268 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1268 BINDING SITE, designated SEQ ID:16885, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49377] Another function of GAM7052 is therefore inhibition of KIAA1268 (Accession XP_291055.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1268.

[49378] KIAA1273 (Accession XP_300760.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1273 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1273, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA1273 BINDING SITE, designated SEQ ID:13714, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49379] Another function of GAM7052 is therefore inhibition of KIAA1273 (Accession XP_300760.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1273.

[49380] KIAA1287 (Accession NP_065799.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1287 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1287, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1287 BINDING SITE, designated SEQ ID:14633, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49381] Another function of GAM7052 is therefore inhibition of KIAA1287 (Accession NP_065799.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1287.

[49382] KIAA1443 (Accession NP_065885.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1443 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1443, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1443 BINDING SITE, designated SEQ ID:3913, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49383] Another function of GAM7052 is therefore inhibition of KIAA1443 (Accession NP_065885.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1443.

[49384] KIAA1456 (Accession XP_040100.3) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1456 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1456, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1456 BINDING SITE, designated SEQ ID:6661, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49385] Another function of GAM7052 is therefore inhibition of KIAA1456 (Accession XP_040100.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1456.

[49386] KIAA1493 (Accession XP_034415.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1493 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1493, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1493 BINDING SITE, designated SEQ ID:9995, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49387] Another function of GAM7052 is therefore inhibition of KIAA1493 (Accession XP_034415.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1493.

[49388] KIAA1518 (Accession XP_170889.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1518 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by KIAA1518, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1518 BINDING SITE, designated SEQ ID:14558, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49389] Another function of GAM7052 is therefore inhibition of KIAA1518 (Accession XP_170889.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1518.

[49390] KIAA1530 (Accession XP_042661.5) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1530 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1530, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of

KIAA1530 BINDING SITE, designated SEQ ID:12327, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49391] Another function of GAM7052 is therefore inhibition of KIAA1530 (Accession XP_042661.5) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1530.

[49392] KIAA1571 (Accession XP_027744.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1571 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1571, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1571 BINDING SITE, designated SEQ ID:9469, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49393] Another function of GAM7052 is therefore inhibition of KIAA1571 (Accession XP_027744.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1571.

[49394] KIAA1615 (Accession NP_066002.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1615, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2, designated SEQ ID:18920 and SEQ ID:15445 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49395] Another function of GAM7052 is therefore inhibition of KIAA1615 (Accession NP_066002.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1615.

[49396] KIAA1617 (Accession XP_166140.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1617 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1617, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illus-

trates the complementarity of the nucleotide sequences of KIAA1617 BINDING SITE, designated SEQ ID:1187, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49397] Another function of GAM7052 is therefore inhibition of KIAA1617 (Accession XP_166140.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1617.

[49398] KIAA1712 (Accession NP_085136.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by KIAA1712, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2, designated SEQ ID:15686 and SEQ ID:16883 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49399] Another function of GAM7052 is therefore inhibition of KIAA1712 (Accession NP_085136.1) . Accordingly, utilities

of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1712.

[49400] KIAA1712 (Accession XP_041497.2) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2 are target binding sites found in untranslated regions of multiple transcripts of mRNA encoded by KIAA1712, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1712 BINDING SITE1 and KIAA1712 BINDING SITE2, designated SEQ ID:16883 and SEQ ID:15686 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49401] Another function of GAM7052 is therefore inhibition of KIAA1712 (Accession XP_041497.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1712.

[49402] KIAA1737 (Accession NP_219494.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1737 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by KIAA1737, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1737 BINDING SITE, designated SEQ ID:3033, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49403] Another function of GAM7052 is therefore inhibition of KIAA1737 (Accession NP_219494.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1737.

[49404] KIAA1827 (Accession XP_290834.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1827 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1827, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1827 BINDING SITE, designated SEQ ID:1496, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49405] Another function of GAM7052 is therefore inhibition of

KIAA1827 (Accession XP_290834.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1827.

[49406] KIAA1829 (Accession XP_030378.2) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1829 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1829, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1829 BINDING SITE, designated SEQ ID:2825, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49407] Another function of GAM7052 is therefore inhibition of KIAA1829 (Accession XP_030378.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1829.

[49408] KIAA1836 (Accession XP_114087.2) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1836 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1836, corre-

sponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1836 BINDING SITE, designated SEQ ID:14962, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49409] Another function of GAM7052 is therefore inhibition of KIAA1836 (Accession XP_114087.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1836.

[49410] KIAA1922 (Accession XP_057040.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1922 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1922, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1922 BINDING SITE, designated SEQ ID:10834, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49411] Another function of GAM7052 is therefore inhibition of KIAA1922 (Accession XP_057040.1) . Accordingly, utilities

of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1922.

[49412] KIAA1940 (Accession XP_086981.2) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1940 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA1940, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1940 BINDING SITE, designated SEQ ID:17635, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49413] Another function of GAM7052 is therefore inhibition of KIAA1940 (Accession XP_086981.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1940.

[49414] KIAA1971 (Accession XP_058720.4) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1971 BINDING SITE1 and KIAA1971 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by KIAA1971, corresponding to target binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1971 BINDING SITE1 and KIAA1971 BINDING SITE2, designated SEQ ID:16885 and SEQ ID:12858 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49415] Another function of GAM7052 is therefore inhibition of KIAA1971 (Accession XP_058720.4) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1971.

[49416] KIAA1987 (Accession XP_113870.1) is another GAM7052 target gene, herein designated TARGET GENE. KIAA1987 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by KIAA1987, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA1987 BINDING SITE, designated SEQ ID:6990, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49417] Another function of GAM7052 is therefore inhibition of

KIAA1987 (Accession XP_113870.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1987.

[49418] KIAA2028 (Accession XP_059415.2) is another GAM7052 target gene, herein designated TARGET GENE. KIAA2028 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by KIAA2028, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KIAA2028 BINDING SITE, designated SEQ ID:17522, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49419] Another function of GAM7052 is therefore inhibition of KIAA2028 (Accession XP_059415.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA2028.

[49420] Killer cell lectin-like receptor subfamily c, member 3 (KLRC3, Accession NP_002252.1) is another GAM7052 target gene, herein designated TARGET GENE. KLRC3 BINDING SITE is a target binding site found in the 3` un-

translated region of multiple transcripts of mRNA encoded by KLRC3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of KLRC3 BINDING SITE, designated SEQ ID:12994, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49421] Another function of GAM7052 is therefore inhibition of Killer cell lectin-like receptor subfamily c, member 3 (KLRC3, Accession NP_002252.1), a gene which is a receptor for the recognition of mhc class i hla- e molecules by nk cells and some cytotoxic t- cells. Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLRC3.

[49422] The function of KLRC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM2624.1.Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) is another GAM7052 target gene, herein designated TARGET GENE. LAMP3 BINDING SITE is a target binding site found in the 3` un-

translated region of mRNA encoded by LAMP3, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LAMP3 BINDING SITE, designated SEQ ID:1656, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49423] Another function of GAM7052 is therefore inhibition of Lysosomal-associated membrane protein 3 (LAMP3, Accession NP_055213.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP3.

[49424] Lipoma hmgic fusion partner (LHFP, Accession NP_005771.1) is another GAM7052 target gene, herein designated TARGET GENE. LHFP BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LHFP, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LHFP BINDING SITE, designated SEQ ID:3333, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49425] Another function of GAM7052 is therefore inhibition of Lipoma hmgic fusion partner (LHFP, Accession NP_005771.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHFP.

[49426] LNIR (Accession NP_112178.1) is another GAM7052 target gene, herein designated TARGET GENE. LNIR BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LNIR, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LNIR BINDING SITE, designated SEQ ID:5115, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49427] Another function of GAM7052 is therefore inhibition of LNIR (Accession NP_112178.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNIR.

[49428] LNK (Accession NP_005466.1) is another GAM7052 target gene, herein designated TARGET GENE. LNK BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LNK, corresponding to a target

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LNK BINDING SITE, designated SEQ ID:8674, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49429] Another function of GAM7052 is therefore inhibition of LNK (Accession NP_005466.1), a gene which links T- cell receptor activation signal to phospholipase c- gamma- 1, grb- 2 and phosphatidylinositol 3- kinase (by similarity). Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNK.

[49430] The function of LNK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to GAM130.1.LOC112687 (Accession XP_053145.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC112687 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112687, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC112687 BINDING SITE, designated SEQ ID:11096, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49431] Another function of GAM7052 is therefore inhibition of LOC112687 (Accession XP_053145.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112687.

[49432] LOC112817 (Accession NP_612422.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC112817 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC112817, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC112817 BINDING SITE, designated SEQ ID:12527, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49433] Another function of GAM7052 is therefore inhibition of LOC112817 (Accession NP_612422.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC112817.

[49434] LOC113444 (Accession NP_612437.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC113444 BINDING SITE1 and LOC113444 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC113444, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC113444 BINDING SITE1 and LOC113444 BINDING SITE2, designated SEQ ID:13633 and SEQ ID:9691 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49435] Another function of GAM7052 is therefore inhibition of LOC113444 (Accession NP_612437.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113444.

[49436] LOC115648 (Accession NP_663299.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC115648 BINDING SITE1 and LOC115648 BINDING SITE2 are target binding sites found in untranslated re-

gions of mRNA encoded by LOC115648, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC115648 BINDING SITE1 and LOC115648 BINDING SITE2, designated SEQ ID:5621 and SEQ ID:3028 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49437] Another function of GAM7052 is therefore inhibition of LOC115648 (Accession NP_663299.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115648.

[49438] LOC118490 (Accession XP_060981.3) is another GAM7052 target gene, herein designated TARGET GENE. LOC118490 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC118490, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118490 BINDING SITE, designated SEQ ID:13356, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:296.

[49439] Another function of GAM7052 is therefore inhibition of LOC118490 (Accession XP_060981.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118490.

[49440] LOC118812 (Accession NP_849154.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:13816, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49441] Another function of GAM7052 is therefore inhibition of LOC118812 (Accession NP_849154.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118812.

[49442] LOC118812 (Accession XP_058346.2) is another

GAM7052 target gene, herein designated TARGET GENE. LOC118812 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC118812, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC118812 BINDING SITE, designated SEQ ID:13816, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49443] Another function of GAM7052 is therefore inhibition of LOC118812 (Accession XP_058346.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118812.

[49444] LOC121952 (Accession XP_062872.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC121952 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC121952, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC121952 BINDING SITE, desig-

nated SEQ ID:18973, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49445] Another function of GAM7052 is therefore inhibition of LOC121952 (Accession XP_062872.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121952.

[49446] LOC125061 (Accession XP_058889.3) is another GAM7052 target gene, herein designated TARGET GENE. LOC125061 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC125061, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC125061 BINDING SITE, designated SEQ ID:13952, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49447] Another function of GAM7052 is therefore inhibition of LOC125061 (Accession XP_058889.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC125061.

[49448] LOC126257 (Accession XP_059009.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC126257 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC126257, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC126257 BINDING SITE, designated SEQ ID:18559, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49449] Another function of GAM7052 is therefore inhibition of LOC126257 (Accession XP_059009.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126257.

[49450] LOC128387 (Accession XP_059243.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC128387 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC128387, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC128387 BINDING SITE, designated SEQ ID:10834, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49451] Another function of GAM7052 is therefore inhibition of LOC128387 (Accession XP_059243.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128387.

[49452] LOC129039 (Accession XP_059329.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC129039 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC129039, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC129039 BINDING SITE, designated SEQ ID:10993, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49453] Another function of GAM7052 is therefore inhibition of LOC129039 (Accession XP_059329.1) . Accordingly, utili-

ties of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129039.

[49454] LOC130639 (Accession XP_059464.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC130639 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC130639, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130639 BINDING SITE, designated SEQ ID:19669, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49455] Another function of GAM7052 is therefore inhibition of LOC130639 (Accession XP_059464.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130639.

[49456] LOC130813 (Accession XP_065904.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC130813 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by

LOC130813, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:2257, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49457] Another function of GAM7052 is therefore inhibition of LOC130813 (Accession XP_065904.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813.

[49458] LOC135293 (Accession XP_072402.4) is another GAM7052 target gene, herein designated TARGET GENE. LOC135293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135293 BINDING SITE, designated SEQ ID:18228, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49459] Another function of GAM7052 is therefore inhibition of LOC135293 (Accession XP_072402.4) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135293.

[49460] LOC135763 (Accession NP_612639.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC135763 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC135763, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC135763 BINDING SITE, designated SEQ ID:19515, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49461] Another function of GAM7052 is therefore inhibition of LOC135763 (Accession NP_612639.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135763.

[49462] LOC137886 (Accession XP_059929.3) is another GAM7052 target gene, herein designated TARGET GENE.

LOC137886 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC137886, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC137886 BINDING SITE, designated SEQ ID:2107, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49463] Another function of GAM7052 is therefore inhibition of LOC137886 (Accession XP_059929.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137886.

[49464] LOC142826 (Accession XP_084355.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC142826 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC142826, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC142826 BINDING SITE, designated SEQ ID:6899, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49465] Another function of GAM7052 is therefore inhibition of LOC142826 (Accession XP_084355.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142826.

[49466] LOC142948 (Accession XP_096364.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC142948 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC142948, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC142948 BINDING SITE, designated SEQ ID:4637, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49467] Another function of GAM7052 is therefore inhibition of LOC142948 (Accession XP_096364.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142948.

[49468] LOC143241 (Accession NP_620167.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC143241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC143241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC143241 BINDING SITE, designated SEQ ID:16432, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49469] Another function of GAM7052 is therefore inhibition of LOC143241 (Accession NP_620167.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143241.

[49470] LOC143916 (Accession XP_084664.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC143916 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC143916, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC143916 BINDING SITE, designated SEQ ID:19303, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49471] Another function of GAM7052 is therefore inhibition of LOC143916 (Accession XP_084664.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143916.

[49472] LOC144100 (Accession NP_778228.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC144100 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC144100, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144100 BINDING SITE, designated SEQ ID:18030, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49473] Another function of GAM7052 is therefore inhibition of LOC144100 (Accession NP_778228.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC144100.

[49474] LOC144248 (Accession XP_084786.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC144248 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144248, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144248 BINDING SITE, designated SEQ ID:12527, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49475] Another function of GAM7052 is therefore inhibition of LOC144248 (Accession XP_084786.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144248.

[49476] LOC144742 (Accession XP_084949.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC144742 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC144742, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC144742 BINDING SITE, designated SEQ ID:13167, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49477] Another function of GAM7052 is therefore inhibition of LOC144742 (Accession XP_084949.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144742.

[49478] LOC145268 (Accession XP_085072.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC145268 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145268, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145268 BINDING SITE, designated SEQ ID:10250, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49479] Another function of GAM7052 is therefore inhibition of

LOC145268 (Accession XP_085072.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145268.

[49480] LOC145453 (Accession XP_085120.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC145453 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145453, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145453 BINDING SITE, designated SEQ ID:6583, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49481] Another function of GAM7052 is therefore inhibition of LOC145453 (Accession XP_085120.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145453.

[49482] LOC145678 (Accession XP_096832.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC145678 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC145678, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145678 BINDING SITE, designated SEQ ID:20072, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49483] Another function of GAM7052 is therefore inhibition of LOC145678 (Accession XP_096832.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145678.

[49484] LOC145757 (Accession XP_085227.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC145757 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC145757, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC145757 BINDING SITE, designated SEQ ID:15280, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:296.

[49485] Another function of GAM7052 is therefore inhibition of LOC145757 (Accession XP_085227.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145757.

[49486] LOC146177 (Accession NP_778229.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC146177 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146177 BINDING SITE, designated SEQ ID:2107, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49487] Another function of GAM7052 is therefore inhibition of LOC146177 (Accession NP_778229.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146177.

[49488] LOC146346 (Accession XP_085430.1) is another

GAM7052 target gene, herein designated TARGET GENE. LOC146346 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146346, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146346 BINDING SITE, designated SEQ ID:10470, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49489] Another function of GAM7052 is therefore inhibition of LOC146346 (Accession XP_085430.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146346.

[49490] LOC146429 (Accession XP_096998.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC146429 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146429, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146429 BINDING SITE, desig-

nated SEQ ID:8011, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49491] Another function of GAM7052 is therefore inhibition of LOC146429 (Accession XP_096998.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146429.

[49492] LOC146443 (Accession XP_085461.6) is another GAM7052 target gene, herein designated TARGET GENE. LOC146443 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146443, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146443 BINDING SITE, designated SEQ ID:4286, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49493] Another function of GAM7052 is therefore inhibition of LOC146443 (Accession XP_085461.6) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC146443.

[49494] LOC146820 (Accession XP_085603.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC146820 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC146820, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146820 BINDING SITE, designated SEQ ID:10012, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49495] Another function of GAM7052 is therefore inhibition of LOC146820 (Accession XP_085603.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146820.

[49496] LOC146894 (Accession NP_660316.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC146894 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC146894, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC146894 BINDING SITE, designated SEQ ID:1234, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49497] Another function of GAM7052 is therefore inhibition of LOC146894 (Accession NP_660316.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146894.

[49498] LOC147071 (Accession XP_054031.5) is another GAM7052 target gene, herein designated TARGET GENE. LOC147071 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC147071, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147071 BINDING SITE, designated SEQ ID:1525, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49499] Another function of GAM7052 is therefore inhibition of LOC147071 (Accession XP_054031.5) . Accordingly, utili-

ties of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147071.

[49500] LOC147166 (Accession XP_085722.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC147166 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC147166, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147166 BINDING SITE, designated SEQ ID:3032, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49501] Another function of GAM7052 is therefore inhibition of LOC147166 (Accession XP_085722.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147166.

[49502] LOC147791 (Accession XP_097293.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC147791 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by

LOC147791, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147791 BINDING SITE, designated SEQ ID:8528, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49503] Another function of GAM7052 is therefore inhibition of LOC147791 (Accession XP_097293.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147791.

[49504] LOC147817 (Accession XP_085903.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC147817 BINDING SITE1 and LOC147817 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC147817, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147817 BINDING SITE1 and LOC147817 BINDING SITE2, designated SEQ ID:18468 and SEQ ID:16859 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated

GAM RNA, also designated SEQ ID:296.

[49505] Another function of GAM7052 is therefore inhibition of LOC147817 (Accession XP_085903.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147817.

[49506] LOC147841 (Accession XP_085924.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC147841 BINDING SITE1 and LOC147841 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC147841, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC147841 BINDING SITE1 and LOC147841 BINDING SITE2, designated SEQ ID:8527 and SEQ ID:2989 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49507] Another function of GAM7052 is therefore inhibition of LOC147841 (Accession XP_085924.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147841.

[49508] LOC148198 (Accession XP_047554.4) is another GAM7052 target gene, herein designated TARGET GENE. LOC148198 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148198, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC148198 BINDING SITE, designated SEQ ID:16957, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49509] Another function of GAM7052 is therefore inhibition of LOC148198 (Accession XP_047554.4) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148198.

[49510] LOC148203 (Accession XP_086095.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC148203 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC148203, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC148203 BINDING SITE, designated SEQ ID:2820, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49511] Another function of GAM7052 is therefore inhibition of LOC148203 (Accession XP_086095.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148203.

[49512] LOC149466 (Accession XP_086546.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC149466 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149466, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149466 BINDING SITE, designated SEQ ID:19862, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49513] Another function of GAM7052 is therefore inhibition of LOC149466 (Accession XP_086546.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC149466.

[49514] LOC149478 (Accession XP_086536.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC149478 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149478, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149478 BINDING SITE, designated SEQ ID:4344, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49515] Another function of GAM7052 is therefore inhibition of LOC149478 (Accession XP_086536.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149478.

[49516] LOC149506 (Accession XP_097661.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC149506 BINDING SITE1 and LOC149506 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC149506, corresponding to

target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE1 and LOC149506 BINDING SITE2, designated SEQ ID:15681 and SEQ ID:12482 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49517] Another function of GAM7052 is therefore inhibition of LOC149506 (Accession XP_097661.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149506.

[49518] LOC149692 (Accession XP_097706.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC149692 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC149692, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC149692 BINDING SITE, designated SEQ ID:12440, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49519] Another function of GAM7052 is therefore inhibition of LOC149692 (Accession XP_097706.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149692.

[49520] LOC150054 (Accession XP_097797.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC150054 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150054, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150054 BINDING SITE, designated SEQ ID:3913, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49521] Another function of GAM7052 is therefore inhibition of LOC150054 (Accession XP_097797.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150054.

[49522] LOC150225 (Accession XP_097870.1) is another GAM7052 target gene, herein designated TARGET GENE.

LOC150225 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150225, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150225 BINDING SITE, designated SEQ ID:5964, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49523] Another function of GAM7052 is therefore inhibition of LOC150225 (Accession XP_097870.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150225.

[49524] LOC150282 (Accession XP_086852.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC150282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150282 BINDING SITE, designated SEQ ID:9847, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49525] Another function of GAM7052 is therefore inhibition of LOC150282 (Accession XP_086852.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150282.

[49526] LOC150397 (Accession XP_086907.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC150397 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC150397, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150397 BINDING SITE, designated SEQ ID:11386, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49527] Another function of GAM7052 is therefore inhibition of LOC150397 (Accession XP_086907.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150397.

[49528] LOC150587 (Accession XP_097917.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC150587 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC150587, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC150587 BINDING SITE, designated SEQ ID:9025, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49529] Another function of GAM7052 is therefore inhibition of LOC150587 (Accession XP_097917.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150587.

[49530] LOC151057 (Accession XP_097998.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC151057 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151057, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC151057 BINDING SITE, designated SEQ ID:14936, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49531] Another function of GAM7052 is therefore inhibition of LOC151057 (Accession XP_097998.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151057.

[49532] LOC151475 (Accession XP_098063.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC151475 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC151475, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151475 BINDING SITE, designated SEQ ID:6688, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49533] Another function of GAM7052 is therefore inhibition of LOC151475 (Accession XP_098063.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC151475.

[49534] LOC151636 (Accession NP_612144.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC151636 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC151636, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC151636 BINDING SITE, designated SEQ ID:7366, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49535] Another function of GAM7052 is therefore inhibition of LOC151636 (Accession NP_612144.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151636.

[49536] LOC152620 (Accession XP_011108.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC152620 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152620, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152620 BINDING SITE, designated SEQ ID:11229, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49537] Another function of GAM7052 is therefore inhibition of LOC152620 (Accession XP_011108.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152620.

[49538] LOC152667 (Accession XP_087500.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC152667 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC152667, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152667 BINDING SITE, designated SEQ ID:5099, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49539] Another function of GAM7052 is therefore inhibition of

LOC152667 (Accession XP_087500.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152667.

[49540] LOC152719 (Accession XP_098257.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC152719 BINDING SITE1 and LOC152719 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC152719, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152719 BINDING SITE1 and LOC152719 BINDING SITE2, designated SEQ ID:726 and SEQ ID:14742 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49541] Another function of GAM7052 is therefore inhibition of LOC152719 (Accession XP_098257.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152719.

[49542] LOC152804 (Accession XP_098266.2) is another GAM7052 target gene, herein designated TARGET GENE.

LOC152804 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC152804, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC152804 BINDING SITE, designated SEQ ID:2898, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49543] Another function of GAM7052 is therefore inhibition of LOC152804 (Accession XP_098266.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152804.

[49544] LOC153077 (Accession XP_098307.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC153077 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC153077, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC153077 BINDING SITE, designated SEQ ID:4990, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49545] Another function of GAM7052 is therefore inhibition of LOC153077 (Accession XP_098307.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153077.

[49546] LOC154282 (Accession XP_098505.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC154282 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154282, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154282 BINDING SITE, designated SEQ ID:19732, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49547] Another function of GAM7052 is therefore inhibition of LOC154282 (Accession XP_098505.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154282.

[49548] LOC154739 (Accession XP_098602.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC154739 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC154739, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154739 BINDING SITE, designated SEQ ID:16887, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49549] Another function of GAM7052 is therefore inhibition of LOC154739 (Accession XP_098602.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154739.

[49550] LOC154822 (Accession XP_098618.3) is another GAM7052 target gene, herein designated TARGET GENE. LOC154822 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC154822, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC154822 BINDING SITE, designated SEQ ID:1649, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49551] Another function of GAM7052 is therefore inhibition of LOC154822 (Accession XP_098618.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154822.

[49552] LOC154866 (Accession XP_088059.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC154866 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC154866, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154866 BINDING SITE, designated SEQ ID:17476, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49553] Another function of GAM7052 is therefore inhibition of LOC154866 (Accession XP_088059.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC154866.

[49554] LOC154877 (Accession XP_098626.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC154877 BINDING SITE1 through LOC154877 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC154877, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE1 through LOC154877 BINDING SITE3, designated SEQ ID:14460, SEQ ID:19863 and SEQ ID:2182 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49555] Another function of GAM7052 is therefore inhibition of LOC154877 (Accession XP_098626.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877.

[49556] LOC157531 (Accession XP_212210.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC157531 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of

mRNA encoded by LOC157531, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157531 BINDING SITE, designated SEQ ID:1954, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49557] Another function of GAM7052 is therefore inhibition of LOC157531 (Accession XP_212210.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157531.

[49558] LOC157858 (Accession XP_098833.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC157858 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC157858, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC157858 BINDING SITE, designated SEQ ID:6270, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49559] Another function of GAM7052 is therefore inhibition of LOC157858 (Accession XP_098833.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157858.

[49560] LOC158436 (Accession XP_098942.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC158436 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158436 BINDING SITE, designated SEQ ID:14740, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49561] Another function of GAM7052 is therefore inhibition of LOC158436 (Accession XP_098942.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158436.

[49562] LOC158476 (Accession XP_098955.1) is another GAM7052 target gene, herein designated TARGET GENE.

LOC158476 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158476, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158476 BINDING SITE, designated SEQ ID:12099, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49563] Another function of GAM7052 is therefore inhibition of LOC158476 (Accession XP_098955.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158476.

[49564] LOC158527 (Accession XP_088594.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC158527 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158527, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158527 BINDING SITE, designated SEQ ID:17909, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49565] Another function of GAM7052 is therefore inhibition of LOC158527 (Accession XP_088594.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158527.

[49566] LOC158668 (Accession XP_045161.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC158668 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC158668, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158668 BINDING SITE, designated SEQ ID:14574, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49567] Another function of GAM7052 is therefore inhibition of LOC158668 (Accession XP_045161.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158668.

[49568] LOC158865 (Accession XP_099000.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC158865 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC158865, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC158865 BINDING SITE, designated SEQ ID:4005, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49569] Another function of GAM7052 is therefore inhibition of LOC158865 (Accession XP_099000.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158865.

[49570] LOC160897 (Accession XP_090573.3) is another GAM7052 target gene, herein designated TARGET GENE. LOC160897 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC160897, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC160897 BINDING SITE, designated SEQ ID:15778, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49571] Another function of GAM7052 is therefore inhibition of LOC160897 (Accession XP_090573.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160897.

[49572] LOC162967 (Accession XP_091890.6) is another GAM7052 target gene, herein designated TARGET GENE. LOC162967 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC162967, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162967 BINDING SITE, designated SEQ ID:15400, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49573] Another function of GAM7052 is therefore inhibition of LOC162967 (Accession XP_091890.6) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC162967.

[49574] LOC162993 (Accession XP_091914.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC162993 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC162993, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC162993 BINDING SITE, designated SEQ ID:16333, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49575] Another function of GAM7052 is therefore inhibition of LOC162993 (Accession XP_091914.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162993.

[49576] LOC163227 (Accession NP_775802.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC163227, corresponding to

target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC163227 BINDING SITE1 and LOC163227 BINDING SITE2, designated SEQ ID:12740 and SEQ ID:12735 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49577] Another function of GAM7052 is therefore inhibition of LOC163227 (Accession NP_775802.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163227.

[49578] LOC164091 (Accession XP_089356.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC164091 BINDING SITE1 and LOC164091 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC164091, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC164091 BINDING SITE1 and LOC164091 BINDING SITE2, designated SEQ ID:8838 and SEQ ID:7689 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated

GAM RNA, also designated SEQ ID:296.

[49579] Another function of GAM7052 is therefore inhibition of LOC164091 (Accession XP_089356.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164091.

[49580] LOC168451 (Accession XP_095114.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC168451 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC168451, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC168451 BINDING SITE, designated SEQ ID:17863, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49581] Another function of GAM7052 is therefore inhibition of LOC168451 (Accession XP_095114.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168451.

[49582] LOC169611 (Accession XP_095809.4) is another

GAM7052 target gene, herein designated TARGET GENE. LOC169611 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC169611, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC169611 BINDING SITE, designated SEQ ID:11251, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49583] Another function of GAM7052 is therefore inhibition of LOC169611 (Accession XP_095809.4) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169611.

[49584] LOC196264 (Accession XP_113683.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC196264 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC196264, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC196264 BINDING SITE, desig-

nated SEQ ID:2824, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49585] Another function of GAM7052 is therefore inhibition of LOC196264 (Accession XP_113683.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196264.

[49586] LOC199725 (Accession XP_117119.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC199725 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC199725, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199725 BINDING SITE, designated SEQ ID:9306, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49587] Another function of GAM7052 is therefore inhibition of LOC199725 (Accession XP_117119.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC199725.

[49588] LOC199858 (Accession XP_114040.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC199858 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC199858, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199858 BINDING SITE, designated SEQ ID:1343, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49589] Another function of GAM7052 is therefore inhibition of LOC199858 (Accession XP_114040.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199858.

[49590] LOC199899 (Accession XP_117153.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC199899 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC199899, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC199899 BINDING SITE, designated SEQ ID:9143, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49591] Another function of GAM7052 is therefore inhibition of LOC199899 (Accession XP_117153.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199899.

[49592] LOC200339 (Accession XP_117226.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC200339 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC200339, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200339 BINDING SITE, designated SEQ ID:12277, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49593] Another function of GAM7052 is therefore inhibition of LOC200339 (Accession XP_117226.1) . Accordingly, utili-

ties of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200339.

[49594] LOC200491 (Accession XP_117239.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC200491 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC200491, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC200491 BINDING SITE, designated SEQ ID:11368, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49595] Another function of GAM7052 is therefore inhibition of LOC200491 (Accession XP_117239.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200491.

[49596] LOC201164 (Accession XP_290750.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC201164 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of

mRNA encoded by LOC201164, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201164 BINDING SITE, designated SEQ ID:3032, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49597] Another function of GAM7052 is therefore inhibition of LOC201164 (Accession XP_290750.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201164.

[49598] LOC201164 (Accession NP_849158.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC201164 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC201164, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201164 BINDING SITE, designated SEQ ID:3032, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49599] Another function of GAM7052 is therefore inhibition of LOC201164 (Accession NP_849158.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201164.

[49600] LOC201292 (Accession NP_775818.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC201292 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201292, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201292 BINDING SITE, designated SEQ ID:9524, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49601] Another function of GAM7052 is therefore inhibition of LOC201292 (Accession NP_775818.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201292.

[49602] LOC201562 (Accession XP_114343.2) is another GAM7052 target gene, herein designated TARGET GENE.

LOC201562 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC201562, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC201562 BINDING SITE, designated SEQ ID:16775, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49603] Another function of GAM7052 is therefore inhibition of LOC201562 (Accession XP_114343.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201562.

[49604] LOC202400 (Accession XP_117397.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC202400 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC202400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202400 BINDING SITE, designated SEQ ID:9253, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49605] Another function of GAM7052 is therefore inhibition of LOC202400 (Accession XP_117397.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202400.

[49606] LOC202934 (Accession XP_117486.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC202934 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC202934, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE, designated SEQ ID:18974, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49607] Another function of GAM7052 is therefore inhibition of LOC202934 (Accession XP_117486.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934.

[49608] LOC219731 (Accession XP_167596.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC219731 BINDING SITE1 and LOC219731 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC219731, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219731 BINDING SITE1 and LOC219731 BINDING SITE2, designated SEQ ID:5076 and SEQ ID:3064 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49609] Another function of GAM7052 is therefore inhibition of LOC219731 (Accession XP_167596.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219731.

[49610] LOC219735 (Accession XP_167601.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC219735 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC219735, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC219735 BINDING SITE, designated SEQ ID:3029, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49611] Another function of GAM7052 is therefore inhibition of LOC219735 (Accession XP_167601.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219735.

[49612] LOC220074 (Accession NP_660352.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC220074 BINDING SITE1 and LOC220074 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC220074, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC220074 BINDING SITE1 and LOC220074 BINDING SITE2, designated SEQ ID:14319 and SEQ ID:12482 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49613] Another function of GAM7052 is therefore inhibition of

LOC220074 (Accession NP_660352.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220074.

[49614] LOC221540 (Accession XP_168133.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC221540 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC221540, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221540 BINDING SITE, designated SEQ ID:8853, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49615] Another function of GAM7052 is therefore inhibition of LOC221540 (Accession XP_168133.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221540.

[49616] LOC221814 (Accession XP_168226.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC221814 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC221814, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC221814 BINDING SITE, designated SEQ ID:16581, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49617] Another function of GAM7052 is therefore inhibition of LOC221814 (Accession XP_168226.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221814.

[49618] LOC222068 (Accession XP_166556.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC222068 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC222068, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222068 BINDING SITE, designated SEQ ID:1573, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:296.

[49619] Another function of GAM7052 is therefore inhibition of LOC222068 (Accession XP_166556.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222068.

[49620] LOC222159 (Accession XP_212100.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC222159 BINDING SITE is a target binding site found in the 5` untranslated region of multiple transcripts of mRNA encoded by LOC222159, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222159 BINDING SITE, designated SEQ ID:11226, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49621] Another function of GAM7052 is therefore inhibition of LOC222159 (Accession XP_212100.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222159.

[49622] LOC222224 (Accession XP_168473.1) is another

GAM7052 target gene, herein designated TARGET GENE. LOC222224 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC222224, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC222224 BINDING SITE, designated SEQ ID:9925, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49623] Another function of GAM7052 is therefore inhibition of LOC222224 (Accession XP_168473.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222224.

[49624] LOC253612 (Accession XP_172985.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC253612 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253612, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253612 BINDING SITE, desig-

nated SEQ ID:11867, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49625] Another function of GAM7052 is therefore inhibition of LOC253612 (Accession XP_172985.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253612.

[49626] LOC253842 (Accession XP_173230.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC253842 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC253842, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253842 BINDING SITE, designated SEQ ID:9847, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49627] Another function of GAM7052 is therefore inhibition of LOC253842 (Accession XP_173230.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC253842.

[49628] LOC253981 (Accession XP_171064.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC253981 BINDING SITE1 and LOC253981 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC253981, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC253981 BINDING SITE1 and LOC253981 BINDING SITE2, designated SEQ ID:3391 and SEQ ID:2107 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49629] Another function of GAM7052 is therefore inhibition of LOC253981 (Accession XP_171064.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253981.

[49630] LOC254532 (Accession XP_172961.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC254532 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC254532, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC254532 BINDING SITE, designated SEQ ID:4317, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49631] Another function of GAM7052 is therefore inhibition of LOC254532 (Accession XP_172961.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254532.

[49632] LOC282905 (Accession XP_212606.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC282905 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC282905, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282905 BINDING SITE, designated SEQ ID:14138, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49633] Another function of GAM7052 is therefore inhibition of

LOC282905 (Accession XP_212606.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282905.

[49634] LOC282916 (Accession XP_212603.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC282916 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282916, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282916 BINDING SITE, designated SEQ ID:8853, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49635] Another function of GAM7052 is therefore inhibition of LOC282916 (Accession XP_212603.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282916.

[49636] LOC282943 (Accession XP_212647.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC282943 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC282943, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282943 BINDING SITE, designated SEQ ID:14138, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49637] Another function of GAM7052 is therefore inhibition of LOC282943 (Accession XP_212647.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282943.

[49638] LOC282953 (Accession XP_212644.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC282953 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC282953, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC282953 BINDING SITE, designated SEQ ID:8853, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:296.

[49639] Another function of GAM7052 is therefore inhibition of LOC282953 (Accession XP_212644.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC282953.

[49640] LOC283012 (Accession XP_210847.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283012 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283012, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283012 BINDING SITE, designated SEQ ID:13809, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49641] Another function of GAM7052 is therefore inhibition of LOC283012 (Accession XP_210847.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283012.

[49642] LOC283089 (Accession XP_210885.1) is another

GAM7052 target gene, herein designated TARGET GENE. LOC283089 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283089, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283089 BINDING SITE, designated SEQ ID:16357, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49643] Another function of GAM7052 is therefore inhibition of LOC283089 (Accession XP_210885.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283089.

[49644] LOC283177 (Accession XP_210903.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283177 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283177, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283177 BINDING SITE, desig-

nated SEQ ID:3679, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49645] Another function of GAM7052 is therefore inhibition of LOC283177 (Accession XP_210903.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283177.

[49646] LOC283215 (Accession XP_208555.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC283215 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283215, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283215 BINDING SITE, designated SEQ ID:8183, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49647] Another function of GAM7052 is therefore inhibition of LOC283215 (Accession XP_208555.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC283215.

[49648] LOC283241 (Accession NP_787089.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283241 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283241, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283241 BINDING SITE, designated SEQ ID:1942, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49649] Another function of GAM7052 is therefore inhibition of LOC283241 (Accession NP_787089.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283241.

[49650] LOC283293 (Accession XP_210962.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283293 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283293, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283293 BINDING SITE, designated SEQ ID:10694, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49651] Another function of GAM7052 is therefore inhibition of LOC283293 (Accession XP_210962.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283293.

[49652] LOC283335 (Accession XP_210981.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283335 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283335, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283335 BINDING SITE, designated SEQ ID:14245, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49653] Another function of GAM7052 is therefore inhibition of LOC283335 (Accession XP_210981.1) . Accordingly, utili-

ties of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283335.

[49654] LOC283377 (Accession XP_208647.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283377 BINDING SITE1 and LOC283377 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283377, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283377 BINDING SITE1 and LOC283377 BINDING SITE2, designated SEQ ID:9023 and SEQ ID:18130 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49655] Another function of GAM7052 is therefore inhibition of LOC283377 (Accession XP_208647.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283377.

[49656] LOC283387 (Accession XP_211007.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283387 BINDING SITE is a target binding site found in

the 3` untranslated region of mRNA encoded by LOC283387, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283387 BINDING SITE, designated SEQ ID:1113, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49657] Another function of GAM7052 is therefore inhibition of LOC283387 (Accession XP_211007.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283387.

[49658] LOC283400 (Accession XP_211024.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283400 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283400, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283400 BINDING SITE, designated SEQ ID:16677, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:296.

[49659] Another function of GAM7052 is therefore inhibition of LOC283400 (Accession XP_211024.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283400.

[49660] LOC283432 (Accession XP_211032.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283432 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283432, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283432 BINDING SITE, designated SEQ ID:9847, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49661] Another function of GAM7052 is therefore inhibition of LOC283432 (Accession XP_211032.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283432.

[49662] LOC283454 (Accession XP_211049.1) is another

GAM7052 target gene, herein designated TARGET GENE. LOC283454 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283454, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283454 BINDING SITE, designated SEQ ID:8011, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49663] Another function of GAM7052 is therefore inhibition of LOC283454 (Accession XP_211049.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283454.

[49664] LOC283487 (Accession XP_211062.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283487 BINDING SITE is a target binding site found in the 3` untranslated region of multiple transcripts of mRNA encoded by LOC283487, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283487

BINDING SITE, designated SEQ ID:10199, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49665] Another function of GAM7052 is therefore inhibition of LOC283487 (Accession XP_211062.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283487.

[49666] LOC283507 (Accession XP_211075.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283507 BINDING SITE1 and LOC283507 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283507, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283507 BINDING SITE1 and LOC283507 BINDING SITE2, designated SEQ ID:1226 and SEQ ID:4986 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49667] Another function of GAM7052 is therefore inhibition of LOC283507 (Accession XP_211075.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC283507.

[49668] LOC283523 (Accession XP_208097.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283523 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283523, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283523 BINDING SITE, designated SEQ ID:5965, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49669] Another function of GAM7052 is therefore inhibition of LOC283523 (Accession XP_208097.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283523.

[49670] LOC283624 (Accession XP_211126.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283624 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283624, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283624 BINDING SITE, designated SEQ ID:12482, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49671] Another function of GAM7052 is therefore inhibition of LOC283624 (Accession XP_211126.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283624.

[49672] LOC283637 (Accession XP_211134.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283637 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283637, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283637 BINDING SITE, designated SEQ ID:19555, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49673] Another function of GAM7052 is therefore inhibition of

LOC283637 (Accession XP_211134.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283637.

[49674] LOC283641 (Accession XP_208764.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283641 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283641, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283641 BINDING SITE, designated SEQ ID:5466, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49675] Another function of GAM7052 is therefore inhibition of LOC283641 (Accession XP_208764.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283641.

[49676] LOC283655 (Accession XP_211144.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283655 BINDING SITE1 and LOC283655 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283655, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283655 BINDING SITE1 and LOC283655 BINDING SITE2, designated SEQ ID:16035 and SEQ ID:19485 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49677] Another function of GAM7052 is therefore inhibition of LOC283655 (Accession XP_211144.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283655.

[49678] LOC283690 (Accession XP_211167.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283690 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283690, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283690 BINDING SITE, designated SEQ ID:4911, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49679] Another function of GAM7052 is therefore inhibition of LOC283690 (Accession XP_211167.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283690.

[49680] LOC283701 (Accession XP_211170.3) is another GAM7052 target gene, herein designated TARGET GENE. LOC283701 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283701, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283701 BINDING SITE, designated SEQ ID:12676, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49681] Another function of GAM7052 is therefore inhibition of LOC283701 (Accession XP_211170.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283701.

[49682] LOC283857 (Accession XP_211236.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283857 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC283857, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283857 BINDING SITE, designated SEQ ID:13947, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49683] Another function of GAM7052 is therefore inhibition of LOC283857 (Accession XP_211236.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283857.

[49684] LOC283861 (Accession NP_787095.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283861 BINDING SITE1 and LOC283861 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283861, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the com-

plementarity of the nucleotide sequences of LOC283861 BINDING SITE1 and LOC283861 BINDING SITE2, designated SEQ ID:4775 and SEQ ID:3638 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49685] Another function of GAM7052 is therefore inhibition of LOC283861 (Accession NP_787095.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283861.

[49686] LOC283863 (Accession XP_208875.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283863 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC283863, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283863 BINDING SITE, designated SEQ ID:12833, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49687] Another function of GAM7052 is therefore inhibition of LOC283863 (Accession XP_208875.1) . Accordingly, utili-

ties of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283863.

[49688] LOC283889 (Accession XP_208899.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283889 BINDING SITE1 and LOC283889 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC283889, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283889 BINDING SITE1 and LOC283889 BINDING SITE2, designated SEQ ID:5077 and SEQ ID:765 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49689] Another function of GAM7052 is therefore inhibition of LOC283889 (Accession XP_208899.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283889.

[49690] LOC283928 (Accession XP_208909.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC283928 BINDING SITE1 through LOC283928 BINDING

SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC283928, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC283928 BINDING SITE1 through LOC283928 BINDING SITE3, designated SEQ ID:5120, SEQ ID:10915 and SEQ ID:10829 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49691] Another function of GAM7052 is therefore inhibition of LOC283928 (Accession XP_208909.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC283928.

[49692] LOC284001 (Accession XP_208958.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC284001 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284001, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284001 BINDING SITE, designated SEQ ID:15850, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49693] Another function of GAM7052 is therefore inhibition of LOC284001 (Accession XP_208958.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284001.

[49694] LOC284023 (Accession XP_208983.3) is another GAM7052 target gene, herein designated TARGET GENE. LOC284023 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284023, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284023 BINDING SITE, designated SEQ ID:15391, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49695] Another function of GAM7052 is therefore inhibition of LOC284023 (Accession XP_208983.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284023.

[49696] LOC284063 (Accession XP_208992.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284063 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284063, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284063 BINDING SITE, designated SEQ ID:6628, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49697] Another function of GAM7052 is therefore inhibition of LOC284063 (Accession XP_208992.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284063.

[49698] LOC284080 (Accession XP_211322.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284080 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284080, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284080 BINDING SITE, designated SEQ ID:7784, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49699] Another function of GAM7052 is therefore inhibition of LOC284080 (Accession XP_211322.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284080.

[49700] LOC284098 (Accession XP_209008.3) is another GAM7052 target gene, herein designated TARGET GENE. LOC284098 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284098, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284098 BINDING SITE, designated SEQ ID:4384, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49701] Another function of GAM7052 is therefore inhibition of LOC284098 (Accession XP_209008.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284098.

[49702] LOC284102 (Accession XP_211327.3) is another GAM7052 target gene, herein designated TARGET GENE. LOC284102 BINDING SITE1 through LOC284102 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284102, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284102 BINDING SITE1 through LOC284102 BINDING SITE3, designated SEQ ID:16386, SEQ ID:12703 and SEQ ID:10012 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49703] Another function of GAM7052 is therefore inhibition of LOC284102 (Accession XP_211327.3) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284102.

[49704] LOC284116 (Accession XP_211338.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC284116 BINDING SITE is a target binding site found in

the 5` untranslated region of mRNA encoded by LOC284116, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284116 BINDING SITE, designated SEQ ID:8308, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49705] Another function of GAM7052 is therefore inhibition of LOC284116 (Accession XP_211338.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284116.

[49706] LOC284117 (Accession XP_209024.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284117 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284117, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284117 BINDING SITE, designated SEQ ID:7907, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also desig-

nated SEQ ID:296.

[49707] Another function of GAM7052 is therefore inhibition of LOC284117 (Accession XP_209024.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284117.

[49708] LOC284135 (Accession XP_209032.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284135 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284135, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284135 BINDING SITE, designated SEQ ID:12522, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49709] Another function of GAM7052 is therefore inhibition of LOC284135 (Accession XP_209032.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284135.

[49710] LOC284155 (Accession XP_211354.1) is another

GAM7052 target gene, herein designated TARGET GENE. LOC284155 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284155, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284155 BINDING SITE, designated SEQ ID:15851, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49711] Another function of GAM7052 is therefore inhibition of LOC284155 (Accession XP_211354.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284155.

[49712] LOC284171 (Accession XP_209051.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284171 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284171, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284171 BINDING SITE, desig-

nated SEQ ID:6477, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49713] Another function of GAM7052 is therefore inhibition of LOC284171 (Accession XP_209051.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284171.

[49714] LOC284183 (Accession XP_209059.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284183 BINDING SITE1 and LOC284183 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284183, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284183 BINDING SITE1 and LOC284183 BINDING SITE2, designated SEQ ID:8749 and SEQ ID:10894 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49715] Another function of GAM7052 is therefore inhibition of LOC284183 (Accession XP_209059.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284183.

[49716] LOC284260 (Accession XP_211408.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284260 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284260, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284260 BINDING SITE, designated SEQ ID:17615, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49717] Another function of GAM7052 is therefore inhibition of LOC284260 (Accession XP_211408.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284260.

[49718] LOC284281 (Accession XP_211415.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284281 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284281, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284281 BINDING SITE, designated SEQ ID:7059, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49719] Another function of GAM7052 is therefore inhibition of LOC284281 (Accession XP_211415.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284281.

[49720] LOC284286 (Accession XP_211419.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284286 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284286, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284286 BINDING SITE, designated SEQ ID:19098, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49721] Another function of GAM7052 is therefore inhibition of

LOC284286 (Accession XP_211419.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284286.

[49722] LOC284289 (Accession XP_209105.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284289 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284289, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284289 BINDING SITE, designated SEQ ID:3340, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49723] Another function of GAM7052 is therefore inhibition of LOC284289 (Accession XP_209105.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284289.

[49724] LOC284305 (Accession XP_211425.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284305 BINDING SITE1 and LOC284305 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284305, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284305 BINDING SITE1 and LOC284305 BINDING SITE2, designated SEQ ID:16484 and SEQ ID:16775 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49725] Another function of GAM7052 is therefore inhibition of LOC284305 (Accession XP_211425.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284305.

[49726] LOC284311 (Accession XP_302720.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284311 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284311, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284311 BINDING SITE, designated SEQ ID:15828, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49727] Another function of GAM7052 is therefore inhibition of LOC284311 (Accession XP_302720.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284311.

[49728] LOC284356 (Accession XP_211437.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284356 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284356, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284356 BINDING SITE, designated SEQ ID:7004, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49729] Another function of GAM7052 is therefore inhibition of LOC284356 (Accession XP_211437.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284356.

[49730] LOC284362 (Accession XP_211435.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284362 BINDING SITE1 and LOC284362 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284362, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284362 BINDING SITE1 and LOC284362 BINDING SITE2, designated SEQ ID:1466 and SEQ ID:11728 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49731] Another function of GAM7052 is therefore inhibition of LOC284362 (Accession XP_211435.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284362.

[49732] LOC284396 (Accession XP_211452.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284396 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284396, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of

Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284396 BINDING SITE, designated SEQ ID:15146, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49733] Another function of GAM7052 is therefore inhibition of LOC284396 (Accession XP_211452.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284396.

[49734] LOC284426 (Accession XP_209198.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284426 BINDING SITE1 through LOC284426 BINDING SITE3 are target binding sites found in untranslated regions of mRNA encoded by LOC284426, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284426 BINDING SITE1 through LOC284426 BINDING SITE3, designated SEQ ID:5116, SEQ ID:5145 and SEQ ID:12481 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49735] Another function of GAM7052 is therefore inhibition of

LOC284426 (Accession XP_209198.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284426.

[49736] LOC284436 (Accession XP_290862.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284436 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284436, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284436 BINDING SITE, designated SEQ ID:8011, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49737] Another function of GAM7052 is therefore inhibition of LOC284436 (Accession XP_290862.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284436.

[49738] LOC284454 (Accession XP_209216.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284454 BINDING SITE1 and LOC284454 BINDING

SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284454, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284454 BINDING SITE1 and LOC284454 BINDING SITE2, designated SEQ ID:13118 and SEQ ID:15855 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49739] Another function of GAM7052 is therefore inhibition of LOC284454 (Accession XP_209216.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284454.

[49740] LOC284577 (Accession XP_211522.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284577 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284577, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284577 BINDING SITE, designated SEQ ID:5969, to the nucleotide sequence of

GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49741] Another function of GAM7052 is therefore inhibition of LOC284577 (Accession XP_211522.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284577.

[49742] LOC284585 (Accession XP_209277.2) is another GAM7052 target gene, herein designated TARGET GENE. LOC284585 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284585, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284585 BINDING SITE, designated SEQ ID:5500, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49743] Another function of GAM7052 is therefore inhibition of LOC284585 (Accession XP_209277.2) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284585.

[49744] LOC284591 (Accession XP_211529.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284591 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284591, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284591 BINDING SITE, designated SEQ ID:507, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49745] Another function of GAM7052 is therefore inhibition of LOC284591 (Accession XP_211529.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284591.

[49746] LOC284628 (Accession XP_211561.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284628 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284628, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nu-

cleotide sequences of LOC284628 BINDING SITE, designated SEQ ID:11163, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49747] Another function of GAM7052 is therefore inhibition of LOC284628 (Accession XP_211561.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284628.

[49748] LOC284708 (Accession XP_209332.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284708 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284708, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284708 BINDING SITE, designated SEQ ID:17993, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49749] Another function of GAM7052 is therefore inhibition of LOC284708 (Accession XP_209332.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC284708.

[49750] LOC284723 (Accession XP_211602.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284723 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284723, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284723 BINDING SITE, designated SEQ ID:7366, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49751] Another function of GAM7052 is therefore inhibition of LOC284723 (Accession XP_211602.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284723.

[49752] LOC284805 (Accession XP_209371.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284805 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284805, corresponding to a target binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284805 BINDING SITE, designated SEQ ID:2369, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49753] Another function of GAM7052 is therefore inhibition of LOC284805 (Accession XP_209371.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284805.

[49754] LOC284865 (Accession XP_211672.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284865 BINDING SITE1 and LOC284865 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284865, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284865 BINDING SITE1 and LOC284865 BINDING SITE2, designated SEQ ID:14664 and SEQ ID:15707 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49755] Another function of GAM7052 is therefore inhibition of LOC284865 (Accession XP_211672.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284865.

[49756] LOC284874 (Accession XP_209394.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284874 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284874, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284874 BINDING SITE, designated SEQ ID:18809, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49757] Another function of GAM7052 is therefore inhibition of LOC284874 (Accession XP_209394.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284874.

[49758] LOC284934 (Accession XP_211696.1) is another GAM7052 target gene, herein designated TARGET GENE.

LOC284934 BINDING SITE is a target binding site found in the 5` untranslated region of mRNA encoded by LOC284934, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284934 BINDING SITE, designated SEQ ID:16887, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49759] Another function of GAM7052 is therefore inhibition of LOC284934 (Accession XP_211696.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284934.

[49760] LOC284947 (Accession XP_211705.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284947 BINDING SITE1 and LOC284947 BINDING SITE2 are target binding sites found in untranslated regions of mRNA encoded by LOC284947, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284947 BINDING SITE1 and LOC284947 BINDING SITE2, desig-

nated SEQ ID:10834 and SEQ ID:7168 respectively, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49761] Another function of GAM7052 is therefore inhibition of LOC284947 (Accession XP_211705.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC284947.

[49762] LOC284950 (Accession XP_211703.1) is another GAM7052 target gene, herein designated TARGET GENE. LOC284950 BINDING SITE is a target binding site found in the 3` untranslated region of mRNA encoded by LOC284950, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.8. Table 4 illustrates the complementarity of the nucleotide sequences of LOC284950 BINDING SITE, designated SEQ ID:8376, to the nucleotide sequence of GAM7052 RNA, herein designated GAM RNA, also designated SEQ ID:296.

[49763] Another function of GAM7052 is therefore inhibition of LOC284950 (Accession XP_211703.1) . Accordingly, utilities of GAM7052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with